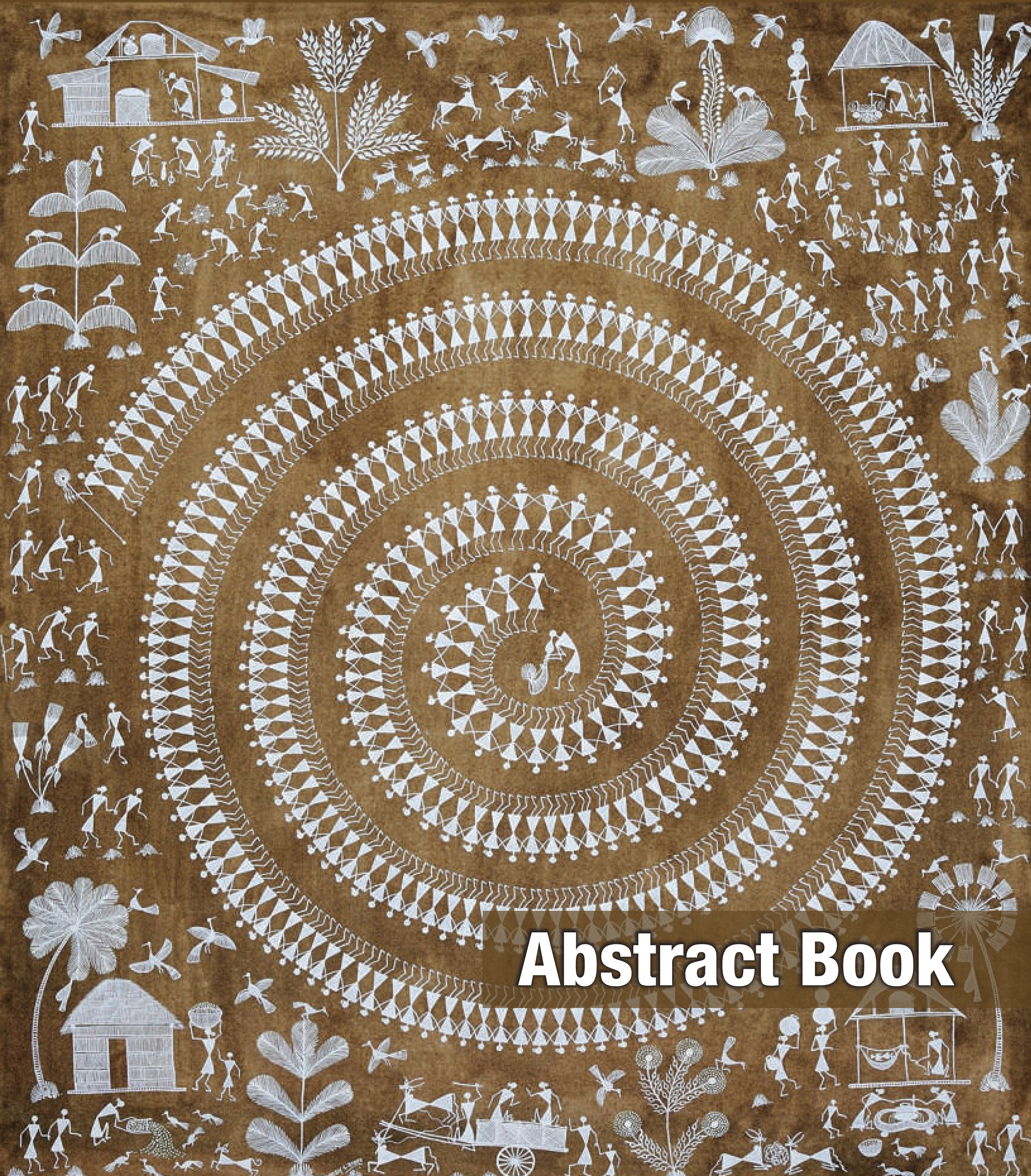
1st International Agrobiodiversity Congress

November 6-9, 2016 | New Delhi, India



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Preface

We are delighted to present the Abstract Book of the 1st International Agrobiodiversity Congress (IAC2016). This publication is unique as it carries abstracts based on the research and development in conservation and use of genetic resources of plants, animals, fishes, microbes and insects for food and agriculture. 545 abstracts included here offer a cross-sectional view of the ongoing work in the area of agrobiodiversity management.

The abstracts are presented in the order of Technical Program of the IAC2016. Spanning the four days of IAC2016, there will be eight plenary and two evening lectures, 72 invited lectures and 50 rapid oral presentations in the technical sessions and 30 presentations in the four satellite sessions. Extended summaries of invited talks are published as a special issue of the Indian Journal of Plant Genetic Resources. This book contains the abstracts of contributions presented as posters and rapid oral contributions.

Organizers acknowledge the contributors who submitted the abstracts in camera-ready form and editors for compiling in the publication by racing against the time.

Date: October 26, 2016 **Technical Program Committee**

Acknowledgements

IAC2016 is a great opportunity for us, as both organizers and participants, to share mutual experience in such an important field. IAC2016 will be attended by 800 delegates from 51 countries. Participants include 35 genebank representatives, 129 students and 55 farmers and community representatives. We acknowledge the enthusiasm and interest of the participants and look forward to the interactions.

We place on record the guidance received from the members of International Advisory Committee, National Steering Committee and Technical Program Committee, right from the conception of IAC2016. Success of the IAC2016 shall be attributed to the whole-hearted participation of each member of the Core Organizing Committee, Local Organizing Committee, Registration Committee, Publicity, Press and Media Committee, Invitation Committee, Accommodation Committee, Transport Committee, Publication Committee, Exhibition Committee, Cultural Programme Committee, Food and Hospitality Committee, Poster Session Committee and Stage and Hall Management Committee.

IAC2016 is projected to be a mega-event in recent times to deliberate on science, technology, policy and partnership driving the agrobiodiversity management. An event of this scale cannot be successful without financial support from our organizing partners, co-organizers and sponsors. We express our sincere appreciation to institutional and industry partners for joining hands with us in this endeavor.

We draw our strength from the support of colleagues from the five Bureaus on Genetic Resources, farmers and exhibitors. A confluence of global intellectuals would not have been possible without the cooperation of many government departments and scientific institutions. We thank each one of them for their role in organizational steps.

Date: October 26, 2016 **Editors**

Technical Session 1-A :

Food Nutrition and Environmental Security

Concurrent Session :

Plant Genetic Resources

54 (O-1)

Traditional Land and Food Systems: A Case of Uttarakhand State in North-western Indian Himalayas

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Like most of India, agriculture is one of the significant sectors of the economy of Uttarakhand state. About 86% of the state consists of hills, traditionally growing diverse crops as polycultures and sustaining about 50% of its population. As the contribution of agricultural biodiversity for local food and nutritional security of farming communities is often undervalued, the present communication succinctly documents the important features of traditional small-holder farming of Uttarakhand hills. About 70-80% of the native people living in rural areas depend on farming for their livelihoods, with the majority relying on small scale crop-livestock systems, including those that are integrated with long haul pastoral systems. The integration of crop and livestock production systems increases the diversity, along with environmental sustainability, of both sectors. At the same time it provides opportunities for increasing overall production and economics of farming. Being rich in agricultural biodiversity and food culture, use of locally available traditional food resources should be part of frontline strategies for nutrition interventions in Uttarakhand hills. The revitalization of local food systems is believed to be an imperative starting point in the local, regional and national framework of agrobiodiversity conservation, dietary diversification and food sovereignty in the Himalayan highlands. The communication also suggests the need of a proactive alliance between local communities and their key allies across agriculture, food, and public health sectors in collaboratively creating a research and advocacy agenda in support of agrobiodiversity and the revival of local food systems and landscapes within the broader framework of food sovereignty.

Keywords: Traditional hill farming, Food sovereignty, Community nutrition and Health

1391 (O-2)

Synecological Farming for Mainstreaming Biodiversity in Smallholding Farms and Foods: Experiments in Japan and Burkina Faso

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We experimented a novel system of small-scale truck farming, namely synecoculture, in temperate zone of Japan and semi-arid tropic in Burkina Faso. Synecoculture is based on highly biodiverse mixed polyculture of crops, including underutilized and neglected species, on the basis of no-till, no-fertilizer, and no-chemical practices. Spontaneous organization of ecosystem functions in response to the diversity of plant community is a major hypothesis that was expected to be compatible with productivity and various regulation services. We monitored between 2010-2016 on 3000 m^2 in Japan, and 2015-2016 on 500 m^2 in Burkina Faso, a mixture of 150-300 species in each plot. The productivity as measured by sold benefit after cost deduction rose to 5 fold in Japan with respect to conventional monoculture systems. Field ecosystems also augmented spontaneous biodiversity. The component analyses of products revealed increased expression of plant secondary metabolites and increased concentration of minerals, which contributed to enrich nutrition profile. The experiment in Burkina Faso recovered a sane functioning of ecosystem exposed to desertification, and marked more than 30% increase for major 10 crops compared to traditional farming methods. The total profit of products resulted in more than 100 fold income compared to average annual salary. These results are important in recovering biodiversity in both environment and food products lost by excessive exploitation of conventional agriculture. Wider introduction of synecoculture could be expected to support sustainable food production, especially in arid tropics where desertification of arable land, poverty and malnutrition of smallholders form a vicious cycle upon conventional methodology.

Keywords: Agrobiodiversity, Ecological Optimum, Neglected and Underutilized Species, Nutrition Diversity, Smallholder

1468 (O-3)

Strategies for Conservation and Sustainable Use of Biodiversity for Food and Nutrition in Sri Lanka

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The project funded by GEF, with the goal of mainstreaming biodiversity conservation and sustainable use for improved human nutrition and well-being (BFN), shows a great promise in Sri Lanka. Baseline surveys in 3 pilot sites revealed a rich level of utilization of the available agro-biodiversity by the households but poor consumption of a balanced diet. The study also revealed the prevalence of food secure, food insecure without hunger, food insecure with moderate hunger and food insecure with severe hunger as 40%, 57.4%, 7.1% and 1.4% respectively. As project interventions, BFN started collection of existing nutritional data and started composition analysis of 64 priority, local, agricultural biodiversity species/varieties in collaboration and development of information portal on BFN in comply with INFOODs data base. Several awareness programs on BFN have being planned and conducted at selected pilot sites including establishment of school home gardens, promotion of diversity and food fairs. At the national level several activities are underway; to establish marketing strategies for under-utilized, traditional crop varieties including local root & tuber crops; the development of demonstration plots; traditional knowledge documentation and dissemination; production and marketing of novel value added products; empowerment and self-employment programmes for women to popularize the use of nutritious herbal food and beverages; festivals of under-utilized fruits; increasing local fruit and vegetable consumption of Sri Lankans through '*helabojun*' sales centres; and development of a model urban home gardens. The policies encompassing biodiversity, food and health are being also currently reviewed in addition to integration of BFN concerns in to NBSAP document for 2016-2022.

Keywords: Agrobiodiversity, Dietary diversity, Local food, Nutrition

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1448 (O-4)

Little Millet, *Panicum sumatrense*, An Under-utilized Multipurpose Crop

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Little millet is a native crop of India, and well adapted to varied soil and environmental conditions, short duration with considerable within species diversity, and has huge potential to produce good grain yield and high biomass with limited water supply under marginal lands of Indian condition. To assess the grain and biomass yield potentials, 200 accessions, including core collection (56) were evaluated in an alpha-design using two replications. The residual maximum likelihood (REML) analysis indicated that variance due to genotypes was significant for important traits including grain and biomass yields. A large variability was observed for days to flowering (range 38 to 97 days), plant height (94 to 198 cm), basal tillers (7.8 to 13.32), grain yield (5 to 12 g plant^{-1}) and dry matter yield (23 to 159 g plant^{-1}). Accessions belonging to race *robusta* were late flowering (79 days after sowing), taller (167 cm) and having higher dry matter yield (88 g plant^{-1}) and slightly greater grain yield (7.8 g plant^{-1}) than that of race *nana*. Accessions producing higher grain yield (>10 g plant^{-1}; IPMr# 1021, 841, 1017, 1063, 983, 712, 1040) and for higher dry matter yield (>133 g plant^{-1}; IPMr# 858, 1043, 1070, 1063, 877) were identified. Due to its short duration and high biomass yield, little millet an under-utilized crop has potential as bioenergy crop besides providing food and fodder. Research is in progress to assess sequence variations linked with grain and biomass yields, and other important agronomic traits.

Keywords: Biomass, Dry matter yield, Grain yield, Little millet

1823 (P-1)

Assessing Diversity in Wild African Oil Palm Germplasm in India

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Wild oil palm (Elaeis guineensis, Jacq.) germplasm resources namely Guinea Bissau, Tanzania, Zambia and Camaroon were assessed for diversity based on principal Component analysis and cluster analysis for yield, vegetative and bunch quality characteristics. Tanzanian and Zambian accessions could outperform Guinea Bissau for most of the yield components. Except few Guinea Bissau palms, there were clear grouping observed among different sources. Overall genetic diversity was high in Guinea Bissau source followed by Camaroon, Zambia, Tanzania and indigenous hybrids. Oil palm is an important industrial and highest oil yielding forest crop Narrow genetic base is the main obstacle for crop improvement. In order to develop varieties for different agro-climatic conditions, genetic diversity of wild germplasm planted under rain fed condition was assessed. African germplasm recourses namely Guinea Bissau, Tanzania, Zambia and Camaroon were assessed for genetic diversity.The results revealed that Guinea Bissau recorded maximum bunch numbers. Maximum Fresh Fruit Bunch yield was recorded in TS 9 followed by ZS 7. GB 35/314 source had short rachis length (2.39 m). The sources namely, CA 15, GB 6/ 302, GB 51/320, TS 9, TS 2 showed vigorous vegetative growth. The lowest shell thickness (2.30 mm) was reported in Tanzania . The highest shell thickness was reported in ZS-7. The range of value of CV (%) recorded for important traits (rachis length, leaflet length and inter nodal length) are 18.26, 14.34 and 22.85, respectively. The variation reported for shell thickness and oil to bunch are 11.50 and 27.69. Overall genetic diversity was high in Guinea Bissau source followed by Camaroon, Zambia, Tanzania, D Ã— P Palode source. Tanzanian and Zambian accessions could outperform Guinea Bissau for most of the desirable characteristics. Except few Guinea Bissau palms, there were clear grouping observed among Guinea Bissau, Tanzania and Zambia accessions.

Keywords: Wild, African germplasm, Diversity, Desirable traits, India

911 (P-2)

Phytoremediation of Heavy Metals from Polluted Water Using *Bacopa Monnieri* L

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The scarcity coupled with increased contamination/pollution of water is a global concern warranting immediate attention. Out of 70% water of the planet, only 3% is freshwater, used for the consumption of humans being, farm animals and for agricultural use. *Bacopa monnieri* L. (Schrophulareaceae), a well-known traditional medicinal plant, besides the cognitive properties, has the ability to remediate few metal ions from water. Experiments were conducted to validate the feasibility of the herb to remediate metal ions like Chromium (Cr) and Cadmium (Cd). Activated carbon (AC), extracted from *in vitro* propagated as well as agro net grown plants of *B. monnieri* (IC-554588) was used to test its ability to remove heavy metals from synthetic wastewater and from water effluent obtained from industrial areas which release significant heavy metal into nearby water bodies. In the results obtained thus far, Cr and Cd were found to be successfully remediated with an increase in the concentration of AC with respect to time. Further AC from *in vitro* propagated shoots (MS + 0.2mg/l BA) was more efficacious with 50-70% of heavy metal removal. Germplasm collected from different eco-geographic regions need to be tested for their efficacy to remediate the industrial wastewater. Keeping in view easy availability of source material, eco-friendly and cost-effective experimental set-up coupled with easy handling of biomaterial, this may be a viable approach to address the problem of water pollution. However, results need to be validated and scale up steps optimized for its potential application.

Keywords: *Bacopa monnieri,* Heavy metals, Phytoremediation, Water pollution

614 (P-3)

Important Landraces and its Salient Traits in Major Vegetable Crops of Goa State

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Major vegetable crops of Goa are brinjal, okra, chilli, cucurbits, sweet potato, vegetable cowpea, amaranthus etc. Goa also harbours minor and under utilized vegetables like yams, aroids, chinese potato, edible ferns *etc.* In brinjal, two local land races *viz., Taleigao* and *Agassim*. The Taleigao type produces violet, round fruits, the average fruit weight being 350g and per plant yield about 2.5-3.5kg. The other type *Agassim* produces violet- purple, elongated fruit of 300g and gives about 2-2.5kg fruits/plant. The *Agassim* type has soft and puffy flesh where as it is hard in *Taleigao*, which accounts to longer shelf life, compared to the earlier one. In bhendi, majority of the local types are long fruited, tender and light green in colour, which retain their tenderness, even when they attain length of 20-22 cm. In amaranthus, thirty accessions were evaluated for yield and yield contributing characters during 2013-15 in Goa. The fresh weight of plant ranged from 4.89 g (AMAR-20) to 33.25 g (AMAR-4). The same accessions recorded the highest plant weight without root also. The highest plant height of 20.4cm was recorded in AMAR-9 followed by 14.45cm in AMAR-13. Chilli was first introduced by Portuguese to India more particularly to Goa. Presently, there are three basic types of chillies *viz., Tarvatti, Lovongi and Portugali* based on its place of cultivation, usage, pungency *etc.* Local type called “*Kholla* chilli” named after its place of cultivation in Goa, is a pungent chilli, exclusively used for *papad* making and fetches premium price in the market.

Keywords: Diversity, Goa, Quality, Vegetable crops

674 (P-4)

Winter Weeds: A Potential Source of Green Herbaceous Forage in Indian Central Himalaya

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The rain-dependent agriculture in mountainous part of Indian Central Himalaya poses challenges to farmers of availability of green forage during winters. The current study presents systematic practice of traditional usage of wild weed flora that occupy shaddy and moist niches in crop land and terrace walls. Botanical surveys conducted involving the local farmers, especially the women flok, of the mountainous part between 1000-1800 m asl recorded 52 herbaceous weed species as the only green winter forage source. The study investigates relative contribution of commonly used species to green forage biomass, collection period, animal preference and mode of utilization. The most preferred species are: *Cardamine impatiens*, *Chenopodium album*, *Cynodon dactylon*, *Dicliptera bupleuroides*, *Justicea simplex, Lathyrus aphaca, Lepidium virginicum, Melilotus alba, Medicago denticulate, Silene conoidea, Solanum nigrum, Sonchus spp.,Stellaria media, Trigonella emodi, Vicia* spp. and *Vigna* spp. Analysis of data on proximate composition, mineral profile and vitamins utilizing the published studies on some of the recorded weed forages revealed superiority for Melilotus alba, Silene spp., Sonchus spp., Stellaria media and Vicia spp. similar to or more than the superior cultivated forages- Medicago sativa and Avena sativa. It is concluded that the present scientific development on forage resources should value such weed flora as potential green winter forages for rainfed agriculture. Collection and improvement of their germplasm and / or introduction of elite materials of these species can boost green herbage availability in Himalayan mountains for improving livestock husbandry and rainfed- agriculture.

Keywords: Wild weed, Winter green herbaceous forages, Biomass and Nutrient potential, Indian Central Himalaya

746 (P-5)

Making Millets Matter in Madhya Pradesh

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Minor millets are central to traditional rainfed farming systems of Gond and Baiga peoples in Madhya Pradesh but their use is declining as livelihoods have shifted toward wage labor and purchase of subsidized grains (rice/ wheat). Farmers limited time and land is focused on paddy and maize. Under increasingly drought-prone conditions, farmers are recognizing that hardy millets are more reliable but weak market channels, low productivity, and difficult processing are constraints to upscale their use. Action for Social Advancement is working to enhance cultivation and use of minor millets in Madhya Pradesh to support climate change adaptation as part of a global initiative coordinated by Bioversity International. A holistic approach is being applied involving inter-disciplinary and inter-sectoral initiatives along each segment of the value chain. The initiative is targeted at improving availability of quality seed to enhance yields, raising the price farmers receive for millet grain, and increasing consumer demand. Farmer producer companies (FPC) have been key in these efforts. Participatory selection and production of high quality millet seed have been organized, which the FPCs make available through their storefronts. To achieve a better price, aggregation and basic processing of millet has been organized by the FPCs to reduce the number of transactions between the farmers and consumers. Millet festivals have been organized in local villages and Bhopal to promote consumer interest in millets. Millet promotion in Madhya Pradesh is in the early stages but there are many emerging opportunities and growing interest for these climate hardy and nutritious grains.

Keywords: minor millets, value chains, seed, collective action

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1910 (P-6)

Crop Wild Relatives in a Changing Climates

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Crop wild relatives, non-domesticated crop genetic resources, are sources of traits and genetic diversity for agriculture. Plant breeding has benefited from crop wild relatives to develop more nutritious plant varieties, as well as varieties tolerant to biotic and abiotic stresses. Their use in plant breeding is expected to continue growing thanks to the steady advances of plant hybridization and biotechnology. For being effectively used, crop wild relatives need to be available through genebanks to plant breeders and researchers. However, large gaps in *ex situ* collections have been recently identified, highlighting the need for enhancing conservation efforts to secure the future availability of these genetic resources. Little time remains for taking action, as existing threats, such as rapid-land use change, deforestation, and climate change are likely to continue affecting the natural habitats where these plants are found. Here we assess the potential effects of climate change on the distributions of the wild relatives of twenty-nine crops and identify areas where collections for *ex situ* conservation should be prioritized, as well as climate-stable areas of potential *in situ* conservation. Our results suggest that crop wild relative taxa may lose an average of 20.8% of their current distributions, with the wild relatives of potato, finger millet and cowpea the worst affected. Highest value *in situ* conservation target regions include parts of the Andes, Central America, the Near East and Northern Australia.

Keywords: Agrobiodiversity, Crop genetic resources, Conservation, Food security

20 (P-7)

Towards Genetic Identification of the Zambian Common Bean (*Phaseolus vulgaris*) Landraces

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The common bean (*Phaseolus vulgaris* L.) landraces continue to be grown in Zambia by small scale farmers, allowing for both local and regional consumption needs, as well as the conservation of genetic diversity, besides being a major source of dietary protein, and a key component for soil fertility improvement. Farmers, plant breeders, conservation biologists, and molecular biologists rely on the use of landraces to enhance and promote genetic diversity. Therefore, this study was conducted to assess the identity, genetic diversity and the structure of the four predominant Zambian common bean landraces of Lusaka Yellow, Lundazi, Mbala Mixture and Solwezi, alongside six CIAT reference lines, using 28 molecular markers. Allele frequencies were estimated by number of alleles per locus, expected heterozygosity (H_e), observed heterozygosity (H_o), Nei's diversity index, and polymorphic information content (PIC) using GenAlEx, R package, and PopGene. Results showed that the four Zambian common bean landraces were clearly distinguished into Andean genepool (Lusaka Yellow and Lundazi), and Mesoamerican genepool (Mbala Mixture and Solwezi), although Andean genepool predominates. Principal component analysis (PCoA) and population structure showed a similar results too. Nei's genetic diversity indices was highest in the order of Mbala mixture (0.502), Solwezi (0.440), Lundazi (0.433) and Lusaka yellow (0.196) for the landraces. A high levels of heterozygosity was observed for the landraces compared to the CIAT reference lines. Individual admixture were observed among these four populations of landraces and was highest for Mbala Mixture. Hence, incorporating these landraces into the National Bean Breeding Program of Zambia will promote high level of genetic diversity, their conservation, and Biodiversity.

Keywords: Genetic Diversity, Landrace, Microsatellite Markers, *Phaseolus vulgaris*, Population Structure

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30 (P-8)

New Crop Species for Agricultural Diversification

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Food for human beings is dependent on an average of 103 species and the exploitation of plant diversity remains far lower than what is existing. About 30 plant species are cultivating to meet 95%of the world's energy requirements. The diversification of agriculture with new species of major crops may enhance plant productivity, quality, nutritional value and reduce environmental stresses caused due to monoculture. Some species of potential importance are not yet fully utilized because of their limited competitiveness with major crops in mainstream agriculture. New health foods like oats, quino, chia, flax and sunflower seeds are getting popular in urban masses due to emphasis on healthy life style. These crops also fetch premium price in market since these are being imported in bulk for consumption directly. Identification of those species and their use for agricultural diversification, food security and balanced diet is yet to be explored. Some potential species other than cultivated already species like in Cereals (*Secale cereale*, hulled wheat); Pulses (*Lupinus* spp.); Vegetables (*Capparis* spp., *Malva* spp., *Scolymus* spp.); Fruits (*Pistacia vera, Ceratonia siliqua*); Forages (*Atriplex halymus*; *Salsola* spp., *Hedisarum* spp.); Medicinal and aromatic (*Thymus* spp., *Rosmarinus* spp.); Ornamentals (*Iris* spp.; *Limonium* spp., *Cercis siliquastrum*) need to be given priority. Increased diversification of crops species will not only enhance nutritional security but would allow farmers to have number of options to face the uncertain weather conditions associated with the increased climate variability. Efforts to introduce new species at ICAR-NBPGR for diversification are highlighted in the paper

Keywords: Climate, Diversity, Diversification, Wild species

36 (P-9)

Chia (*Salvia hispanica*) – A New Potential Nutritional Crop

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Functional foods have gained tremendous attention these days. Now a days due to stress and disease, healthier life styles are being adopted. NBPGR is making constant efforts for introduction of new crops which have not been commercially utilized. Recently ‘chia’ has gained popularity and used as a major food crop. It is grown commercially in Mexico, Bolivia, Argentina, Ecuador, Nicaragua, Guatemala, and Australia. Seed is used as healthy oil supplement for humans and animals. It is cultivated and commercialized for its seed, a food that is rich in omega-3 fatty acids, since the seeds yield 25–30% extractable oil, including α-linolenic acid. Seeds are rich source of the vitamins, thiamine and foliate. It is also a rich source of the dietary minerals and has antioxidant properties. The cultivation of *S. hispanica* requires light to medium clay or sandy soils. The plant prefers well-drained, moderately fertile soils, but can cope with acid soils and moderate drought. Presently, no major pests or diseases affect chia production. Essential oils in chia leaves have repellant properties against insects, making it suitable for organic cultivation. In India the *Salvia* species were introduced from Slovakia, Denmark, Hungary, Russia, Germany, Japan, USA, France, Austria, UK, Holland, England, Bulgaria, Poland, Netherlands, Italy. Being a new potential crop, this can be commercialized in India for diversity in agriculture and food security.

Keywords: Chia, New Crop, Nutrition, PGR

47 (P-10)

Collection, Characterization, Conservation and Utilization of *Perilla frutescens* (Linn.) Britt. Landraces in Northeastern Hill (NEH) Region of India

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Perilla is one of the important potential oilseed crops of Northeastern hill (NEH) region of India. Being a rich source of oil and protein the tribal communities use the seeds and leaves of *Perilla* for preparing various traditional dishes. The agro-climatic heterogeneity of NEH region offers a great deal of diversity in agro-morphology of *Perilla* germplasm. A total of 62 landraces, collected in different exploration trips from Meghalaya, Nagaland, Arunachal Pradesh, Manipur, Mizoram, Sikkim states of NEH region. The collected landraces were grown in experimental field of the ICAR-NBPGR Regional Station, Umiam, Meghalaya in a Randomized Complete Block Design (RCBD) in three replications with four checks (Jaintia, Shillong, Check III and Check IV) and observation on 22 agro-morphological traits were recorded. Considerable variation was recorded for early plant vigour, plant shape, leaf colour, seed colour and seed size, whereas variation was less for inflorescence structure and secondary branches. Among the quantitative traits, number of inflorescence/plant, yield/plant, 1000-seed weight, main inflorescence length and plant height had recorded high coefficients of variation.

Keywords: Collection and Characterization, North eastern India, *Perilla*, Traditional Uses

134 (P-11)

Characterization and Evaluation of Jack bean [*Canavalia ensiformis* L. (DC)], an Underutilized Wild Legume collections from Peninsular India

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Conservation and utilization of less known edible legume genetic resources is an essential element for increasing food and nutritional security and maintaining the environment. In view of the accelerated depletion/ genetic erosion of natural diversity due to increasing biotic pressure, systematic collection, characterization, evaluation, conservation and documentation of underutilized edible legume species like Jack bean (*Canavalia ensiformis*) is of immense practical utility. This will enable identification of genotypes with superior traits as high protein content/ nutritive value and resistance/ tolerance to different biotic/abiotic stresses. Thirty eight accessions of Jack bean augmented from Peninsular India were characterized during 2010-14 and considerable variation was found among the genotypes for morphological characters *viz.,* growth habit (pole and bush), leaf density (sparse, intermediate and dense), stem colour (light green, purple and dark purple), flower colour (purple and white), pod shape (straight, intermediate and curved), pod colour (light green and green), pod beak length (short, medium and long), pod curvature (straight, curved and highly curved), pod surface (smooth and wrinkled) and seed colour (brown, reddish - purple, white, grayish-yellow and grayish-orange). While the protein content ranged between 16 - 21%, the oil content ranged between 0.4 - 2.3% with fatty acids oleic, linoleic and palmitic being predominant. The plant height, pod weight, number of pods per plant, and test weight were observed with high genetic variability and direct selection would be rewarding for Jack bean improvement in India.

Keywords: *Canavalia ensiformis*, Germplasm, Jack bean

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137 (P-12)

Genetic Divergence Among Sunflower Inbred Lines and Their Convergent Improvement for Yield, Quality and Disease Resistance

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Ninety sunflower inbred lines from different agro-ecological origins were evaluated to study the genetic divergence for seed yield and its components and quality attributes *viz*., days to 50% flowering, days to maturity, duration of reproductive phase, plant height, stem girth, head diameter, 100-seed weight, seed filling percentage, hull content (%), protein content (%), oil content (%) and seed yield per plant (g). Genetic diversity in parental lines is a pre-requisite for exploiting high heterosis. Based on D^2 values, the 90 inbred lines were grouped into 8 clusters indicating considerable amount of genetic diversity. The character, seed filling percentage contributed maximum towards genetic divergence, followed by hull content and seed yield per plant. The genotypes were also screened against Alternaria blight and Powdery mildew. The genotype, AKSFI-54-3 exhibited the highest value of genotypic worth followed by EC-601957, RHA-3, RHA-859, AKSFI-33, EC-623015 and EC-601767. Mating among these genotypes shall be worthwhile to further expand genetic variability among populations and for selection of elite inbreds through convergent improvement for seed yield and its components, oil content and quality and disease resistance for developing superior hybrids and/or elite populations through recurrent selection for composite varieties.

Keywords: Divergence, Heterosis, Improvement.

146 (P-13)

Aromatic Rices (*Oryza sativa* L.) of Northeastern Hill Region of India: Analysis of Genetic Diversity

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Aromatic rice is a special class of rice with high market value due to its superior grain qualities and pleasant aroma. The Northeastern hill (NEH) region of India possess diverse array of locally adapted non-Basmati aromatic germplasm. Considerable number of aromatic rices have been collected in past, and to utilize such collections breeders need information extent of genetic diversity present within collections. Population genetic analysis of a total of 107 aromatic rice accessions collected from different states of NEH India was carried out with 40 microsatellite markers. Altogether, 322 alleles were amplified with an average of 8.03 alleles per locus. Average gene diversity was 0.67. The NEH aromatic rices can be subdivided into three genetically distinct population clusters: P1, joha rice accessions from Assam, tai rices from Mizoram and those from Sikkim; P2, chakhao rices of Manipur, and P3, aromatic rice germplasm of Nagaland. A combined analysis with a set of structured global rice cultivars revealed two major groups (Indica and Japonica) in NEH aromatic rice germplasm. The aromatic accessions from Assam, Manipur and Sikkim were assigned to the Indica group, while the accessions from Nagaland exhibited close association with Japonica. The taiaccessions of Mizoram along with few chakhao accessions collected from the hill districts of Manipur were identified as admixed. A separate study on 37 chakhao accessions revealed six sub-populations within these landraces. The results suggest that there is scope for exploiting the genetic diversity of aromatic and quality rice germplasm of NE India for rice improvement.

Keywords: *Oryza Sativa*, Aromatic rice, North eastern India, Population structure, SSR

147 (P-14)

Participatory Plant Breeding for Improvement in Rice Landrace Ghansal

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The rice landrace Ghansal grown in the Ajara tehsil of Maharashtra is renowned for its aroma and peculiarity. The variety is popular among urban areas and gains significant demand from various cities with good market price. However, the local farmers are reluctant about its purity. In this context, Participatory Variety Selection (PVS) was carried out with the objectives of varietal purification and genetic improvement in the landrace, through farmers' selection criteria. Seed characteristics *viz*., grain length, grain breadth, Length: Breadth ratio were basic criteria, whereas, consumption qualities refined the selection. Market demand of the variety was the major selection principle. Other factors are secondary for the farmers. Present work increased farmers' awareness and their access to improved variety. This PVS should supplement the formal breeding system to further improve product quality. To accelerate seed dissemination farmer-to-farmer exchange mechanisms was followed. A faster, more efficient and reliable pure-seed supply system than the traditional mechanism is required for proper maintenance of pure seed of the landraces like Ghansal, which can be better achieved through small-scale commercial producers and/or cooperatives.

Keywords: Ghansal, Participatory variety selection, Rice landrace

265 (P-15)

Traditional Wheat (*Triticum aestivum* L.) Genetic Resources for Sustenance and Sustainable Agriculture in Uttarakhand Himalaya

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Wheat (*Triticum aestivum* L.) is one of the first cereals known to have been domesticated and is the third most-produced cereal globally after maize and rice. Although landraces of wheat are no longer grown in Europe and North America, they still continue to be important elsewhere. In traditional small-holder farming of Uttarakhand hills, wheat populations consist of informal farmer-maintained populations often with high levels of morphological diversity. An investigation was, therefore, specifically designed with the objectives of documenting the wheat landrace diversity in production landscapes of Uttarakhand hills. For documenting wheat landrace populations, all the thirteen districts of the state were systematically surveyed and seed samples collected. It was observed that formal breeding efforts have not made much difference in hilly areas of Uttarakhand and there is increasing recognition that the diverse needs of resource-poor farmers cannot be addressed by the breeding of a restricted range of high-yielding and high-input varieties. A total of 38 unique farmer varieties/landrace populations were documented from different parts of the state. The distribution pattern and distinctive features of landrace populations were recorded for their effective conservation and use in crop improvement programmes. Genetically, wheat landrace populations are marked by high level of adaptation to climate and disease, and high variability, and these factors render them essential in plant breeding for their intended use. Further, the recognition, dissemination and wider use of landrace varieties may be both more relevant to the needs of poor farmers and also less damaging to the environment than the use of improved varieties in Himalayan highlands.

Keywords: Uttarakhand Himalaya, Traditional subsistence farming, Wheat landrace diversity

277 (P-16)

Wild Leafy Vegetables of North Eastern Hill Region of India: Diversity and Domestication Potential

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North Eastern Hill region of India, inhabited by more than 200 tribes is geographically located in one of the most biodiversity-rich regions of the world; it occupies about 8 percent of the total geographical area of India and endowed with about 50 percent of country's biodiversity. In this region wild plants used as leafy vegetables occupy an indispensable place in the diet of the tribal people besides ethnobotanical use and income through sale of surplus. Green leafy vegetables are rich sources of protein, vitamins and minerals. These wild leafy vegetables are generally consumed as simple stew- sole or mixed leafy vegetables, steamed, stir-fried, raw, chutney or as an adjunct, garnishing etc. A total of 340 species belonging to 217 genera and 81 families are used in this region as wild leafy vegetables. Among them, major species that are being cultivated in field and kitchen garden are *Centella asiatica* (also used in gastrointestinal problems), *Chenopodium album*, *Clerodendrum glandulosum* (high blood pressure), *Elsholtzia blanda* (sinusitis), *Eryngium foetidum* (indigestion), *Gynura cusimbua* (vermifuge), *Houttuynia cordata* (gastritis), *Phytolacca acinosa* (root juice- sinusitis), *Plukenetia corniculata*, *Zanthoxylum acanthopodium* (fruit pericarp- condiment, pounded fruits for treating dysentery and stomachache) etc. Package of cultivation practices, post harvest management, value chain development for marketing, etc needs to be developed for popularization of these species. Exploration and collecting of germplasm of prioritized species from diverse habitats (field/homestead/wild) across altitudinal and distributional ranges for sustainable utilization and conservation, and screening them for nutritive values and other bioactive compounds, must receive paramount attention.

Keywords: Diversity, Germplasm, North Eastern hill region, Wild leafy vegetables.

316 (P-17)

Agro-Biodiversity Captured in Rescue Missions Executed in Natural Calamities Affected Areas of India

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Rescue collections are conducted when genetic diversity is imminently threatened in an area and *in situ* conservation is not feasible. To capture the diversity from the areas under the influence of natural calamities, four rescue missions were planned and executed. These rescue missions were undertaken in: super cyclones affected parts of Odisha (1999); earthquake hit areas of Gujarat (2001), drought affected areas Gujarat, Rajasthan, Haryana, Odisha, Madhya Pradesh, Uttar Pradesh and Vindhyachal hills region and natural calamity affected areas of Uttarakhand (2013). Total 2413 accessions including cereals/pseudo-cereals (697), millets (147), oilseeds (100), legumes (460), vegetables (384), spices/condiments (67), M&AP (130) and other agri-horticultural crops (428) were collected. Wild relatives *viz. Abelmeochus crinitis, A. manihot, Atylosia scarabaeoides, Citrullus colocynthis, Coccinia indica, Crotalaria burhia, C. medicagenea, Curcuma amada, Lycopersicon pimpinellifolium, Musa acuminata, Oryza granulata, O. nivara, O. rufipogon, Solanum nigrum, S. pimpenifolium, S. sisymbrifolium, S. torvum, S. viarum, Musa* (seeded type) were collected. Rich diversity in paddy landraces exhibiting various traits like, grain size, shape, colour, panicle characteristics, aroma, fineness of the grain, tillering habit, varying plant height, resistance to salinity and water logging in Odisha. Wild ginger (*Zingiber* sp.) having 1.5 metre long rhizome was also collected from Odisha. In present communication germplasm diversity rescued in different crops and awareness on importance & need for conservation of PGR from natural calamities affected areas was discussed. Agro-biodiversity is rapidly eroding from areas under infrastructural development, expansion of highways etc. to the cultivated fields. These areas need to be explored in the country.

Keywords: Conservation, Diversity, Exploration, Germplasm

362 (P-18)

Conservation and Preservation of Native Flora and Fauna in Agro-Biodiversity Park in Telangana State Agricultural University, Hyderabad, India

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The Professor Jayashankar Telangana State Agricultural University, Hyderabad, India has established Agro-Biodiversity park in August, 2008 in Agricultural University campus in 60.0 ha and it is first of its kind in Indian agricultural Universities. The park site is naturally spread with jungle scrub, hillocks, boulders, undulated rocky terrain with sloppy lands covered diverse vegetation such as herbs, shrubs, creepers, trees and grass species besides a natural water tank. In the initial stage, the dangerous invasive species such *as Parthenium hysterophorocous*, *Lantana camera* and *Prosopis juliflora* present in the vicinity were removed and the natural pathways were made with minimum disturbance. The agro-biodiversity park is aimed mainly to preserve, conserve and promote the native flora and fauna through *ex-situ* conservation of species and to establish 15-20 biotic communities including wild relative field crops such as cereals, millets, pulses, oilseeds and fiber crops. As a repository that flourished in the Deccan plateau in the past. The other objectives are to restore and develop the existing dry land and wet land habit to preserve and conserve the genetic resources. Subsequently several plantation blocks were developed in phased manner such as Teak (2200 plants in 2.10 ha), Mahuva (1500, 1.5 ha) plant dominant community blocks and mixed forest tree species block (4600, 2.5 ha). Besides, a separate generic blocks of *viz.*, palm (300, 0.4 ha) medicinal trees (700, 0.7 ha) beal (*Aegel marmelos,* 200, 0.4 ha) and mixed forest tree garden (1200, 1.0 ha). A species diversity Ficus block (225 no. 30 species in 0.4 ha) was also developed and maintained. Of late rare, endemic, endangered threatened species *Ceropegia* (Asclepiadaceae) was identified in 2014. Since then, utmost care was taken for conservation and preservation in agro-biodiversity park. Water ponds and bodies were also created as a source of water for all resident and migratory bio-creatures for promotion of fauna genetic resources. The natural fauna present in agro-biodiversity park are wild boars, field rabbits, small mammalians, field peacocks, reptiles, lizards, avians, amphibians, toads etc., The creation of different plantation blocks has facilitated to increase flora and fauna in University campus. The native flora and fauna was protected by erecting chain link mesh as border fencing against movement of trespass and live stock animals. Every year during monsoon the gap filling was done to maintain greenery in different block plantations.

Keywords: Agrobiodiversity, Conservation, Preservation, Native flora and fauna

369 (P-19)

Wild Edible Plants of District Hamirpur of Himachal Pradesh

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At the global level in many developing countries, a large number of population does not have sufficient food for their daily need and many people are lacking one or more micro-nutrients. The wild edible plants served as a dietary supplements and medicines for thousands of years, particularly in the tribal and rural areas of the Himalayas. Although, they are not consumed in large quantities, their role at regional level cannot be ignored. Keeping the above facts in view, efforts were made to document wild edible plants associated with traditional knowledge from different villages of the Hamirpur district, by interviewing knowledgeable persons of the study area. Hamirpur is the smallest district of Himachal Pradesh, falls in the range of the Shivalik hills. The local people of the district have a direct dependence on the wild plants for their sustenance. The use of local plants and their products for treatment of various health problems have been an old practice. In this context, the present study emphasizes on multifunctional uses of wild edible plant species. There is a dramatic loss of traditional knowledge regarding the use of wild edible plants. Consequently, the recording, preserving and documentation of traditional knowledge to upcoming generation is essential, before it is lost.

Keywords: Himalayas, Shivalik hills, Sustenance, Wild edible

371 (P-20)

Genetic Resources of Underutilized Leguminous Species in Northeastern Hill Region

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Legumes are very important component of global plant genetic resources as they play significant role in human health and nutrition. Northeastern hill region (NEH) being one of the hot-spots of biodiversity, holds rich diversity in underutilized leguminous species. Though the edapho-climatic condition of this region is unsuitable for cultivation of high input demanding crops but can be used for growing low input economically potential leguminous species. Some of the underutilized leguminous species *viz. Canavalia ensiformis* 'Fangra anzamchi', *Canavalia gladiata* 'Naga sem', *Crotalaria tetragona 'Tum-thang'*, *Flemingia vestita* 'Soh-phlang', *Mucuna pruriens* var. *utilis* 'Dimpa', *Parkia timoriana* 'Zawng-tah-lay, *Phaseolus coccineus* 'Tibi-shonglon', *Sesbania grandiflora* 'Bokphool', *Psophocarpus tetragonolobus* 'Sbai daograng', and *Vicia faba* 'sbai maishing' grown in kitchen gardens and consumed as traditionally processed food by natives of NEH region. These legumes are better source of protein, dietary fibers, *etc.* comparable to other common legumes. Keeping in view the rich diversity in above mentioned leguminous species, their systematic collection and conservation (*ex situ/* on farm) is required, as so far very little germplasm accessions have been assembled from this region. Moreover, shifting cultivation (Jhum) is causing a tremendous loss of several underutilized species; hence their proper exploitation can boost income of rural/tribal communities of the region. In the present paper, genetic diversity, traditional uses, economic potential and need for collection and conservation of their genetic resources have been discussed.

Keywords: Genetic Resources, Northeastern Hill Region, Underutilized Leguminous Species

397 (P-21)

Conservation of Indigenous Palm Flora of Bay Islands

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The palm wealth of Andaman and Nicobar Islands are considered very rich and unique with natural regeneration and existence of substantial number of indigenous species. The native palm flora of the Islands consisted 49 species under 18 genera. The important indigenous palm flora distributed in the Island includes *Areca triandra, Arenga westerhoutii, Bentinckia nicobarica, Calamus andamanicus, C.nicobaricus, C.baratangensis, C.dilaceratus,, C.unifarius, Caryota mitis, Corypha macropoda, Daemonorops kurziana, Daemonorops manii, Korthalsia rogersii, Korthalsia laciniosa, K. echinometra, Licuala paludosa, L. spinosa, L. peltata, Phoenix andamanensis, Phoenix paludosa, Pinanga andamanensis, P.coronata, P. manii, Rhopaloblaste augusta and Nypa fruiticans*. The islanders use different palm products for their livelihood, social and cultural importance. The stem, leaves, fruits, inflorescence saps and seeds are utilized for both domestic and industrial purposes. Most of the wild palms have curious shapes and have wide adaptability to grow ex-situ or as pot plants. The massive impact of palms in any landscape gardening cannot be substituted by any other plant because of their distinctly different appearance and elegance. Majority of the palm species enlisted are endemic to these Islands and are threatened in their natural habitat. 30 indigenous palm species are collected through exploratory surveys and conserved at the Institute. . The conservation of endemic palm genetic resources will help to prevent genetic erosion and aid their sustainable utilization. The palm wealth of Bay Islands has tremendous potential in landscape beautification. The promotion of these palms for aesthetic purpose will enhance large scale commercial cultivation which in turn ensures their conservation.

Keywords: Andaman and Nicobar Islands, Conservation, Indigenous, Palm

426 (P-22)

Crop Diversification in Coffee Based Agroforestry Ecosystem for Sustainable Farm Income-planter's Experience

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Coffee occupies a place of pride among plantation crops grown in India. The area under coffee is around 4.15 lakh hectare and annual average production is around 3.10 lakh ton and 75% of this is exported. Crop diversification in coffee based agro forestry eco system is adopted to get sustainable farm income and better utilization of resources apart from conservation of eco system. Coffee in India is grown as a silvi horticultural crop under a tree cover for optimal performance. This situation provides way for inclusion of several economic species together. The shade grown conditions in coffee holdings are ideal for cultivation of many fruit, cash crops and spices. Many planters in coffee growing area's of Western Ghats following the crop diversification in coffee based cropping system. Main crops in the system are Coffee, Silver Oak tree + Pepper, Orange, Banana, Avocado, Areca nut, Jack fruit, other minor fruits, vegetables and permanent shade trees. Also cultivation of annual crops like sweet potato, tapioca, ginger, elephant foot yam in the initial year of plantation also being done to get some revenue. The higher net income from the different diversification system ranges from Rs 1,15,000 to 3,25,000 per acre as compared to Rs 30,000 to 75,000 per acre in mono crop of coffee. Adoption of crop diversification practices in coffee based agro forestry farming systems ensures the sustainable farm income along with support for maintenance of bio diversity in both flora and fauna and management of the ecosystem.

Keywords: Biodiversity, Coffee, Forest ecosystem, Net income

462 (P-23)

Domesticating Sweet Gourd (*Momordica cochinchinensis*) as a Future Crop and also as Genetic Resource of *Momordica* Gourds

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Sweet gourd (*Momordica cochinchinensis* [Lour.] Sprengl.) is a potential under-utilized vegetable of importance as food, medicine, future crop and of ecosystem value. Native of South and South-East Asia, it has an extended distribution to Pacific Islands and has many economically exploitable large fruited forms in Myanmar, Philippines, Vietnam and Formosa. Tender fruits and leaves are nutritious vegetable, ripe fruit yields 'gac pulp' used in Vietnamese cooking as a natural food colorant, flavouring and Vitamin-A source. It is one of the richest sources of β-carotene and lycopene. Characterized by good agronomic traits like ratoonability and heavy fruit yield, it is an ideal vegetable for home gardens as well as commercial farms. Still a wild gathered vegetable in India, its domestication bottlenecks are the extended seed dormancy and non-availability of planting materials. Various propagation methods have been standardized for commercial multiplication. Augmentation of germplasm through introduction of elite types from South-East Asian countries, collection of diversity from North-East India, Andaman Islands, Eastern India and Jharkhand, on farm conservation in homestead, control of root-knot nematodes and Cucumber Stunting Virus are some of the immediate research supports needed for popularizing it. Adapted to tree-based cropping systems, it can be a multipurpose economic plant worth popularizing in various parts of India and a valuable genetic resource for improving teasel gourd, spine gourd and bitter gourd. Its domestication will help to fight Vitamin A deficiency in the humid tropics further adding a new vegetable to the food basket and contributing to farmers' income.

Keywords: On-farm conservation, *Momordica cochinchinensis*, Propagation techniques

522 (P-24)

Community Mobilization for Collective Citrus Gardening and Fund Management

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Gardening of Kachai lemon (*Citrus jambhiri*) on common community land to finance for community development and associated livelihood activities has been highlighted as one of the good practices adopted in Kachai village of Ukhrul district, Manipur in India. Each household provides labour to maintain the garden and during harvesting. New saplings are propagated by local families. Different tribal Women's groups also share their hands in community gardening focussing mainly on value addition like preparation of pickles, squash etc through Kachai lemon. The returns obtained through sale of fruits from such community garden is shared amongst all households on the basis of informal agreement and regulatory norms, with some provision of common fund later used for developing civil amenities. The government recently started supporting the project by providing some necessary inputs. The community has now successfully mobilized the natural capital (e.g. Kachai lemon) together with social and human capital for management of citrus garden for safeguarding social, economic and environmental issues benefiting the receptor community.

Keywords : Community Gardening, Citrus, Natural capital, Kachai lemon

475 (P-25)

Genetic diversity studies in indigenous mango genotypes of Mandya, Karnataka

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The farmer Mr. Mohammed Ghani and his ancestors have been collecting mango genotypes from local and distant places for many generations. At present in their farm, they have 120 different mango genotypes. From these we have collected leaves from 92 genotypes and total genomic DNA was isolated using the modified CTAB method. We have employed previously selected eight SSR microsatellite markers for molecular characterization and assess the genetic diversity. The genetic analysis of microsatellite revealed that expected heterozygosity ranged from 0.670 (for MiIIHR 23) to 0.880 (for MiIIHR 17) with a mean value of 0.818. The polymorphic information content values ranged from 0.613 to 0.863 with a mean value of 0.792. These parameters indicate high diversity in their collection. Cluster analysis grouped the genotypes into three broad groups. This is a remarkable effort from a farmer family. Mr. Ghani family needs appreciation for their effort and sustained interest in mango collection and conservation. In recognition of their effort, many state and national awards were conferred on them.

Keywords: CTAB, characterization, farm, genetic, microsatellite, genotypes, heterozygosity

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642 (P-26)

Swarna Safal: An Improved Vegetable Faba Bean Variety for Jharkhand

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Faba bean (*Vicia faba*) is an important winter vegetable legume of Jharkhand state of India whose green pods used as cooked vegetable. To overcome the low productivity of the crop, the need of the hour is to develop high yielding and better quality varieties. So, an improvement programme was initiated through collection, evaluation and utilization of genetic variability of the crop. This resulted in development of an improved vegetable Faba bean line HAVFB-41. During 2008-11, HAVFB-41 proved its worthiness in respect of green pod yield (24.25 t/ha) with 24.04% yield increase over the check variety Pusa Sumeet (19.55 t/ha). During 2012-14, the variety also exhibited its superior performance regarding green pod yield and quality at farmers' fields in three agro-climatic zones of Jharkhand. The line comes to 50% flowering stage in 35-40 days after sowing. The green pods become ready for harvest in 89-94 days after sowing. The green pods are 3.0-3.3 g in weight and 5.4-6.0 cm in length. HAVFB-41 was resistant to Chocolate spot (*Botrytis fabae*) and was least infested by pod borer under field conditions. Per 100g edible portion, the green pods contained 2.95g protein, 5.81g carbohydrate, 25mg calcium, 115mg phosphorus, 194mg potassium, 32mg magnesium, 33mg sulphur, 0.65mg copper, 0.39mg manganese and 0.11mg iron. Due to its high nutritive value, better yield potential and consumer preference, this vegetable Faba bean line HAVFB-41 has been released as Swarna Safal (IC 617240) by the State Variety Release Committee of Jharkhand in 2015 for large scale commercial cultivation in Jharkhand.

Keywords: Faba bean, Green Pod yield, Swarna Safal, Chocolate spot

476 (P-27)

Evaluation of genetic diversity among the local mango (*Mangifera indica* L.) genotypes in Coorg District, Karnataka

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Coorg district is situated in the Western Ghats region, a hot spot of tropical biodiversity in Karnataka state. In this region we have surveyed and collected local mango genotypes. We have examined the diversity present in this population using microsatellite markers. Total genomic DNA was isolated from leaves using modified CTAB method. We have employed highly polymorphic eight microsatellite markers for amplification of mango DNA. The results of genetic analysis of data from microsatellite markers showed that the expected heterozygosity values ranged from 0.704 to 0.937 with a mean value of 0.835. The average allele per locus was 15.5. The polymorphic information content values ranged from 0.670 (MiIIHR 34 locus) to 0.920 (MiIIHR 18) with a mean value of 0.813. The dendrogram analysis showed three main groups among mango genotypes. These parameters indicate the existence of high genetic diversity among mango genotypes collected from the Coorg district.

Keywords: Western Ghats, Coorg, Population, Microsatellite, Genotypes, Heterozygosity, Diversity

646 (P-28)

Genetic Diversity of Jack Fruit in Goa State

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Goa is a small state located in the Western coast of India, holding and nurturing large biodiversity within it. There is a wide variability found in native fruit trees like jack fruit, karonda, ber, jamun, jagoma, kokum *etc*., Research attempts are being made to document and catalogue the enormous diversity of jack fruit in Goa. In order to study the variability in jack fruit, field surveys were conducted in Bicholim, Canacona, Pernem, Ponda and Bardez talukas during May-July 2013, 2014 and 2015. Based on descriptor, fruit characters of the accessions were recorded. There was wide variation recorded in traits like, stalk length (5.6 to 11.5 cm), fruit weight (3.62 to 19.36 kg), fruit length (31.2 to 68.2 cm), fruit girth (52.2 to 94.2 cm) rachis length (11.9 to 42.3 cm), rachis diameter (5.1 to 11.0 cm), number of bulbs per fruit (48 to 271) bulb weight without seeds per fruit (0.51 to 5.57 kg), weight of seeds per fruit (0.2 to 1.38), weight of inedible waste per fruit (2.05 to 8.2 kg) *etc.* The bearing ranges from early to late season; fruit rind colour yellow to blackish green; fruit shape oblong/ ellipsoidal/ irregular; spine shape flat to pointed; spine density sparse to dense; fruit quality poor to excellent; bulb colour creamy white to deep orange; seeds with shapes ranging from elongate to reniform; seed surface plain or with striations. The study is being carried out for the past three seasons and accessions from Kindelkatta and Loutalim are found promising for yield and quality traits.

Keywords: Diversity, Goa, Jackfruit

660 (P-29)

Species Interrelationship and Derivation in Vegetable Amaranths

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Amaranths are the leading group of plants having great potentiality to alleviate malnutrition especially in the low income food deficient countries. The species of *Amaranthus* are mostly annual weeds; few are utilized as vegetables and ornamentals. At least 50 tropical countries grow vegetable amaranths in quantities far from negligible. Vegetable amaranths are considered as the most popular vegetable crops grown in the humid tropical lowlands of Africa, Asia and Caribbean islands for their unique food value. Though a number of species are consumed as vegetable the two species – *Amaranthus tricolor* and *A. blitum* are most important. Both are very rich in morphological variability represented by different morphotypes and varieties, conforming two species complex –"tricolor complex" and "blitum complex" respectively. Morphological variability was evaluated morphometrically and new varieties and species were introduced (*A. tricolor* var. *acutus* S.Das; *A. bengalense* Saubhik Das & Iamonico, *A. parganensis* Saubhik Das). The genus *Amaranthus* also unique in showing wide range of sexuality ranging from gynomonoecy, monoecy to dioecy and variability in mating behavior from self compatibility to obligate outcrossing. Monoecy in Amaranths might have transmitted from co-sexual species of Cheno-Amaranth alliance through gynomonoecy. Taxonomic delimitation in vegetable amaranths is still not clearly resolved. The presence of large number of morphotypes, varieties, landraces, overlapping morphological features, and large number of morphotypes have made taxonomic delimitation very complicated. Any idea about putative progenitor and phylogenetic linkage among them is also lacking which are very important for proper utilization of genetic resources and sexual variability may be very instrumental in this aspect.

Keywords: Morphological variability, Morphotypes, Phylogeny, Sexual diversity, Vegetable *Amaranthus.* .

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696 (P-30)

Effect of Suberization on Sprouting and Survival of Cactus pear in Arid Region, India

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Cactus pear (*Opuntia ficus-indica*) is being viewed as a potential forage and fruit crop for arid and semi-arid regions of India. Since, planting of cladode in field immediately after detaching it from mother plant has not been so successful, therefore, 120 Cladodes/pads having similar dimension were separated from different Cactus pear and moisture loss treatment from 10-60 percent (suberization) were analysed on sprouting and survival of Cactus pear. Of the moisture loss cladode from 10-60 percent, the best performance in term of sprouting, number of new cladode and growth has been observed in treatment having 10-20% moisture loss treatment. The sprouting kids/cladode was influenced significantly by various moisture content of cladode. The maximum number of sprouting kids (1.66/cladode) and significantly more number/cladode were recorded at the 20 percent moisture loss (T-2) than other treatment. The maximum kids (46) were produced in the 20% reduced moisture treatment with cent percent sprouting pads, while lowest (15) in the 60% reduced moisture treatment with 50 percent sprouting pads. The average number of kids produced per pad were increased with the increase in the weight of pad. The maximum kids/pad were produced when the weight of pad was more than 140 g. The cladode with 10% and 20% reduced moisture treatment was the best treatment since it gave the maximum sprouting kids/pad in field after planting in comparison to other treatment.

Keywords: Cactus pear, Cladode, Sprouting and Survival

698 (P-31)

Genetic Diversity Studies of Brinjal Hybrids (*Solanum Melongena* L.) in Chhattisgarh State

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Brinjal or eggplant (Solanum melongena L.) is an important solanaceous crop of sub-tropics and tropics. Several studies have been conducted on vegetable crops to know the knowledge and adoption of recommended cultivation practices but very few research studies have been conducted on brinjal crop in Chhattisgarh. The experiment was carried out during the year 2011-12 in Rabi season at Horticulture Research cum Instructional Farm, Department of Horticulture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) Crosses involving genetically divergent parents were expected to show a broad spectrum of genetic variability, would contributing characters in brinjal hybrids. High GCV and PCV were found in some characters viz., number of flowers per cluster, number of fruits per cluster, per cent fruit set, fruit weight, pericarp thickness, number of fruits per plant and fruit yield per hectare. A correlation was significant in case of number of fruits per plant with fruit yield at both genotypic and phenotypic levels. Fruit yield was significantly and positively associated with number of fruits per plant at phenotypic level whereas, characters like number of fruits per plant, number of fruits per cluster, fruit yield per plant at genotypic level. It shows negative relationship with days to first flowering, days to first picking and TSS at genotypic level. The path analysis revealed that the number of fruits per plant had maximum and positive direct effect on fruit yield followed by fruit length, TSS, number of branches per plant, fruit yield per plant, pericarp thickness, number of fruits per cluster, fruit girth.

Keywords: Brinjal, Correlation, Genetic diversity, Path analysis, Vegetable

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753 (P-32)

Assessing the Diversity of Traditional Landraces of Rice (*Oryza sativa* L.) from Goa, India using Multivariate Technique

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Goa state of India has rich diversity with respect to traditional rice landraces. The utilization of genetic diversity in landraces which possess many useful genes/alleles is the key to breed new varieties. Hence, the present study was undertaken to assess the genetic diversity among the rice landraces native to Goa state using different agro-morphological characters. The landraces were characterized for 30 qualitative and 16 quantitative characters. The unweighted pair group method with arithmetic mean (UPGMA) cluster analysis, and principal component analysis (PCA) were used to analyze the diversity. Cluster analysis for qualitative characters grouped the genotypes into two major clusters with two sub-clusters in each of the main cluster with a similarity coefficient varying between 0.38 and 0.87. Principal component analysis indicated that the first four components explained about 80.60% of the total variation among the 16 quantitative characters. Principal component one (PC1), with eigenvalue of 5.99 contributed 37.49% of the total variability, PC2 with eigenvalue of 3.35 accounted for 20.98%, PC3 with eigenvalue of 2.37 accounted for 14.87%, and PC4 with eigenvalue of 1.16 accounted for 7.26% of total variability. The result of the PCA suggested that traits such as plant height, flag leaf width, straw yield per plant in PC1, grain width, test weight and grain length in PC2, and grain yield per plant, grains per panicle and length to breadth ratio in PC3 were the principal discriminatory characters. The genetic variability present in above important agro-morphological characters can well be exploited for future genetic improvement programmes.

Keywords: Landraces, Genetic diversity, Goa, Principal component analysis.

766 (P-33)

Genetic Divergence in Pigeonpea (*Cajanus Cajan* (L) Millsp.) Germplasm

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Eastern India, being the centre of origin of pigeonpea (*Cajanus cajan* (L) Millsp.) boasts tremendous germplasm diversity in this important legume crop. A total of 100 diverse pigeonpea germplasm collected from Jharkhand were subjected to genetic divergence study for yield and its component traits. Ward's minimum variance dendrogram clustering based on standardized Euclidean distances grouped 100 germplasm accessions under study into 11 distinct non-overlapping clusters. The number of clusters and the inter-cluster distances indicated presence of very high genetic diversity in the collected germplasm. Cluster I comprised of 14 genotypes which were maximum in any cluster followed by cluster X with 13, cluster V with 11 genotypes, cluster VII and IX with 10 genotypes each, cluster III, IV and XI with 9 genotypes each and cluster II, VI and VII with 6, 5 and 4 genotypes respectively. The cluster II had lowest mean number of days to maturity (211.38) and cluster VII had maximum mean yield per plant (153.08). The Euclidian inter-cluster distance was maximum between cluster II and VI (38.13) and it was minimum between clusters VIII and IX (11.65). The complex trait yield per plant exhibited maximum contribution (47%) towards divergence followed by plant height (40%), number of days to 50% flowering (6%), number of days to 80% maturity (6%) and primary branches per plant (1%). The geographic site of collection and genetic divergence lacked a definite relationship. Based on this study the genotypes belonging to the clusters with maximum inter-cluster distance are expected to yield better hybrids upon crossing.

Keywords: *Cajanus cajan*, Germplasm, Genetic divergence

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800 (P-34)

Crossability Barriers in Interspecific Hybridization of Ricebean (*Vigna Umbellata*) with other Vigna Species

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Ricebean is one of the underutilized crop which keeps great potential to solve the food and nutritional problem. It is a multipurpose grain legume crop mainly cultivated for food, fodder and green manure and is important crop of. It has emerged as a good alternative to other pulse crops such as black gram and green gram in Mid-Himalayan region which do not flourish in this region due to their susceptibility to cold temperature stress. Despite having all the favourable traits; it is not much popular among the farmers due to the late maturity and indeterminate growth habit. A little genetic improvement with respect to maturity and growth habit can revive its cultivation. Since variability for these traits is very low in this crop, inter-specific hybridization of ricebean with other Vigna species can lead to its improvement. Thus, in the present study inter-specific hybridization was performed among ricebean, adzukibean, mash and mung to introgress desired traits into otherwise high yielding genotypes. It revealed that there was no free crossing in these species. In the present study, successful pod set was observed in 10 crosses out of 72 interspecific crosses with mash (*V. mongo*) and mung (*V. radiata*). Highest crossability was observed in *V. mungo* and *V. umbellata* crosses while moderate crossability in *V. radiate* and V. umbellata crosses. Crossing of adzukibean with ricebean showed poor or no pod set percentage among all the cross combinations.

Keywords: Inter-specific hybridization, Synchronous maturity, Introgression

810 (P-35)

Glycine max (Kala Bhat) – A Potential Pulse Crop of Uttarakhand

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Soybean [*Glycine max* (L.) Merr.] is an important legume crop, native of south-eastern Asia used as a valuable protein supplement food in south-east Asia including India. In India it is under cultivation from ancient times with variability in seed (yellow, chocolate and black) in the hilly tracts of Assam, Bengal, Manipur and Khasi and Naga hills (upto 2,000m) and in Uttarakhand, Himachal Pradesh and Sikkim. In Uttarakhand black soybean called '*kala bhat'* is a local/landrace used as traditional food consumed as *dal* (soup) or as staple foods (bhatwani in Garhwal; churkani in Kumaon). Seeds are rich in iron (11.5mg./100g), phosphorus (0.69%) and protein (43.2%) and eaten boiled in soups, as roasted and pods/seeds cooked. It is also known for curing beriberi, lockjaw, promoting blood circulation and reducing cholesterol. Keeping in view of the shrinking area of its cultivation under traditional farming and depletion of '*kala bhat'* in Uttarakhand an exploration was undertaken in Ramgarh, Bhimtal and Kaladhungi areas of Nainital district in October 2015. The farmers have discontinued its cultivation and replaced it by vegetables or white seeded soybean which is mostly traded in market. So far ICAR-NBPGR has collected over 4,000 accessions of soybean among them only 230 accessions of *kala bhat* from Uttarakhand (203), Himachal Pradesh (22), Arunachal Pradesh and Sikkim (5). In view of the erosion of its landraces, there is need to collect its germplasm from unrepresented areas of Himachal Pradesh, parts of Sikkim and Arunachal Pradesh to conserve, evaluate and utilize the diversity.

Keywords: Kalabhat, Potential pulse, Uttarakhand

821 (P-36)

Rice Biodiversity at Indira Gandhi Krishivishwavidyalaya, Raipur

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Landraces acquired precious genes and replaced by various high yielding semi dwarf rice varieties which leading to drastic reduction in variability. So, it was important to collect and conserved the land races. About 23000 land races of rice are conserved and maintained at Indira Gandhi KrishiVishwavidyalaya, Raipur in the Department of Genetics and Plant Breeding. In which 4557 accessions (early group), 5069 accessions (medium group) and 7915 accessions (late group). Some of the entries in this germplasm are of unique characteristics *viz.* Double grain quality type (Do-dana and Ram-Laxman), Clustered spikelet (Amaruthi, Koudidhool etc.), Spikelets with typical long sterile glume (Suapankhi, Pankhi etc.), Longest grain (Dokra-dokri), shortest grain (Ramjeera), Bold grained and suitable for Poha (Rice flakes) (Hathipanjara, Barhasal (Scented flakes), Cheptigurmatia etc.), Nutrient rich (high iron) accessions (Ganga balu etc) high zinc (Lalu 14, Badshahbhog etc.), high protein (Vishnubhog, Jalpa etc.), scented accessions (Badshahbhog, Atmasheetal etc.) and extra early accessions Sathia and late accessions like Korma etc. Based on Agro-morphological characteristics three catalogues had been published with characterization of about 17,000 accessions of early medium and late group rice.Since 1982 these germplasm are being utilized for release of new varieties in rice like Kranti, Cross 116, Madhuri, Mahamaya, Indira SugandhitDhan-1, Karma Mahsuri, Maheshwari, IGKVR-1 (Rajeshwari), IGKV R-2 (Durgeshwari), IndiraBarani Dhan-1, Indira aerobic dhan 1, Dubraj Selection-1, Badshahbhog Selection-1, Vishnubhog Selection-1, Tarunbhog selection-1, Chhattisgarh sugandhit bhog-1 and Chhattisgarh Madhuraj55.

Keywords: Agro-morphological characteristics, Biodiversity and Landraces

861 (P-37)

Variability and Correlation Studies for Yield and Quality Traits in Garden Pea (*Pisum sativum* L.)

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Legume played important role in the progress human civilization providing, food, fodder and help in maintaining the environment. Food legume satisfies basic nutritional requirement of human by providing protein, carbohydrate, minerals and vitamins. Beside this they are the unique sources for various secondary metabolites having antioxidant potential. Among legumes, pea is an important vegetable and also rich source of secondary metabolites especially phenolics. In India various genotypes of peas have been growing for long times. Although information on the basic nutritional composition is available, limited documentation has been carried out on antioxidant activities of pea genotype. In the present experiment, 22 genotypes including released varieties and advance breeding lines belonging to early, mid and late maturity group were selected and assayed for antioxidant phytochemicals. Antioxidant activity of these genotypes were evaluated by four different methods *viz.* Ferric Reducing Antioxidant Power (FRAP), Cupric Reducing Antioxidant Capacity (CUPRAC), Trolox Equivalent Antioxidant Capacity (TEAC) and the 2,2-diphenyl-1-picrylhydrazyl (DPPH). Among 22 genotypes, EC-9485 and VRP-233 bearing purple colour flower, were found to be the highest sources of total phenol (128.64 and 104.01 mg GAE/100g) and flavonoids (45.84 and 36.84mg CE/100g). This two genotype also showed strong antioxidant potential (26.79 and 20.96µ Mol TE/g). Cultivar belonging to early group like VRP-100, VRP-101, VRP-25, VRP-5, VRP-6, AP-3 and Arkel, possessed comparatively lower amount of phenolics, flavonoids and antioxidant potential. The positive correlation between total phenols, flavonoid with antioxidant activities indicates phenolics and flavonoids are the main component for antioxidant activity of pea genotype.

Keywords: Antioxidants, Flavanoid, Legume, Phenol, *Pisum sativum*

863 (P-38)

Genetic Variability and Inter-Relationships of Total Phenolics, Anthocyanins and Antioxidant Activity in Coloured Radish (*Raphanus sativus* L.)

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Radish belong to Brassicaceae family and is an important salad vegetable consumed throughout the world for fleshy roots and soft leaves which has numerous categories of roots (colour, shape and flavor) and leaves (incision, shape, colour and surface). The uses of coloured radishes in the salads and their anthocyanins as colorants are gaining popularity because of the colour characteristics and health benefits. However, information on the genetic variability, heritability and inter-relationship of total phenolics, anthocyanins and antioxidant activities in coloured tropical radish is very limited, but pre-requisite to initiate breeding programme; and therefore investigated in the present study. There were significant variability for all the antioxidants; ranged from 12.4-61.7 mg/100g for total phenolics, 4.6-166.3 µg/g for anthocyanins content, 1.14-5.66 µmol/g for FRAP activity and 2.73-11.01 µmol/g for CUPRAC activity; and the genotypes alone account for >97% of total variations. Furthermore, there were meager differences between phenotypic and genotypic coefficient of variation indicating the greater role of genotypes and lesser influence of the environment on the biosynthesis and accumulation of pigments and antioxidants. Significantly positive correlations along with higher magnitude for anthocyanins content, total phenolics, FRAP activity and CUPRAC activity (0.823-0.964) could be used as indirect selection criteria for improving levels of antioxidant compounds. The estimates of heritability and genetic advance indicate the role of additive and non-additive genes for biosynthesis of antioxidants and root development, respectively; therefore, recurrent selection would be the best breeding approach to improve the both traits (yield and antioxidants) simultaneously in coloured radish.

Keywords: Anthocyanin, Antioxidant, Variability, Correlation, Radish

951 (P-39)

Evaluation of Maize Landraces for Some Yield and Quality Traits

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131 maize landraces, collected from different parts of North Eastern Hill Region, were evaluated for thirteen yield and quality traits over three consecutive years i.e. *kharif* season of 2013, 2014 and 2015. Among these 131 landraces, six landraces namely GP 40, GP 47, GP 63, GP 105, GP 121 and GP 124 were found heat tolerant. Further, five (GP 32, GP 40, GP 102, GP 116 and GP 127), seven (GP 32, GP 40, GP 47, GP 87, GP 102, GP 127 and GP 131) and four landraces (GP 32, GP 40, GP 102 and GP 127) were found tolerant to stem borer infestation, cob borer infestation and stem borer and cob borer infestation both, respectively over the three years. Furthermore, six (GP 24, GP 31, GP 48, GP 79, GP 91 and GP 98), five landraces (GP 13, GP 16, GP 26, GP 27 and GP 29) and four (GP 65, GP 72, GP 116 and GP 122) were screened for high 1000 seed weight, number of seeds/row and number of rows in cob, respectively.

Keywords: Maize, Landraces, Cob diameter, 1000 seed weight, Dry cob weight.

1065 (P-40)

Mangroves and Mangrove Associates of Puthuvypin of Ernakulam District, Kerala (South India)

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Puthuvypin is a fast developing industrial area in Kochi (Ernakulam district) in the Indian state of Kerala (South India). Given its close proximity to the city and to the international sea route Puthuvypin has attracted many development projects in the near past. Further, of late, Government of Kerala decided to set up a mega oceanarium project together with a Marine Biological Research Centre at Puthuvypin with the objective of imparting awareness on the marine resources of the Arabian Sea. Though the various development projects contribute to a wide range of advancements in the social and economic fronts and overall growth of the region, they may also bring in adverse effects on the environmental quality, if adequate precautions are not taken to prevent them. Therefore, there is a pertinent need to collect information on the prevailing environmental conditions of the development area and surroundings prior to the implementation of the project. A comprehensive database on the baseline environmental characteristics is a pre- requisite for an integrated assessment of environmental impacts, if any, with respect to pre-construction, construction and post-construction phases of the project. The present study which forms part of a larger integrated study was meant to collect information on mangroves which are among the most dynamic but fragile eco systems. The main objective of the study was to document the mangroves and mangrove associates in and around Puthuvypin with a view to act as a baseline data for future studies on the impact of the project on the environment. In the study 11 species of true mangroves and 32 species of mangrove associates were found to occur in the study area. The various bio diversity threats to mangroves and mangrove associates in the area were also identified and discussed in the paper.

Keywords: Mangroves, Mangrove associates, Puthuvypin

1068 (P-41)

Underutilized Vegetables: Opportunities to Grasp for Livelihood Improvement

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Underutilized vegetables have an important role in indigenous people's nutrition around the world. The term 'underutilized plant species' covers an enormous range of plants that have the potential to contribute to food and nutritional security and poverty alleviation. India being blessed with varied climatic conditions provides habitat to a number of green foods, some of which are still underutilized and their knowledge is confined to some tribal and ethnic communities living in close conformity to the nature. These plant species are found resilient, adaptive and tolerant to adverse climatic conditions, and can be raised at lower management costs even on poor marginal lands. They have remained underutilized due to lack of awareness and popularization techniques for utilization. The wild, semi-cultivated or neglected vegetables and fruits are regarded worldwide as an important area of the nutritional and phytotherapic research. This necessitates the importance of inclusion of underutilized/ neglected vegetables which feature promptly in the food security, socio-economic conditions and health promoting benefits. Underutilized vegetables (UUVs) like Tree tomato, Tree bean, Jack bean, Scarlet bean, Sword bean, Winged bean, *Moringa*, *Dolichos spp*., *Luffa*, *Colocasia, Amorphophallus, Alocasia, Xanthosoma*, cucurbits, *Dioscorea spp.*, leafy vegetables and numerous others are known to be good source of micronutrients and also high in antioxidants and anti-microbial photochemicals. Therefore, enhancing the role of UUVs holds promise for improved nutrition, healthy diet, and diversified income generation in home garden and commercial farming systems in India.

Keywords: Under utilized vegetables, Nutrition, Diversity, Food security, Antioxidants.

1224 (P-42)

An Assessment of Crop Genetic Diversity in the Central Himalaya

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Crop genetic diversity, which evolved traditionally over the time, not only provide basic nutritional requirements as a food security, but also maintain their own sustainable agriculture system for centuries. In recent years, however there is significant change in crops and cropping pattern due to change in life style and other pressing factors. In the present study, we investigate crop genetic diversity of 24 villages from two development blocks of the district Bageshwar, Uttarakhand, India. Data on crop genetic diversity was gathered through extensive field surveys using structured/semi-structured questionnaire and interview schedules. The study revealed a total of 104 landraces of cereals (47), pseudo cereals (05), millets (09), pulses (10), vegetables (20), spices (07), oil yielding (05) and fibre yielding (01) crops. Maximum genetic diversity was recorded for rice (38 cultivars) of which 18 cultivars are still under cultivation. Twenty cultivars of rice are not being cultivated and considered eroded. The possible reason for erosion of traditional varieties/cultivars are climatic changes, wild animal damage, low yield, change of cropping sequence, migration, adoption of HYV. The present study was focused with the objective of understanding the *in-situ* (on-farm) conservation of agro-biodiversity in traditional agro-ecosystems for subsistence of traditional knowledge related resource management and uses. It is suggested that, promotion and conservation of the crop-genetic pool erosion on food security should be done through sustainable use of on-farm mangement.

Keywords: Crop genetic diversity, Landraces, Food security, Uttarakhand, Central Himalaya.

1282 (P-43)

Role of Food Habit of Tai Phake Community in the Buildup of Local Biodiversity in Assam

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Assam is a state situated in the extreme north-eastern region of India. The river Brahmaputra flows almost in the middle of the state with 42 major tributaries. The Brahmaputra valley with abundant rain and humid climate is gifted with some of the most productive soils and thus makes the foundation for the great Brahmaputra biodiversity. Tai Phake community is one of the 20 major tribes of Assam with a very small population living in Dibrugarh and Tinsukia districts along the areas of Dihing river, a tributary of Brahmaputra. The study assessed the food consumption patterns of 100 Tai Phake farm families belonging to four selected villages with the help of structured questionnaires and personal interviews. Tai Phake community lives in the stilt houses (*chang-ghar*) built on raised platform with bamboo structures which help them live safely during flood and rear varieties of livestock in the ground stairs. Rice being the staple, they grow paddy using family members following traditional practices. The community catches fish from the adjacent river and natural wet lands for daily consumption and preserve by fermentation, smoking, sun drying etc. All the families are found to consume food grains, fruit and vegetables including indigenous greens from their own harvest and also from the nearby forest. They adopt a balanced farm and home resource allocation strategy. They also follow traditional herbal medicine for treating various ailments. Their age old practices add to input utilization, resource conservation, environment replenishment and capital formation ensuring a sustainable food and nutrition security.

Keywords: Tai Phake, Food habit, Traditional food, Resource conservation, Food security

1315 (P-44)

Agro-Morphological Variation in Kenaf (*Hibiscus cannabinus* L.) Exotic Germplasm

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Kenaf or Mesta (*Hibiscus cannabinus* L.) is second most important Malvaceous bast fibre crop after jute in India. The crop species is valued for fibre, paper pulp and biofuel production round the globe. A total of 325 exotic accessions of kenaf were evaluated for 21 agro-morphological traits at ICAR-CRIJAF, Barrackpore. Each accession was grown in two rows of 3 meter length at 30 cm x 5-7 cm spacing. Data were collected on five randomly selected plants from each accessions for fifteen quantitative (plant height, basal diameter, middle diameter, top diameter, core diameter, no. of nodes, dry fibre weight, dry stick weight, dry biomass, harvest index, petiole length, leaf length, leaf width, days to 50% flowering, 1000 seed weight) and six qualitative characters (stem colour, stem pubescence, leaf pubescence, flower colour, fruit colour, seed shape). Plant height varied from 125 to 398 cm with a general mean of 276 cm while dry fibre weight/plant ranged from 2.0 to 24.0g. Highest coefficient of variation was noticed for stick weight/plant (39.76%). Two types of stem and fruit pigmentation (green/red), two types of seed shape (reniform, angular), three types of flower pigmentation (yellow/yellow with purple throat/ violet with purple throat) and two types of seed coat colour was observed in kenaf germplasm under study. *Hierarchical* clustering grouped 325 kenaf accessions into 11 clusters based on usual Euclidean distance coefficient. In conclusion the present germplasm accessions were found to be diverse for fibre yield and attributing traits hence could be used in kenaf improvement programme.

Keywords: Kenaf, Fibre, Variability

1398 (P-45)

Characterization and Utilization of Oil Palm (*Elaeis Guineensis* Jacq) Genetic Resources from African Sources

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Oil palm (*Elaeis guineensis* Jacq.) an introduced crop in India has narrow genetic base which poses a major constraint in its genetic advancement through breeding. An attempt was made to import oil palm germplasm from African countries, especially the centres of origin, in order to increase the genetic diversity and to explore the possibility of their utilization directly. Oil palm germplasm from Cameroon (15 nos. of accessions), Guinea Bissau (13 nos.), Tanzania (7 nos.) and Zambia (8 nos.) were planted in September 1998; evaluated and being utilized at ICAR – IIOPR, Pedavegi (aged 17 years by 2015). Traits of interest include higher oil productivity (achieved through higher FFB (Fresh Fruit Bunches) yield coupled with higher oil/bunch ratio), slow vertical growth (dwarfness measured in terms of annual height increment) and higher water use efficiency (drought tolerance). Data on the performance of African germplasm indicated that mean FFB yield was highest in Tanzanian source but numbers of dura mother palms (37.15%) selections were maximum from Zambian source. The Zambian source has also recorded slow vertical growth (lowest mean annual height increment of 33.9 cm and 38.5 cm during 2011-12 and 2012-13, respectively. Physiological studies resulted in characterization of the germplasm as drought tolerant (TS -11, ZS-3, ZS-2 and GB-21/310) and drought susceptible (ZS-5, ZS-8, TS-9 and GB-25/314). Selected palms based on FFB yield, slow vertical growth and higher water use efficiency are being utilized in generating advanced planting material for crop improvement trials and for commercial hybrid (DxP) seed production.

Keywords: African Oil palm, Drought tolerance, Dwarfness, Oil productivity, Water use efficiency

1401 (P-46)

Traditional Minor Millets and Tree Fodder Species for Food, Fodder and Ecosystem Services in North Western Himalayas

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In North Western Himalayas minor millets constitute an important staple diet, but their productivity is low. The area is predominantly rainfed with monocropping as a common practice. The ecosystem services of prevailing land use systems are rarely investigated, though these systems are in vogue since time immemorial. The present studies were envisaged with a view to (1) Assess the productivity potential of traditional minor millets along with agroforestry multipurpose trees (MPTs) of the area. (2). Quantify the ecosystem services provided under different land use systems in terms of arresting soil loss and conservation of natural run off water. The average productivity of improved varieties of finger millet and barn yard millet was 13.6 and 11.3 per cent higher than local varieties, respectively. The average productivity of finger millet and barn yard millet under *Grewia optiva* was 10.6 and 9.2 q ha^{-1}, while it was 9.1 and 7.9 q ha^{-1} under *Morus alba*, showing differential tree x crop interactions. The ecosystem services provided under different land use systems were quantified during 2009-2015 by measuring the soil loss and runoff water. Average soil loss under cultivated fallow was 24.5 t ha^{-1} in comparison to 15.0 t ha^{-1} recorded in mulberry + barnyard millet. Similarly, the runoff loss of water was 44.1% in cultivated fallow which declined to 23.7% in mulberry + finger millet combination. Thus, trees crops and tree + crop combinations, were quite effective in controlling the runoff rain water and soil loss in ascending order, thereby providing valuable ecosystem services.

Keywords: Improved varieties, Minor millets, Fodder trees, Resource conservation

1427 (P-47)

Challenges in Augmentation, Multiplication, Conservation and Utilization of Sunflower Genetic Resources in India

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Sunflower crop was introduced in India during late 1960's. It is an important oilseed crop after soybean, groundnut and rapeseed mustard. The first attempt to augment and conserve sunflower genetic resources was made during 1969 with introduction of four varieties of Russian origin, *viz*. 'VNIIMK 8931' (EC 68413), 'Peredovick' (EC68414), 'Armavirskij-3497' (EC 68415), and 'Armaverts' (EC 69874). Augmentation, systematic characterization, evaluation and documentation of accessions is of prime importance for effective utilization of the genetic resources. There are several issues with regard to augmentation, multiplication, conservation and exploitation of sunflower genetic resources in the breeding programme in India. Very few initial introductions from USA USDA, were exploited in the breeding programmes and access to other international gene banks is limited. The multiplication of sunflower is labour intensive owing to its cross pollinated and self incompatible nature. The major challenge in the conservation of sunflower genetic resources including wild species is the establishment and maintenance of the augmented sunflower accessions under Indian situations. Special techniques are required for germination of the wild sunflower species due to small seed size. Another problem is the non viability of the seed due to prolonged storage under normal conditions where viability is reduced upto 20 to 30% with one year storage. The accessions with viability less than 50 per cent are multiplied on a regular basis to maintain the germplasm. Germplasm characterization is inadequate thus restricting the identification of promising accessions with agronomically desirable attributes in the breeding programme. Overcoming incompatibility barriers with the exception of diploid annuals is a major challenge for exploitation of wild species in genetic improvement of cultivated sunflower. The present paper discusses about the challenges and strategies to be followed for effective utilization of the genetic resources in sunflower.

Keywords: Sunflower, Augmentation, Multiplication, Conservation and Utilization

1536 (P-48)

Resurrecting Browntop Millet (*Brachiaria Ramosa* (L.) Stapf): A Less Known, Endemic and Endangered Small Millet Crop of South Indian Origin

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Browntop millet (*Brachiaria ramosa* (L.) Stapf) is an endemic crop originally evolved and domesticated by farming communities in the drier belts bordering Karnataka and Andhra Pradesh in South India. It is a short duration, dual purpose crop mainly grown in pure stands for its grain and fodder known as *Korle* (Kannada) and *Andakorra* (Telugu). The grain is considered superior to other millets due its protein content and the straw is relished by cattle. Rice made out of Browntop millet is useful in diabetes and the flour is mixed with finger millet for *ragi mudde* and at least nine traditional foods are also prepared from it. Due to commercialization of agriculture and changing food habits, this crop is under tremendous pressure of replacement by other profitable crops. In order to salvage this crop, an exploration was undertaken in collaboration with AICSMIP in parts of Karnataka and Andhra Pradesh which resulted in the collection of 28 germplasm accessions facilitating long term conservation of diversity of this crop in the NGB for the first time. Significant variability was observed in the germplasm for plant height (68.7-144.3 cm), panicle length (13.2-18.3 cm), panicle branches (1.3-17.0), panicle compactness (open/ semi-open/ compact) and maturity (67-94 days) as well. Browntop millet being rainfed is highly adapted and suitable to arid situations especially under climate change scenario as *Brachiaria* grasses are known to inhibit green house gases. Efforts are being made to revive this crop in existing cropping systems for enhancing resilience and strengthening nutrition and livelihood support.

Keywords: *Brachiaria*, Browntop millet, Conservation, Germplasm

1663 (P-49)

Harnessing Maize Germplasm for Nutritional Security: Status and Prospects

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Deficiency of essential amino acids, vitamins, and minerals in staple crop like maize imposed health problems called ‘hidden hunger’ that afflicts millions of people worldwide and it can be effectively addressed with the utilization of diverse maize germplasm along with effective policy implementation. Biofortification has emerged as a sustainable approach to overcome malnutrition. At CIMMYT, breeders have successfully developed quality protein maize (QPM) genotypes by combining *opaque2* allele with endosperm modifiers. Then, a series of QPM composites and hybrids have been released and notified in India. Further, using marker- assisted selection (MAS) strategy, several normal hybrids have been converted into QPM versions. Furthermore, combining the novel *opaque16* with *opaque2* showed promising effects on enrichment of lysine. Across Africa and Mexico, millions of hectares have been covered by QPM varieties. Efforts towards development of high methionine maize are underway. Scientific advances revealing higher accumulation of kernel -Fe and -Zn in *opaque2* genotypes offers possibility of development of Fe- and Zn-rich QPM hybrids. Additionally, *lpa2-2* allele that enhances bioavailability of minerals by lowering phytic acid has been successfully introgressed into Indian inbreds. Four MAS-derived hybrids possessing a maximum of 21.5 μg/g provitamin A (proA) and high proA inbreds with 5.3-8.1 μg/g have been developed in India and China, respectively. Developing countries like Zambia, Nigeria and Ghana have released several proA-enriched synthetics and hybrids. Similarly, *ZmVTE4* introgression enhanced vitamin E from 29.1 to 51.5 μg/g in sweet corn genotypes. Thus, pyramiding of genes/ QTLs imparting elevated essential micronutrients in agronomically superior QPM hybrids could pave way for strengthening the global nutritional security.

Keywords: Maize, Micronutrients, Biofortification, Nutritional security

1848 (P-50)

Genepool of Cotton (*Gossypium* spp.) at ICAR – Central Institute for Cotton Research, Nagpur, India

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Genetic resources are key drivers for improvement of crop and development of improved commercial derivatives. ICAR – Central Institute for Cotton Research, Nagpur, Maharashtra is maintaining 11559 geographically and genetically diverse germplasm lines of four cultivated species, land races, perennials, and wild species of *Gossypium*. The huge collection includes National collection and exotic collection from all over the world, especially major cotton growing countries like USA, Soviet Union, Australia, Egypt and Africa etc. The germplasm material possesses a wealth of variability for qualitative and quantitative traits viz., yield, ginning outturn, fibre spectrum and boll weight. However, vast amount of variability is available for morpho-economic traits, plant stature, leaf shape and size, canopy, boll shape and size, locules and seeds per boll, trichome density, gossypol glands distribution pattern, nectary variation, floral attributes, resistance reactions to environment stress, pests and pathogens, etc. The 49 unique genetic stocks and introgressed derivatives coupled with novel traits were registered with NBPGR, New Delhi during 2009–2015 to protect the sovereignty of cotton genetic stock resources in the country.

Keywords: Cotton, Genepool, Germplasm, Genetic stock

1852 (P-51)

Conservation and Propagation of *Rhodiola*- A High Value Medicinal Plant of Trans Himalaya

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Rhodiola sp. (Golden root, rose root, arctic root or Shrolo), belonging to the family *Crassulaceae*, is an important medicinal plant distributed in trans-Himalayan cold desert regions in India, Pakistan, Tibet, China, Nepal and many other countries. *Rhodiola* species have been used as traditional medicines for the treatment of long term illness and weakness, in Tibet and other Himalayan region for over 1000 years. Recent pharmacological studies have showed that *R. imbricata* possess immuno-stimulatory, anticancer, cytoprotective, radioprotective, antioxidant, free radical scavenging, metal chelating, anti-lipid peroxidation, anti-hemolytic activity, dermal wound healing activity, anti-hypoxic, anti-inflammatory, anti-tumour, and adaptogenic activity. In Amchi and Tibetian system of traditional medicine, the roots are used against lung problems, cold, cough, fever, loss of energy and pulmonary complaints. Due to various anthropogenic activities and ecological imbalance this high value medicinal herb is facing a critical existence in Trans-Himalayan Ladakh region. As conservation and propagation of this wonder herb is a tedious process, therefore our present study focuses on conservation of *Rhodiola imbricata through* various biotechnological approaches which involve *in-vitro* as well as *in-situ* conservation. As germination through seed is a tedious process in fields and takes long time to develop into whole plant therefore seed germination using different media and plant growth hormone *in-vitro* have been the best method to conserve and propagate *Rhodiola.* Recent ongoing research in the plant revealed vital bioactivity in shoot/rhizome of the plant tested in different solvents. Initial preliminary HPLC results evaluated traces of bioactive compounds in *in-vitro* shoots However, the active principles in these extracts still remained unrevealed. This is the first ever study on seed germination, propagation and conservation of *R. imbricata* through various *in-vitro* techniques such as protoplast isolation and regeneration.

Keywords: Conservation, Propagation, *Rhodiola,* Medicinal Plant, Trans Himalaya

1912 (P-52)

Plant Genetic Resources in North-Eastern Region of India: Collecting Status and Future Thrusts

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The North-Eastern Hill (NEH) region of India is a centre of origin/diversity of a number of agri-horticultural crops. Although over 200 explorations had already been undertaken till 201 but still this region is a potential site for germplasm collection due to prevalence of rich diversity, high endemism. A special drive for germplasm collection was launched by the Bureau during 2011-2016. A total of 3,103 germplasm samples (190 taxa) were collected in 45 exploration trips in all eight states viz. cereals and millets (992), pseudocereals (104), pulses (265), oilseeds (107), fibres (61), vegetables (964), fruits (158), spices and M&AP (73), crop wild relatives (322) and minor economic species (57). Maximum collections were of paddy (411) followed by maize (386), chilli (138) and finger millet (112). In paddy, besides collecting germplasm of known landraces (300), trait-specific germplasm (scented, deep-water and cold tolerance) and its wild genepool were also collected. In pulses, prevalent diversity in French bean (102), rice bean (55) and pigeonpea (82) were collected. Gossypium arboreum races (26 acc.) known for various traits was collected from Mizoram and Manipur. In vegetables, rich diversity was collected in leafy mustard, chilli, brinjal, garlic, cowpea and cucurbits. Among native crops of region – buckwheat (90), job's tear (19), Perilla (50), scarlet eggplant (15), etc. was collected. Two new crops – Plukenetia corniculata (leafy vegetable) and Cucumis metulifer (salad vegetable) were published. Some rare species specific to NEH region collected for the first time are Citrus ichangensis, Vigna nepalensis, Cucumis javanicus, Trichosanthes himalensis, T. cordata,

Keywords: Plant genetic resources, North-east India, crop wild relatives,

1939 (P-53)

Utilization Pattern of Some Wild Edible Plant Biodiversity under Ethno-Agricultural System by the Tribal, Forest Dwellers and Rural People of Jharkhand

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Jharkhand is the great home of ethnic wisdom, indigenous plant-lore with rich biodiversity occurs in ambient vegetation and natural forests. Although, there are now changes according to modern life style, concept of modern cities and urbanization of the state; however still in the rural areas and hilly tracts the native people as well as forest dwellers having affinity with plant based indigenous knowledge related to meeting there day to day needs of edible and healthcare purpose. In the present communication, our emphasis is on some edible plants particularly cooked as vegetables and growing by the farmers in own methods referred as Ethno-agricultural system. It has been observed that some of the herbaceous annual and seasonal plant species usually cultivated in their farming and utilizing as traditional vegetable. Some of the potential species are *viz. Boerhaavia difusa* ('Khapra- sag'), *Centella asitica* ('Beng- sag'), *Limnophila indica* ('Hemcha-sag'), *Portulaca* spp. ('Nuni-sag', 'Jitia- sag') etc. have been observed utilized by almost tribal, rural and forest dwellers. The above plant species have also significant medicinal uses. The comparative studies on the above plants used for edible purpose and *vis-a vis* their known medicinal uses, there are interesting results have been observed. Certainly, the above species should promote for more scientific researches for validation of nutritional claim of indigenous people. Further, it has been observed that the above species are less sold in the local market in abundant availability. It is fact that the plant biodiversity utilizes by the ethnic people is also considerable under agro biodiversity. The native agro-technology, cultivation and harvesting methods, utilization pattern as alternative and supplement vegetable, details knowledge and experiences for their uses for healthcare are herewith communicated.

Keywords: Agrobiodiversity, Edible plant, Jharkhand

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825 (O-5)

Innovative Integrated Systems for Intensification of Banana, Pig and Cattle Production in Yunnan Province of Southwest China

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Yunnan is one of the biggest banana producing regions in China and is also one of the original centers of banana and its wild relatives. The landscapes have retained much of their original ecological integrity, and are suitable for the development of high-grade, top quality bananas due to temperature differences between day and night, etc. However, Yunnan, and the national and global banana industry, is facing serious challenges from fungal, soil-borne diseases, especially banana Fusarium wilt disease tropical race 4 (TR4), which is a direct threat to the income of local farmers and the banana value chain. In the meanwhile, after harvesting fruits huge biomasses of banana plants are generated which are underutilized. We have identified two potential innovation platforms on integrated systems intensification. One is “Livestock (pig)-Waste-Banana” ecological recycling production system in Yuanyang, Yunnan, China. This system has advantages of combing planting and husbandry, integrating water and fertilizer, saving resources and protecting environment. The second case is “Banana–Cattle–Waste–Banana (or other crops)” ecological recycling production system. This system has advantages of combing recycling huge banana biomass with integrating organic fertilizer, saving resources, promoting husbandry enterprises protecting environment as soil and plant health-oriented management. In order to understand the mechanism and enhance productivity and resilience in farms and rural landscapes, this innovative sustainable banana, pig and cattle integrated production system, comprehensive ecosystem services in banana plantation should be further investigated.

Keywords: Innovative integrated systems, Banana, Pig, Cattle production

852 (O-6)

Role of Veterinary Type Culture Collection in Capturing Equine Microbial Biodiversity

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Microbial repository presents excellent resource for understanding the richness in microbial diversity of animals. We present a synopsis of equine bacterial biodiversity maintained at NCVTCC in the last decade. The equine disease outbreaks of industry, defense, and farmer’s background were attended and outbreak history was collected. The pathological samples collected were brought to laboratory on ice and processed for microbial isolation. Isolates were purified and identified by phenotypic and biochemical testing. Selected isolates were identified upto species level by 16S rRNA gene cloning, sequencing, phylogenetic analysis and homology searches using 3 ribosomal databases. 392 bacterial isolates were obtained from 170 samples collected from Uttarakhand, Rajasthan, J&K, Delhi and Haryana. The identification of microbial isolates obtained from disease outbreaks in equine has lead to discovery of a diverse set of bacterial isolates, out of which many strains were hitherto unreported from India. Out of the 31 genera, 18 were Gram-negative viz., *Actinobacillus, Bordetella, Escherichia, Klebsiella, Enterobacter, Serratia, Pseudomonas, Pantoea, Kluyvera, Providencia, Citrobacter, Shigella, Comamonas, Acinetobacter, Flavobacterium, Aeromonas, Achromobacter, Ignatzchineria* and the remaining 13 were Gram-positive *viz.*, *Corynebacterium, Streptomyces, Streptococcus, Staphylococcus, Rhodococcus, Nocardia, Nocardiopsis, Microbacterium, Bacillus, Brevibacillus, Lysinibacillus, Barrientosiimonas* and *Enterococcus.* Significant pathogens previously unreported from Indian equines were *Bordetella bronchiseptica, Actinobacillus equilli,* and *Streptococcus equi* ssp. *ruminatorum*. Equines are source of important opportunistic pathogens of public-health importance. The *ex-situ* conservation for the characterization of new emerging animal microbes in clinical and epidemiological context is critical for their ecological understanding in health and disease.

Keywords: Biodiversity, Equine, Pathogens, 16S rRNA

1659 (O-7)

Partial Gene Characterization of Candidate Functional Gene Mstn Encoding Growth and Muscle Development in Trachinotus Mookalee and Trachinotus Blochii

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Aquaculture production can be enhanced by genetic improvement of fish. Quantitative trait loci (QTL) linked genetic markers can be used as a tool for marker-assisted selection (MAS) in selective breeding programs for genetic improvement of fish. Trachinotus blochii and Trachinotus mookalee belonging to carangidae family are promising candidate species for mariculture due to their attractive appearance, fast growth rate, adaptability to culture environment, acceptability to formulated feed, high domestic and international market demand. Growth is an important economic trait in all a cultured species. Myostatin (MSTN) also known as Growth Differentiation Factor-8 (GDF-8) can negatively regulate the growth of finfish in aquaculture. Molecular characterization of MSTN will help to study the association between the polymorphisms and phenotypic growth trait in finfish thereby aiding marker assisted selection and selective breeding based on phenotype. In this study partial characterization of the candidate functional gene MSTN comprising of three exons and two introns were done in T. mookalee and T. blochii. The primer pairs used to amplify MSTN gene from the genomic DNA were Myo-pro & Myo-L8, Myo-UP1 & Myo-L1, Myo-UP3 & Myo-L3 and Myo-UP5 & Myo-L5. The amplified PCR products were sequenced and subjected to homology search analysis using BLAST. The analysis showed 90-95% similarity with MSTN genes of Lates calcarifer (EF672685.1) and Lates niloticus (EF681885.1). Further studies are being carried out to characterize the complete MSTN gene, to elucidate the intron-exon boundaries and to study the polymorphisms within the gene.

Keywords: Candidate Gene, Genetic Improvement, Polymorphism

1761 (O-8)

Conservation and Sustainable Management of Seahorses (Family: Syngnathidae) in the Gulf of Mannar and Palk Bay, South-East Coast of India

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The declining seahorse population has become a global concern in much of its distributional range. However, there is an increasing demand for seahorses in Traditional Chinese Medicines, aquarium trade and curios. In India, collection of seahorses concentrated mainly in Gulf of Mannar and Palk Bay, and contributed substantially to the livelihood of fishermen. With increasing demand in international markets, there has been a targeted fishery since 1992 which expanded rapidly during 1996-1997. Consequently as catches declined, Government of India banned collection and trade of all species of syngnathids (seahorse and pipefish) and listed them under Schedule I of Indian Wildlife (Protection) Act, 1972. The study was envisaged to understand the impact of listing and to come out with policy guidance for conservation and management of seahorse. Our study from January to May, 2015 revealed a diversity of six species in the Gulf of Mannar dominated by Hippocampus trimaculatus and five in Palk Bay dominated by Hippocampus kuda. The total estimated catch in trawl ranged from 609 to 8964 numbers in the Gulf of Mannar while in Palk Bay, it ranged from 949 to 9,184 numbers. In country trawl, the estimated catch was highest in Palk Bay and ranged from 1675 to 25,864 numbers. The males of H. kuda with full brood pouch comprised 16.95 to 37.5% and H. trimaculatus from 11.54 to 34.29%, indicating a serious threat to recruitment. Although ban exists, illegal collection and trade thrives. The measures for conservation and sustainable management of seahorse are discussed in detail.

Keywords: Conservation, Management, Sea horse

34 (P-54)

Arbuscular Mycorrhiza Fungal Biodiversity in Rainfed Upland Agro-Ecology of Jharkhand Plateau, India

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Arbuscular-mycorrhiza fungal (AMF) symbiosis with plant roots promotes plant acquisition of less mobile nutrients like phosphorus, zinc etc. and imparts biotic (diseases) and abiotic (drought, heavy-metal toxicity, salt toxicity etc.) stresses tolerance. Depending on crop multiplicity and soil ecology, AMF diversity varies. A diversified AMF population is more efficient in rendering ecosystem services to plants. AMF diversity under several cropping systems in uplands was documented as a tool to manipulate native AMF activities in favor of plants. Soil samples (5-20 cm) from fields with different cropping systems under unfavorable-uplands (10-20% slope, pH 5.6-6.5), favorable-uplands (3-5% slope, pH 6.4-6.8) and medium-lands (terraced/plain, pH 6.8-7.9) of CRURRS research farm (Hazaribag, Jharkhand) were collected during mid-monsoon (August) and post-monsoon (November) in 2010 and 2011. AMF spores were isolated following standard wet-sieving-decanting method, observed under stereo-zoom microscope (20X) and identified (genus) based on morphology using INVAM description (www.invam.caf.wvu.edu/). Spore densities, relative-spore-frequencies for predominant AMF genus were computed. Infective propagule populations were monitored following standard Infection-point analysis method. Native AMF population increased in post-monsoon (November) compared to monsoon (August) irrespective of cropping systems and land situations. Spore density was highest under direct seeded rice (DSR) and pigeon-pea in unfavorable uplands followed by that of DSR-chick-pea sequence-cropping in favorable uplands. Both unfavorable and favorable uplands were dominated by genus *Glomus* with that of *Gigaspora* in medium-lands. The results indicated anaerobic adaptation of *Gigaspora* and suggested developing native *Glomus* and *Gigaspora* based inoculums respectively for uplands and medium-lands.

Keywords: Arbuscular-mycorrhiza fungi, Diversity, Upland agro-ecology

56 (P-55)

Documentation of Kashmir Geese Germplasm and Rearing Practices

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A study on Kashmir Geese was undertaken to document their morphologic, morphometric, anatomic, behavioural, physiological, biochemical and production parameters along with the product quality, parasitic load, rearing practices and socioeconomic status of their rearers. Geese-rearing was predominant around water bodies. Some birds showed presence of knob, dewlap and paunch. Ample variation was seen in plumage, eye and bill colour but not in shanks. Males had significantly higher body weight, larger bill, knob and neck dimensions, and longer body-length and wing-span but females had longer jejunum-length. Copulatory organ in males was spiral and left testicle significantly larger. 19 cervical, 5 thoracic and 7 coccygeal vertebrae, 9 pairs of ribs, boat-shaped sternum and U-shaped clavicle was seen. Different behaviours and variation in vocalizations were recorded. E.C.G. revealed P, QRS & T waves with inverted QRS complex. Significant difference between sexes was found in heart-rate and temperature but not in haemato-biochemical parameters. Parasitogical study revealed presence of various eggs and parasites. Fast juvenile growth and low egg-production was recorded. Significant difference was seen in slaughter and cutability characteristics. Geese egg and meat was likable and of good quality. Rearers had varied occupations, land and livestock holdings, flock-size and preferences, along with different practices of rearing, housing, feeding, incubation, sex-determination and identification methods. Eggs were kept for incubation while geese sold through middlemen in city. The study provided a baseline data for characterization of Kashmir Geese and future geese development programmes.

Keywords: Characterization, Germplasm, Kashmir-Geese

187 (P-56)

Understanding Species Diversification of Parasitic Hymenoptera Associated with Agroecosystem: Current Knowledge and New Approaches

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Diversity of parasitoids, though eminent in biological control, is taxonomically challenging as many taxa are extremely tiny (average size < 2mm), morphologically homogeneous, and highly speciose. The parameters chosen for analyses− traditional taxonomy, associated hosts, host-parasitoid specificity, and molecular characterization. Diversity estimates revealed that 82.67% of braconid diversity is yet to be explored in India. Hence current approach of combining three different sets of data (morphology, host records, and molecular phylogenetic analyses) were integrated in order to generate accurate boundaries between species for highly speciose genera. First successful attempt was made for genus *Glyptapanteles*. The study based on 60 populations reared from 35 host species from 11 states and one Union territory revealed 26 provisional *Glyptapanteles* species within 8 species-groups which were previously unrecognized (Gupta et al. 2016). An account of 70 cases of egg, larval and pupal parasitism were recorded across four states (Karnataka, Kerala, Maharashtra and Goa during 2010-2016). Parasitism rate was highest for Hesperiidae (62.86%) followed by Lycaenidae (22.22%) and Nymphalidae (11.11%). Percent parasitism was high by Braconidae (56.52%) and low by Eulophidae (10.87%), Tachinidae (8.69%), and Ichneumonidae (8.69%). Species diversity unveiled (number of species in parentheses): Braconidae (26), Tachinidae (4), Eulophidae (5), Ichneumonidae (4), Chalcididae (3), Encyrtidae (2), Eurytomidae (1) and Pteromalidae (1). Forty six species of parasitoids were recovered which exclusively attacked butterflies. The result indicated that parasitoid host specificity was highest in Braconidae and lower in Tachinidae, Eulophidae and Ichneumonidae. This study extrapolates a new range of diversity estimates of the parasitoid species richness.

Keywords: Diversity, India, Parasitoid, Phylogeny, Taxonomy

467 (P-57)

Morphometric Characterization of Teressa Goat (*Capra Hircus*) an: Indigenous breed of A&N Islands, India

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Goats (65324) constitute about 42.21% of the total livestock population (154733) in the Andaman & Nicobar Islands and are an integral part of the livestock system. Teressa goat, an indigenous breed from this island has recently been included in the goat breed of India. With the prime objective to conserve and characterize the indigenous germplasm of this island, the study on characterization of the Teressa goat for its phenotypic characters, feeding and management system and population status was carried out. Results revealed that the Teressa goats were mainly reared by the Nicobari Tribal community and were concentrated in Southern group of Islands. These goats were reared under free range and/ or semi intensive system. They were fed with locally available tree fodders and coconuts. Morphological characters revealed that these goats are generally tall, sturdy, brownish or dark tan or black or white in colour with white and black patches. Black hairs on dorsal midline up to the tail, black colored muzzle, eyelids and hoofs. Peculiar white patch/ line starting from inner canthus of both eyes or from eye brows and extending up to nostrils or mouth. Body weights (kg) at birth, 3, 6, 9, 12, 24 months were 1.40 ±0.07, 7.61 ±0.11, 14.46 ± 0.26, 23.54 ± 0.31, 39.85± 1.03 respectively. The population was higher in Car Nicobar and Teressa islands and presently the population is increasing steadily. The Teressa goats showed higher twinning rate and castrated male showed higher body weight than the uncastrated goats. From the results, it is concluded that the Teressa goat is a precious germplams of the A & N Islands, and efforts for conservation of the indigenous breed should be strengthened by the CIARI and local Animal Husbandry Department.

Keywords: A&N Islands, Characterization, Teressa goat.

535 (P-58)

Diversity of Rhizobia in Food Legumes Growing in Central & Sub-Himalayan Region of India

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Cicer arietinum, *Lens culinaris* and *Trigonella foenum graecum* are important food legumes across globe. It is known that each legume species nodulates with specific rhizobia. The objective of present study was to unravel the rhizobial partner important for effective nitrogen fixation in these legumes in Central and Sub-himalayan region of India. The rhizobia from each of the three legumes were investigated using polyphasic approach. In a pot trial all isolates nodulated their original host. Their genetic diversity was assessed on the basis of amplified rDNA restriction analysis, polymorphism in repetitive sequences, symbiotic genes and full 16S rDNA sequencing. Classically *Cicer* symbionts are identified as *Mesorhizobium* but in this study as *Sinorhizobium* and *Burkholderia*. *Lens culinaris* rhizobia fall in *Rhizobium leguminosarum* and *R. pisi* clade as expected but a few in *Mesorhizobium* and *Burkholderia* clade also. Full 16S rDNA sequence comparisons revealed that rhizobia nodulating *C. arietinum*, *L. culinaris* and *T. foenum graecum* fall very close to clades representing existing species and may represent new biovars of existing species.

Keywords: Diversity, Food legumes, Phylogeny, Rhizobia, 16S rDNA sequencing

653 (P-59)

Genetic Variability, Character Association and Path Analysis in Cowpea [*Vigna unguiculata* (L.) Walp]

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In the present study forty genotypes of cowpea were evaluated for different horticultural traits for genetic variation, character association and cause-effect analysis. All the ten characters under study differed significantly among the genotypes. High to moderate GCV and PCV values were recorded for plant height, number of peduncles and pods per plant, pod length, pod weight and pod yield per plant. Higher estimates of broad sense heritability coupled with the higher genetic advance was obtained for plant height, number of peduncles per plant, number of pods per plant, pod length, pod weight and pod yield per plant. Highly significant correlation coefficient with pod yield per plant was observed for number of branches per plant, number of peduncles per plant and number of pods per plant, pod length and pod weight at genotypic and phenotypic levels. The number of peduncles per plant exerted the maximum positive direct effect on pod yield followed by pod length, number of branches per plant and pod weight. A positive indirect effect of number of peduncles per plant on pod yield was obtained through number of branches per plant and number of pods per plant. The present study indicated that pod length, pod weight and number of pods per plant should be given due importance in selection programmes for yield improvement in cowpea.

Keywords: Correlation Coefficient, Cowpea, Genetic Variability and Path Analysis.

697 (P-60)

Buffalo Genetic Resources of India

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The diversity of farm animal genetic resources is vital to all agricultural systems and more particularly in the developing countries. At present, there are about 74 buffalo breeds are available in the world. In India, so far 13 buffalo breeds have been identified, characterised and registered by ICAR-NBAGR, Karnal. Murrah breed of buffalo is the predominant breed of buffalo in India followed by Surti, Mehsana and Jaffarabadi. Murrah breed has been the breed of choice for improvement of Buffalo genetic resources. Toda and Bhadawari breeds animal are low in numbers hence considered threatened buffalo breeds. Besides well-known breeds, there exists some less known buffalo populations such as Gojri, Tarai, Chhattisgarhi, Dharwadi and Bargur. World buffalo population is estimated to be 198.09 million, out of which 192.28 million (97.06%) of them are in Asia. In India, their population is 108.7 million, which constitutes about 56.53% of total world buffalo and 21.23% of the total livestock population in India. During 2007-12 buffalo population had shown an overall growth of +3.19% and females have grown with +7.99% whereas the males have shown a negative growth (-17.83%). Among the buffaloes both in milk and dry females have shown a positive trend in percent change from 2007-12 with 2.61% and 11.41%, respectively. Buffaloes are an important source of milk, meat, draft power and manure in India and immensely contributes to milk industry, therefore it is imperative to evaluate and improve this important animal genetic resource (AnGR) of India.

Keywords: AnGR, Buffalo, Breed, Diversity

735 (P-61)

Assessment of Phenotypic Variability in Indigenous Cattle of North-East States of India

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The north-east states comprise only 6.57% of total cattle population of the country. There is no registered breed of cattle from the region except Siri in Sikkim. Most of the cattle in the region are non-descript and need description. An attempt has been made to record variability available in indigenous cattle of the region. Study incorporated 364 cattle of Tripura, 363 cattle of Manipur, 237 cattle of Mizoram, 218 cattle of Meghalaya and 68 Siri cattle of Sikkim. Number of Siri cattle declined drastically from 79000 to 12171 during the years 2003 to 2012 and breed falls in risk under vulunerable category of risk status. The State Animal Husbandry Department, Sikkim has started a genetic improvement program on the breed in the field, which needs to be strengthened. Cattle in this region were reared for milk, meat, bullock power and manure. Animals were reared mainly on extensive system of management. Animals were smaller in size with cylindrical type of body. The coat colour varies in different colours and shades i.e. brown, grey and black. Nine different morphometric traits were recorded and compared biometry among the states. Daily milk yield ranged from 0.5 to 5.0 kg. The indigenous cattle of the region showed uniformity in physical characteristics. It was observed that in some places, cows had good potential for milk production especially in the difficult areas. Therefore, there is urgent need to study these cattle in detail, register as breed if suitable and plan genetic improvement programs to improve the productivity.

Keywords: Indigenous cattle, Siri, Physical characters, Performance

801 (P-62)

Characterization of Indigenous Dog Biodiversity

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Dog, first domesticated animal by human being and kept for guarding, hunting and as companion animal. There are some dog breeds in India viz., Combai, Chippiparai, Rajapalayam, Rampur Hound, Mudhol Hound, Indian Mastiff, etc., which are being used for shepherding of livestock and guarding farm and farm houses. So far adequate attention has not been given for characterization of Indian dog. Keeping this in view for the first time survey methodology was developed for characterization of Indian dog breeds, Rajapalayam and Chippiparai breeds were characterized comprehensively. Rajapalayam dogs are medium in size with compact body, tucked-up abdomen, white coat colour / pink skin, nostrils and eyelids, semi-dropping ears and straight top line. Chippiparai dogs are medium in size with coat colors varying from fawn to dark brown, brownish black and black. Rajapalayam dogs (22.064±0.45 kg) are significantly heavier in body weight than Chippiparai dogs (20.52±0.35 kg), and observed a highly significant difference in most of the morphometric traits between the two dog populations. Karyology revealed common fundamental chromosome number of 2n=78. The overall PIC by microsatellite analysis was observed to be 0.7230±0.02 and 0.7146 ±0.02 in Rajapalayam and Chippiparai dog respectively. The overall F_{IS} value was 0.0494±0.03 and 0.0472 ±0.02 which is higher than zero indicating a wide heterozygosity of the breeds which may be due to planned matting by the breeders to avoid inbreeding. These unique canine germplasms needs to be documented and registered at National level, which will be beneficial for dog owners, dog breeders and Kennel clubs.

Keywords: Biodiversity, Characterization, Chippiparai, Dog, Rajapalayam

923 (P-63)

Faunal Diversity of Fishes, Crustaceans and Molluscs in Valapatnam River in Kannur District of Kerala (South India)

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Valapatanam river (colonial name Baliapatam river) is the longest river of Kannur district of Kerala (South India). It has a length of 110 km. The river supports a sizeable fishery in the region. In spite of its importance only very few studies were conducted on the fish and fisheries of the river system, in the past. The present study was conducted for two years (from January 2014 to December 2015) with the objective of understanding the diversity of fishes, crustaceans and molluscs and to get an idea about the exploited fishery resources of the river system. 83 species of fin fishes, seven species of crustaceans and six species of molluscs were observed in the river system. These included five species each of endangered and near threatened category as per IUCN categorization. Twenty species of fin fishes, four species of crustaceans and one species of mollusc contributed to the exploited fisheries of the river system. The annual average landing from this river was estimated to be 173.08 metric tonnes (t). Fin fishes contributed 90.67 t (52.39%) followed by crustaceans with 51.36 t (29.67%) and molluscs with 31.05 t (17.94 %). The highest landings were recorded during the pre-monsoon season (56.44%) and the lowest during the monsoon season (14.05%). Alien fishes, tilapia (*Oreochromis mossambicus*), common carp (*Cyprinus carpio*), African cat fish (*Clarias gariepinus*) and Gangetic carps (*Catla catla, Labeo rohita and Cirrhinus mrigala*) were observed to contribute to the fishery substantially (27.64%). In general the fish landings decreased from downstream to upstream portion of the river.

Keywords: Exploited fishery, Fish diversity, Fish resources, Valapatnam river

968 (P-64)

Symbiotic Efficiency of Slow and Fast-growing Soybean Rhizobia of Central India

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Soybean rhizobia are pre-dominantly slow growing but fast growing strains that evolved from natural populations have been reported globally including from several locations in India but have not been evaluated. The symbiotic effectivity of three slow and three fast-growing rhizobial strains isolated from Vertisols of Central India was evaluated on soybean var. JS 97 52 in sterilized sand microcosms in a green house. The N content of nodules, roots and shoots was determined by Kjeldahl method to calculate N uptake. Biological nitrogen fixation was computed form the difference in total plant N in the inoculated and uninoculated series. The data were statistically analysed by Student's t-test to calculate values of least significant difference at p=0.05. At 40 days growth, there was variation in nodulation parameters and growth of soybean with both types of rhizobia but overall, the slow growers were superior to fast growers with respect to nodule number (56%), nodule dry matter (25%), shoot dry matter (11%) and total nitrogen uptake (22%). The slow-growers (genetic homology to *Bradyrhizobium japonicum*) fixed ~25% more nitrogen than fast-growers with homology to *Rhizobium* (*Agrobacterium*) *radiobacter*. The results have very important implications for strain selection during biofertilizer production to maximize biological nitrogen fixation.

Keywords: Nitrogen fixation, Nodulation, Symbiosis, Vertisols

979 (P-65)

Yak: A Declining Alpine Treasures and Genetic Resources for the Future

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Yaks are mountain cattle and are found 3000-5000 meter above sea level in trans-Himalayan region of Ladakh, Arunachal Pradesh, Sikkim, Himachal Pradesh, West Bengal and Uttarakhand of India. The yak population in India is estimated 76,237 according to 19th livestock census which is decline by 7.6% as compared to previous census. The farmers have reared this animal for milk, meat, wool and transportation purpose. Although Indian yaks are sparsely characterized at phenotypic level no systemic documentation was done to call these group of yak as breed. Based on the available information yak found in West Kameng and Tawang district of Arunachal Pradesh are most pure and unique in the world. Present study systematically documented phenotypic characteristics of Aruanchali yaks which are reared under semi-migratory system and 85% of yaks are black in color and lactating female producing on an average 1.3 kg milk per day which is very poor but substantial to prepare different milk products due to high fat (7.45%) percentage. The first calving for Arunachali yak is observed very late at the age of 43-45 months. Although yak milk and wool product are treated as valuable entity for its uniqueness but decreasing population trend of yak has been the serious concern. Yak which is recognized as one of the critical and endangered mountain species need urgent attention for *in situ* and *ex situ* conservation as well as breed characterization. It also needs empowerment of farmers with scientific husbandry and economical remuneration for conservation.

Keywords: Breed, Conservation, Phenotype, Migratory, Yak,

994 (P-66)

Positive Selection and Concerted Evolution Typify the Dynamics of Meiotic Recombination Regulator PRDM9 in Small Ruminants

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Meiotic recombination contributes to increase in genetic diversity, exclusion of deleterious alleles and proper segregation of chromatids. PRDM9 has been identified as the gene responsible for specifying the location of recombination hotspots during meiosis and is also the only known vertebrate gene associated with reproductive isolation between species. PRDM9 encodes a protein with a highly variable zinc finger (ZF) domain which varies between as well as within species. In the present study, zinc finger domain of PRDM9 on chromosome 1 was characterized for the first time in 15 goat breeds and 25 sheep breeds of India. Remarkable variation in the number and sequence of ZF domains was observed. The number of ZF repeats in the ZF array varied from 8 to 12 resulting in 5 homozygous and 10 heterozygous genotypes. The number of different ZF domains was 84 and 52 producing 36 and 26 unique alleles in goats and sheep respectively. The posterior mean of dN/dS or omega values were calculated using Codeml tool of PAMLX to identify amino acids which are evolving positively in goats and sheep as positions -1, +3 and +6 in the ZF domain have been reported to experience strong positive selection across different lineages. Our study identified sites -5, -1, +3, +4 and +6 to be experiencing positive selection. Small ruminant zinc fingers were also found to be evolving under concerted evolution. Put together, our results reinforce vast diversity of PRDM9 in goats and sheep which is in concert with reports in many metazoans.

Keywords: PRDM9, Zinc fingers, Diversity, Goat, Sheep

997 (P-67)

Genetic Variability and Phylogenetic Relationship Establishes Distinctiveness of Local Manipur Poultry of India

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India is rich in chicken biodiversity with 16 distinct registered breeds in addition to many more not characterized and accredited so far. It is imperative to characterize all the poultry populations of the country so as to have better conservation options. Thus, the present study was planned to ascertain genetic diversity of local poultry population of Manipur (*Kaunayen*) and to establish its relationship with registered poultry breeds of India by using 24 microsatellite markers. Large number of observed alleles (212) and heterozygosity (0.66) indicated high genetic diversity. Mean number of alleles observed in *Kaunayen* chicken were 8.83±0.64 and ranged between 4 (MCW250 and LEI174) and 15 (LEI120). Mean effective number of alleles was significantly less (4.11±0.38) than the observed number of alleles. The maximum observed heterozygosity (1.0) was observed in MCW262 locus and the minimum (0.368) in LEI166. The expected heterozygosity (0.706) was more than the observed heterozygosity (0.664±0.036) which points to heterozygote deficiency and was also reflected in positive FIS estimate (0.06) for the population. Non-significant heterozygote excess on the basis of Infinite allele model and Two-phase model along with a normal 'L'-shaped distribution of mode-shift analysis test, indicated an absence of bottleneck. Phylogenetic reconstruction on the basis of genetic distance places *Kaunayen* chicken as a distinct population with respect to other poultry breeds of India. All analysis showed that a significant amount of genetic variation is maintained in local *Kaunayen* chicken which is distinct from the recognized breeds of India and needs recognition as a breed.

Keywords: Bottleneck, Genetic diversity, Indian poultry, Microsatellite markers

1072 (P-68)

Growth Potential of Avikalin Sheep at Farm Conditions of Rajasthan

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Avikalin was evolved by stabilizing the exotic inheritance at 50% level in the crosses of Rambouillet x Malpura at ICAR-CSWRI, Avikanagar. Wool produced by Avikalin is suitable for manufacturing superior carpet. The objectives of wool quality traits were achieved and efforts were made to exploit the growth potential to develop as dual type sheep. Avikalin sheep are being reared under semi-intensive management and growth data of 718 lambs born (2012-16) were analysed. Overall means of body weight at birth, 3, 6, 12 months of age were 2.92, 15.92, 25.18, 31.39 kg, respectively. Corresponding values for male lambs were 3.01, 16.73, 27.12 and 34.01 kg, respectively. Birth weight ranged between 2.87 to 3.05 kg during the different years. Three- month body weight and six-month body weights ranged from 13.15 to 17.89 and 19.39 to 29.54 kg, respectively. Twelve month body weight ranged between 24.96 and 37.22 kg. Effect of year of birth was significant on body weight at different ages. Overall means of average daily gains were 114.4 and 102.9 g for the period 0-3 months and 3-6 months respectively. Avikalin can be successfully reared under the semi-intensive management up to six month of age to attain a good body weight of more than 25 kg and greasy fleece yield of around 800g with improved quality can be obtained before selling the animals for slaughter. Avikalin has been used as an improver breed and has great demand particularly in southern part of India to upgrade nondescript sheep for improving mutton production.

Keywords: Avikalin, Dual type sheep, Mutton production

1147 (P-69)

Morphology and ITS Based Characterization of *Colletotrichum Falcatum* Isolates Collected from South Gujarat

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Although the red rot disease of sugarcane (*Saccharum officinarum* L.) caused by *C falcatum* is prevalent in east coast zone and north central/west part of India, it has also spread to the peninsular part like Gujarat. South Gujarat is a major sugarcane cultivating area but information is not available on pathotypes of *C. falcatum* prevalent, if any. In present research nine isolates obtained from different places and cultivars were characterized for morphological features and internal transcribed spacer (ITS) sequence. All isolates had characteristic fast-growing sparse and fleecy aerial mycelia on PDA with falcate conidia (length x width: varied from 20.0 X 3.89 to 25.52 X 5.34 µm) and blackish to orange acervuli with setae (length x width: varied from 112.37X 2.78 to 167.66 X 6.73 µm). They could divided into two groups on the base of morphology; P1, dense mycelia with concentric growth and P2, sparse mycelia with uneven growth. Genomic DNA isolation followed by PCR amplification with ITS1 and ITS4 primer produced ~550bp amplicons for all isolates. Molecular phylogeny generated by ITS confirmed the variation in isolates and mainly grouped into two clusters; cluster 1 contained CoC671 isolates (cfNAV and cfPAR) and Co86002 isolate (cfTIM). Other isolates cfMAD, cfKAM, and cfMAR were grouped into cluster 2. Remaining isolates did not fall into any cluster. Isolate cfGAN, collected from Co86032 was found highly diverse of all the nine isolates. Furthermore, result indicates that there were no correlation between morphology and ITS based groups.

Keywords: *Colletotrichum falcatum*, ITS, Morphology, Red rot, Sugarcane

1157 (P-70)

Studies on Genetic Diversity using Mitochondrial Genes in Brown Trout (*Salmo salar*) Populations in India

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Brown trout was introduced in Indian high altitude rivers during 18th Centuryby the British for sport. This species also has the potential for farming in Coldwater regions of the Himalaya. Since its dissemination to Indian rivers, there is no information available on the genomics of this species in the country. We had preliminarily initiated the analysis of geographically isolated populations of Brown trout using mitochondrial genes, Cytochrome Oxidase I (COI), Cytochrome b and ATPse 6/8from Jammu & Kashmir, Himachal Pradesh, Sikkim and Uttarakhand. These genes were selected from whole mitochondrial genome sequence of brown trout (developed and characterized by ICAR-DCFR, Bhimtal). The genomic DNA of 10 samples each from 4 populations were used for PCR amplification ofthree mitochondrial genes which were further sequenced. The sequences were aligned, Annotated, and analysed using CLC GenomicsWorkbench 7.5.2. Furthermore, the sequences were examined for phylogeny using maximum likelihood method available in MEGA 7.0. The results obtained from the three genes showed very likeliness/or identity within individuals and among all the populations. We could observe very fewer variations in their nucleotide sequences. Though the populations were from geographically isolated drainage systems, the present findings indicated to have a common ancestor and a possible genetic bottleneck in the brown trout populations.

Keywords: Brown Trout, Genetic Variability, Mitochondrial Genes, Wild Populations

1206 (P-71)

Basic Protocols for Stock and Mass Production of Three Species of Calanoid Copepods Suitable as Live Feed for Fish Larvae

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Copepods are the most abundant and most popular and nutritious natural food fish larvae. Unfortunately, copepods are not popular in hatchery use mainly due to the difficulties in mass production. CMFRI has standardised the technology for stock and mass production of three copepods (*Acartia spinicauda, Pseudodiaptomus serricaudatus* and *Temora turbinata*) and consistently producing in large scale and utilising the same for larval rearing in marine fin fish hatcheries. The first part of the culture is isolation and purification of the copepods from wild collections. Wild collections always contain a mixture of thousands of organisms and individual species wise isolation is essential using a stereozoom microscope and base culture of these can be started in 1-2 litres transparent beakers under the indoor conditions. After developing the base inoculum for about a month, the culture can be upgraded to 30-50l bins which can be permanently maintained as stock culture. The stock culture can be maintained for at least 2-3 months period and after every three months fresh stocks should be prepared from the stock in a fresh container. The stock of 20-30 litres can be used as inoculum for 1000-3000 litre tanks and within 15-20 days tanks will be ready for stocking fish larvae. Aeration, water exchange and waste removal are essential for stock culture and mass culture. Salinity, 30-35ppt, temperature 24-29°C, pH 8-8.5 and 12hr normal light conditions are ideal. Mixture of algae *Nannochloropsis oculata* and *Isochrysis galbana* in the ratio 2:1 and 10000-20000 cells/ml is ideal for feeding.

Keywords: Copepods, Live feed culture, *Acartia spinicauda, Pseudodiaptomus serricaudatus*, *Temora turbinata*

1212 (P-72)

Isolation and Characterization of Plant Growth Promoting Microbes from Rhizospheric Soil of Chickpea (*Cicer Arietinum*)

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Plant growth promoting rhizobacteria facilitate plant growth and development by enhancing the uptake of nutrients by plants. The rhizospheric soil of plants are rich source of PGPR which could be isolated and exploited as bio-fertilizer for increasing crop production. In the present study, rhizospheric soil of Chickpea was explored for the presence of microbes having plant growth promoting activities. Four bacterial strains were isolated and characterized for their morphological, biochemical and nutrient mobilization abilities on plates.These isolates were screened in vitro for their plant growth promoting traits like production of indoleacetic acid (IAA), ammonia (NH3), hydrogen cyanide (HCN), siderophore and phosphate solubilization. Isolates were also tested for their Temperature, Salinity, pH and Drought tolerance. The molecular characterization of these isolates on the basis of 16S rRNA revealed that they belong to genus *Azotobacter, Bacillus* and *Pseudomonas*. The growth promoting ability of these isolates were tested in pots under field conditions by inoculating the Amaranthus seeds with isolates for four hours. It was observed that treated seeds revealed higher germination percentage and plant vigour than untreated seeds.This study demonstrated that PGPR isolated in this study could be used as a non-polluting bio-fertilizer useful in the development of sustainable agriculture.

Keywords: PGPR, Rhizosphere, Indoleacetic acid, Biofertilizer

1221 (P-73)

Freshwater Fish Genetic Resources of Goa - Mapping and Baseline Data

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Of the states in Peninsular India with rivers originating in the Western Ghats, Goa remains the least explored. Located on the West coast between Karnataka and Maharashtra, Goa is drained by two major river systems, Zuari and Mandovi, which share an estuary, in addition to few minor rivers. Some species reported from Goa are poorly known due to the lack of specimens in collection. We conducted explorative surveys to generate baseline data on the freshwater fish genetic resources of Goa. 14 sites covering the variety of habitats in these rivers sampled extensively using different gears over a period of two years, 2013 and 2014. the collected specimens were documented in the field and voucher specimen and tissue samples were preserved. Data on habitat and distribution were also recorded. Barcodes were generated from rare and endemic species to confirm the species identities. The exploratory surveys yielded a total of 55 species of freshwater fish, under 44 genera, in 18 families. In addition interviews of local fishermen revealed the presence of 6 additional species not represented in our collection. Out of these, 27 species are utilised by local residents for food. 21 species have wide spread distribution, while others have restricted distribution. The data generated suggests freshwater habitats in Goa support highly diverse ichthyofauna, which need to be taken account in the planning for conservation and sustainable use.

Keywords: Conservation, Genetic Resources, Goa, Ichthyofauna, Western Ghats

1231 (P-74)

Effect of an Artificial Fish Habitat on Fish Community Structure in a Coastal Ecosystem

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The fish communities in an ecosystem are structured through the local habitat conditions and the environment. In this study, fish communities of an artificial fish habitat (AFH), a 60 year old sunken ship, SS Rita and adjacent natural reef patches in Grande Island, Goa along southwest coast of India were monitored from 2013 to 2016. To compare the fish communities in the artificial fish habitat and natural reef patches, the fish assemblage data were subjected to multivariate analyses including permutation multivariate analysis of variance, analysis of similarity, similarity percentage analysis and non-metric multidimensional scaling. The results suggest that the AFHs contained greater species richness and abundance, with more diurnal fish communities than nocturnal fish communities. The feeding guilds of artificial fish habitats were different from the natural reef patches. The multivariate analyses demonstrated that the AFHs have distinctly different fish assemblages from the natural reef patches. The fish community structure has also revealed that AFHs hold significantly higher abundance and diversity of ecologically vulnerable species compared to natural reef patches. The greater complexity and availability of different structural habitats in AFHs might have resulted in the greater diversity and abundance of fish communities in the habitat. For protection of these AFHs, there should be adequate policy initiatives from the side of the government.

Keywords: Artificial fish habitat, SS Rita, Fish communities, Feeding guild

1296 (P-75)

Understanding the Effect of Cutting on Flowering Phenology in Tropical Forage Grasses

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Grasses play a crucial role in the sustenance of livestock, wild life as well as maintaining the biodiversity of the ecosystem. The natural spread of these range species occurs through seed. The human intervention through cutting has profound effect on flowering phenology of grass species. Eight different range grass species with good forage value were evaluated for their flowering response to cutting. The morphological characters *viz*., tussock diameter, perimeter, panicle length and weight, spikelet number and seed to ovule ratio were recorded along with inflorescence density during flowering period. The changes in the antioxidant enzyme activities and proline content were estimated with respect to cutting in all these grasses. Cutting has positive effect ($p<0.05$) on the number of spikelets and seed setting percentage with highest values observed in *Pennisetum pedicellatum* (415 & 96% respectively). The inflorescence density was more in cut plants and a shift in the peak flowering density was noticed as a result of cutting. Cutting has resulted in higher antioxidant activity and proline content across the species indicating the stress. The stress resulted due to cutting has also manifested into earlier flowering and increased inflorescence density. Thus, cutting has a positive effect on increased seed formation in these grass species.

Keywords: Biochemical changes, Cutting, Grasses, Seed setting

1347 (P-76)

Functional Diversity Among Bacterial Community in Phumdis of Loktak Lake of Manipur State

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Loktak lake is the largest freshwater lake in Northeast India and play an important role in the economy of Manipur. It is also known as the floating lake in the world due to large amount of floating biomass on its surface. Phumdis are unique niche from microbial diversity perspective as these floating bodies are heterogeneous mass of vegetation, soil and organic matter at various stages of decomposition that has been thickened into solid form. Identity of culturable bacterial diversity of the lake was analyzed on the basis of their morphology, biochemical features and molecular analysis. Ninety five bacterial isolates were selected and functional characterization for different enzyme like cellulase, amylase, xylanase, pectinase and protease were performed. Among these isolates, 14 were positive for cellulase, 27 for amylase, 16 for protease, 8 for xylanse and 1 for pectinase activity. The plant growth promoting traits and biocontrol activity against *Macrophomina phaseolina* (causing charcoal rot in soybean) was assessed by employing standard techniques. Twenty isolates were showing siderophore production and seven were showing phosphate solubilization. Further, the selected isolates were identified using 16S rDNA sequence similarity and fatty acid methyl ester (FAME) analysis. Three of the isolates- *Bacillus subtilis* LLP-2, *Bacillus subtilis* LLP-4 and *Serratia marcescens sub sp. sakuensis* LLP-32 were positive for most of the tests performed. *Bacillus subtilis* LLP-2 showed prominent production of enzymes, siderophore and inhibited *Macrophomina phaseolina*. The above results indicate that these three bacteria could be utilized in agriculture for organic matter decomposition and enhancing yield of crops.

Keywords: Loktak Lake, Phumdis, Culturable bacterial diversity, *Bacillus subtilis,*

1410 (P-77)

A Comprehensive Study of Simple Sequence Repeats (SSRs) from the Genome of the *Exiguobacterium Profundum* PHM 11

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Increasing environmental perturbations has largely limited the production of important agricultural crops. To get the enhanced production of vegetables and other crops under abiotic perturbations a number of environment friendly efforts are ongoing by employing the novel plant growth promoting microorganisms. A strain of Exiguobacterium profundum PHM 11 that has shown a number of plant growth promotion traits, salinity and temperature tolerance up to 2.5 M (NaCl) and 45^o C respectively was explored to get the insights about the microsatellites of its genome through different in silico approaches. The presence, density and relative abundance of simple sequence repeat (SSR) markers in PHM 11 were studied. The analysis revealed the occurrence, relative abundance, and density of microsatellites in PHM 11 genome. In general, relative abundance and density of SSRs is not co-related with the genome size; however, positively correlated with the G + C content of the genomes. In this study, a total 3005 SSRs were identified in 2.92 Mb genome of PHM11. Among different classes of repeats; the penta-nucleotide repeats were most abundant in the genome and accounts for ~65.75%, followed by hexa-nuceotide repeats of ~28.75%, mono-nucleotide repeats of ~3.89% while tetra-nucleotide repeats were found to be least ~1.59%. The total relative abundance and relative density of SSRs is 1029 and 10951 respectively. Present *in silico* study provides useful insights about the microsatellites for genotypic fingerprinting and development of diagnostic markers for *E. profundum* and its comparison with other related strains.

Keywords: *Exiguobacterium profundum*, Genotypic fingerprinting. Relative abundance, Relative density, Simple Sequence Repeats

1420 (P-78)

Bacterial Diversity of Municipal Waste; Potential for Waste Management and Plant Growth Promotion

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Growth of population, increasing urbanization and technological innovations has contributed to an increase both in the quantity and variety of solid wastes generated by industrial, agricultural and domestic activities. These solid wastes pose major environmental and ecological problems. The eco friendly management of this environmental pollution is a greatest challenge to the scientists. Bioremediation through application of microorganisms in this context has got an age over other available technologies. Hence there is an immense possibility to screen effective bacterial strains from waste dump sites with valuable applications. In the present study, isolation of bacterial strains from municipal waste of Dafi, Varanasi (Lat. 25.25 & Long. 83.01) was performed with the objective of diversity analysis, evaluating their hydrolytic capacities and suitability for use in bioconversion of specific substrates. A total 34 bacterial morphotypes were isolated which were phenotypically and biochemically characterized. All the isolates were screened in specific culture media for the production of various hydrolytic enzymes. It was found that 22 strains exhibited cellulolytic activity, 17 had proteolytic activity, 25 had amylolytic activity and 21 had xylanolytic activity. These isolates were able to tolerate higher concentration (50-1000 ppm) of heavy metals such as Cr, Cd, Cu and Ni. On the basis of 16S rRNA gene sequencing the taxonomic position of the bacterium was confirmed as *Brevibacillus, Fictibacillus, Ornithinibacillus, Lysinibacillus, Bacillus subtilis, Acinetobacter, Isoptericola and Agromyces.* These results have increased the scope of finding of effective bacteria strains from municipal waste which could be vital source for the industrially useful molecules.

Keywords: Municipal waste, Biodegradation, Hydrolytic enzymes

1439 (P-79)

Nutritional Study of Local Fodder Species in Ahmednagar District of Western Maharashtra

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Most commonly observed fodder grass and tree species grazed by livestock were collected for determining the nutritional quality through proximate analysis in the laboratory. The local grasses species includes *Dicanthum annulatum, Setaria intermedia, Themeda triandra, Heteropogon contortus, Indigofera cordifolia, Apluda mutica, Cymbopogon martini, Tephrosia purpurea*. Among the tree species *Melia azadarach, Azadirachta indica, Prosopis julifera, Grewia asiatica, Clerodendrum multiflorum* were the major tree species commonly available as fodder source. The analysis report indicated that crude protein ranged from 5.61 to 15.46%, crude fiber 18.09 to 34.87%, ether extract 1.00 to 3.24%, Ash 6.44 to 21.56 % and silica was less than 5.31%. It has also indicated that the available fodder species are needed to be selected based on nutritional quality for further multiplication. This study highlighted the importance of local fodder species including grasses, legumes, bushes and trees raising the livestock with low inputs at field conditions. The grass and tress species found in hilly regions are showing tremendous variation in nutritional composition.

Keywords: Fodder species, Nutritional analysis

1479 (P-80)

Fish Diversity in Two Floodplain Wetlands in West Bengal with Implication for Conservation of Indigenous Fishes

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Wetlands plays an enormous role in rural livelihoods and environment as they serve a wide range of functions, including ecosystem balance, flood control, water purification, protection from natural disasters, sources of livelihood, habitat for wildlife, fishes, aquatic plants and animals. The role of agro biodiversity in floodplain wetlands especially the indigenous fishes are significant as thousands of fishermen depend on these water bodies for their livelihood.The present study aimed to investigate the indigenous fish diversity in two floodplain wetlands, Khalsi (seasonally open) and Akaipur (closed) in West Bengal. Indigenous fishes from Khalsi were represented by 30 species whereas in Akaipur only 18 species were recorded. Species diversity assessed revealed Khalsi having rich and diverse indigenous fish fauna more evident from the high biodiversity indices than Akaipur. Seasonally open nature of Khalsi where the river water enters into the wetland during monsoon and aquatic macrophyte coverage has helped to sustain natural fish diversity despite having more fishing pressure in terms of fishing days and fishing effort. High fish stocking density has led to concomitant increase in fish yield in Akaipur, whereas reduced native fish biodiversity was recorded in this closed wetland as a trade off. The present work therefore suggests that for regional persistence and subsequent conservation of these fish communities, maintenance of hydrological connectivity as well as macrophytic coverage is essential. The study recommends appropriate management measures for the sustainability of agrobiodiversity with reference to conservation of indigenous fishes in floodplain wetlands.

Keywords: Aquatic Macrophytes, Floodplain Wetlands, Indigenous Fishes

1494 (P-81)

Microbial Inoculants Modulated Plant Growth Promotion and Nutrient Uptake in Chickpea (*Cicer Arietinum* L.)

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Indiscriminate use of agrochemicals and low purchasing power of the marginal farmers are major threat on sustainability of Indian agriculture. Use of microorganisms can stimulate plant growth, offers environmentally benign solution for nutrient management and sustaining the ecosystem functions. Pulses, especially chickpea, are a major crop from nutrition perspective. Since the information on response of chickpea to inoculation with *Rhizobium* and bacterial inoculants possessing multiple PGP traits is meagre under such situation, therefore a field experiment was carried out during the rabi season (2015-2016) at CSAUA&T Kanpur in field trials to find out the effect of *Rhizobium* and other microbial inoculants on PGP and nutrient uptake in chickpea (*var* Awarodhi). A vast pool of prominent bacterial isolates screened at ICAR-NBAIM was used in talc based bioformulation in 30 consortial combinations with chickpea *Rhizobium* was prepared and tested in chickpea in field. Experiment was carried out in 1.2 × 1 m microplot in triplicates. Statistical analysis done using standard protocol and means were separated by DMRT. The treatments have shown enhanced germination, reduced days to 50% flowering and enhanced root length at 50% chlorophyll content, number of pods per plant, number of seeds per plant, straw yield, protein content and nutrient uptake. Higher seed yield per plot was given by T12 (456.7g) followed by T19 (426.7 g) and T-26 (412.3 g) as compared to control (253.7g). These microbial inoculants were found satisfactory in performance at field level. This consortium can be tested for enhancing productivity of other pulses also.

Keywords: Chickpea, Microbial consortia, Nutrient management, Plant growth promotion, *Rhizobium,*

1496 (P-82)

Formulation of Natural Fortified Whey Beverages with Improved Health Benefits and as a Tool to Control Environmental Pollution

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Whey is a by-product of dairy industry generated during the manufacture of coagulated milk products. Underutilization of whey results in serious environmental pollution due to its high biological oxygen demand (BOD). However, the food industry is now focusing on biodiversity as a tool to food and nutritional security and to balance ecosystem through maximizing the use of underutilized food resources. Whey generated from *paneer* manufactured by coagulating heated milk with 2% citric acid solution (control), lemon or Indian gooseberry (*amla*) extracts were used to develop beverages with the addition of sugar, colour and flavour and further processing and packaging. The physicochemical properties were estimated according to AOAC methods. The antioxidant activity, ascorbic acid, total phenols and tannins were analysed using DPPH, 2, 6-dichlorophenol indo-phenol dye, Folin–Ciocalteau and Folin–Denis's methods respectively. Whey from lemon extract contained higher total solid, fat and protein content than control and *amla* extract. The antioxidant activity was higher in whey from lemon extract (88.77%) than *amla* (81.38%) and control (14.39%). The ascorbic acid content was higher in *amla* (56.5 mg/100g) than lemon whey (6.76 mg/100g) and was non-detectable in control. The total phenols (GAE mg/100g) and tannins (mg/100g) respectively were higher in *amla* (550; 394.45) than lemon (69.23; 4.08) and control (5.86; 0.00). The whey beverages from both the fruit extracts were highly acceptable. Therefore, whey generated from the *paneer* manufacture using both the fruit extracts has a potential for conversion into beverages with improved health benefits as well as minimising the environmental pollution.

Keywords: Beverages, Biodiversity, Phytochemicals, Pollution, Whey

1498 (P-83)

Rhizobium Inoculation Effect On Foliage Cutting On Growth And Seed Yield In Fenugreek (Trigonella Foenum Graecum L.)

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An experiment was conducted during 2013-14 at Vegetable Research Farm, Haryana Agricultural University, Hisar and it was located between 29.15°N latitude 75.69°E longitude with a mean altitude of 215 m above mean sea level. Two sets of genotypes were under taken; one set was without *Rhizobium* inoculation while the second set inoculated with *Rhizobium* culture The experiment was laid out in Randomized Block Design with three replications and comprising of ten genotypes: HM-257, HM-273, HM-291, HM-293, HM-346, HM-348, HM-355, HM-444, Hisar Suvarana and Hisar Sonali with plant spacing of 50x10 cm and plot size was 3.0 x 1.50 m and the observation were recorded among the plots with three level of leaf cuttings: no cutting, one cutting at 30 days, two cuttings at 30 and 40 days after sowing..The observation recorded under following parameters; Plant height (cm) , Days to 50% flowering, Number of branches per plant ,Number of pods per plant , Pod length (cm) , Number of seeds per pod, Leaf yield (q/ha) and Seed yield (q/ha).It is found that inoculation with *Rhizobium* is beneficial, economical and ecological safe and better. Genotype HM-348 was observed the superior in terms of growth and yield parameters. Therefore, seed treatment with *Rhizobium* should be followed for obtaining higher leaf and seed yield along with good quality seed. Significant differences /variability were observed among the genotypes for almost all the growth and yield components. Leaf cutting management has significant impact upon the seed yield and leaf yield.

Keywords: Fenugreek, Leaf cutting, Seed yield

1510 (P-84)

Hard Coral Diversity of Minicoy Island, Lakshadweep

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Present account is based on a detailed underwater biodiversity assessment of lagoon and inshore coral ecosystem of Minicoy conducted during December 2015. Minicoy is the southernmost island of the Lakshadweep archipelago lying south of the Nine Degree Channel along the coordinates Lat 8° 16, N and Lat 73° 01 E. Geo-referenced resource mapping of the distribution and diversity corals was assessed using Line Intercept Transect Method. Diversity and distribution of corals was more in the reef crest and the shallow areas of lagoon. In the open water, the north eastern part of lagoon has a narrow slope where the sub-massive and massive corals are distributed where as in the north western side has a reef flat having branching and plate forming corals. In the present study 75 species of scleractinian corals belonging to 32 genera under 11 families were recorded .The most dominant genera by extent of coral cover were found to be *Acropora* and *Porites*. The most diverse family as per numbers of species is that of Acroporidae with 22 species, followed by Merulinidae, Poritidae, Pocilloporidae, Fungidae, Lobophyllidae, Agaricidae, Mussidae ,Psammocoridae, Euphyllidae and Diploasteridae. The reef showed an average live coral cover of 27.94% and the average dead coral coverage recorded was 30.78%, most of which were covered with algae. Coral mortality index were derived for different transect areas. Bleaching was most commonly noticed in acropoids and diseases were common in the *Porites* genera. Major threats, both natural and anthropogenic faced by the reefs of Minicoy is also elaborated.

Keywords: Blaeaching, Resource mapping, Scleractinian corals, Threats

1528 (P-85)

Screening of Bacterial Endophytes From Pearl Millet With Potential to Enhance Plant Growth

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Pearl millet (*Pennisetum glaucum*) is the most widely grown crop among millets. because of its tolerance to difficult growing conditions such as drought, low soil fertility and high temperature. Endophytic bacteria may in future be even more important than rhizosphere bacteria in promoting plant growth promotion (PGP) and nutrition, as they help to escape competition with rhizosphere microorganisms and achieve a more intimate contact with plant tissues. In this study, pearl millet plants were collected from eastern regions of Indo-Gangetic plains (Mau, Varanasi, Gazipur and Mirzapur) and bacterial endophytes were isolated from various plant parts such as stem, leaf and roots. A total of 102 bacterial isolates were obtained and they were characterized for PGP traits. Four percent of the isolates were found to produce indole acetic acid (IAA), 35 and 2 percent of the isolates were found to solubilize zinc and mineral phosphate. Seventeen, 18 and 15 percent of the isolates were positive for lipase, protease and amylase production, respectively .Out of 102 isolates, 73 were Hydrogen cyanide (HCN) producer whereas, 14 isolates were producing ammonia under *in-vitro* conditions. Average of IAA production and phosphate solubilization index was observed as 6.42µg/ml and 1.41, respectively. The isolates EPP44 and EPP97 were found positive for multiple PGP traits.

Keywords: Pearl millet, Endophytes, Plant growth promotion, Phosphate solubilization index, IAA

1552 (P-86)

Studies on the Genetic Diversity of Chocolate Mahseer (*Neolissochilus Hexagonolepis*) Populations Using Mitochondrial Genes

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The Chocolate Mahseer (*Neolissochilus hexagonolepis*) is an important food fish and endemic to North Eastern states of India, particularly in the Brahmaputra river basin. It is tagged as near- threatened species (IUCN, 2014) based on the inferred population decline in the wild. Studies on genetic variability using different populations is a requirement for future genetic improvement programme. We had initiated preliminarily to analyse seven geographically isolated populations of the chocolate mahseer from Arunanchal Pradesh, Assam and Meghalaya using mitochondrial genes *viz.* Cytochrome oxidase I (COI) and Cytochrome b. The genomic DNA of 10 samples each from seven populations were PCR amplified using two mitochondrial gene specific primers. The sequences of the PCR products were analysed using CLC GenomicsWorkbench 7.5.2 and MEGA 7.0. A total of 856 sites of cytochrome b were used to infer the phylogeny of chocolate mahseer. There were 210 variable sites, out of which 73 were parsimony informative, and 137 were singleton variable sites. The overall mean distance between the taxa was 0.036 ±0.006 while mean inter-population diversity was 2.15. A total of 644 sites of Cytochrome Oxidase I were used forinferring the phylogeny of chocolate mahseer. There were 122 variable sites, out of which 47 were parsimony informative, and 75 were singleton variable sites. The overall mean distance between the taxa was 0.031±0.004 whilemean inter-population diversity was 2.14.

Keywords: ChocolateMahseer, Genetic Variability, Mitochondrial Genes, Wild Populations

1636 (P-87)

Nutrient Composition of Five Snow Trout (*Schizothorax* Spp.) from Western and Central Himalaya and Their Importance in Human Nutrition

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Snow trout (*Schizothorax* spp.), the Indian Himalayan food fish was taken up for exploring their inherent nutritional value from western and central Himalaya based on their availability. Proximate composition, total fat, total cholesterol, triglyceride, fatty acids profile and mineral profiles were analyzed. Protein percentage, in all five fish was found to be same ($P>0.05$) ranging from 15-18%. Moisture (75-82%) and lipid (1.5-8%) values were found to differ prominently ($P<0.05$) in an inverse manner. Total fat (%), total cholesterol (mg/100g) and triglycerides (mg/100g) contents were found in the range of 2.73 to 6.54, 21.31 to 25.76 and 298.89 to 342.22 respectively. The trend of fatty acids, in decreasing order was saturated>monounsaturated>polyunsaturated (n-6>n-3). The sum of n-6 fatty acids value was higher than that of n-3, and major n-6 and n-3 long chain polyunsaturated fatty acids (n-6 and n-3 LC-PUFAs) were arachidonic acid and docosahexaenoic acid respectively. In most of these fish, with slight exception, the profiles of macrominerals reveals the abundance trend as phosphorus>potassium>calcium>sodium>magnesium, while the trend for microminerals was iron>zinc>copper>manganese. The snow trout species with best contribution potential to daily requirement of n-3 LC-PUFAs was found in *S. Esocinus* & *S. niger*, calcium & phosphorus in *S. Plagiostomus* and iron & copper in *S. progastus*. The uniquely distributed snow trout in Indian sub continental Himalaya have the potential to contribute significantly to the nutritional requirements of native inhabitants of the region.

Keywords: Dietary contribution, Nutrient composition, Snow trout

1625 (P-88)

Food Fishes from India - Need for Propagation and Conservation of Nutrismart Species for Nutritional Security and Biodiversity Conservation

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As a rich source of quality animal proteins, ω-3 PUFAs and micronutrients, fish plays an important role in providing food, nutrition and health security to million across the world. India is a mega biodiversity hotspot distributed over 15 agro-climatic zones and it is especially rich in fish diversity harboring about 2200 fish species, which accounts to 11.72% of global fish fauna. As a large variety of fish species are available each with unique nutritional significance, it is necessary to know their nutritional composition for optimal utilization of these valuable natural resources. We have generated nutritional information on > 50 species of food fishes and it is available in the knowledgebase (open access repository) http://www.cifri.res.in/outreach. The information generated could be useful in dietary counseling and public health nutrition; formulation policy guidelines for species prioritization and bringing nutrismart species (those rich in multiple nutrients and therefore useful for public health nutrition, like *Tenualosa ilisha, Anabas testudineus*, small indigenous fishes *Amblypharyngodon mola, Puntius sophore* etc.) into aquaculture on priority basis by developing breeding technology and feeding management and working for successful blue revolution through public private partnership with a social entrepreneurship approach. Where, govt. agencies like NFDB, State Fisheries department, fish farmers' cooperative should work in unison. The important challenges like provision for certified seeds, disease management, vaccine development, feeding management and aquatic resource management need to be addressed for blue revolution. Harnessing the rich fish biodiversity in a knowledge driven and sustainable manner could take us closer to food and nutritional security.

Keywords: Biodiversity Conservation, Fish Fauna, Nutrismart Species, Nutritional Security

1648 (P-89)

The Complete Mitochondrial Genome of two Ornamental Schistura Species and their Phylogeny

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Fishes of the genus Schistura, McClelland are economically important in ornamental fish trade. There are about 202 species of Schistura worldwide, out of which 45 species are distributed in the India. To study the phylogenetic status, we sequenced the complete mitochondrial genome of two Schistura species of Himalayan region namely Schistura sikmaiensis and Schistura reticulofasciata. Their mitogenomes are 16581 bp and 16603 bp in length respectively, and composed of 13 protein-coding genes, 22 tRNAs, 2 rRNAs and one putative control region. The phylogenetic position of the studied species was compared with few Nemacheilidae species. Twelve protein coding genes (except ND6) were aligned together and about 10,939bp were retained for the final phylogeny construction. The results obtained from the complete mitogenome showed variation within species and among all the different genus. There were 5115 variable sites, out of which 4284 were parsimony informative and 831 were singleton variable sites. The overall mean distance between the taxa was 0.258. Maximum divergence (0.263) was observed between Genus Schistura and Tarimichthysa whereas minimum (0.201) between Schistura and Homatula. The evolutionary history was inferred by using the Maximum Likelihood method with a bootstrap value of 1000 replications. The tree with the highest log likelihood (-104970.0851) was computed. All the genus of family Nemacheilidae separated into different clades in phylogenetic analysis. Both the studied species shared the same clade as that of previously reported congeneric species. Hence, the phylogenetic inference with the help of complete mitogenome is more accurate and reliable as compared to single gene.

Keywords: Mitogenome, Phylogeny, Nemacheilidae

1679 (P-90)

Traditional Knowledge on the Edibility of Sea urchin Roe among the Fisher Folk Community of the Gulf of Mannar Region with a Note on their Cuisine

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Sea urchins are marine echinoderms and their body consists of five gonads covered by a calcareous test. The gonads of male and female sea urchins are commonly called 'roe' and have been known a delicacy in several parts of the world. However in India not all the coastal community eat the gonads of sea urchin, but fishers of a fishing village along Gulf of Mannar, have the habit of eating the roe of sea urchin from time immemorial. This works brings into light the consumption of sea urchin roe from the fishing community of Gulf of Mannar and their various culinary preparation methods with an account on the nutritional and health benefit.

Keywords: Gulf of Mannar, Roe, Sea urchin

1686 (P-91)

Perna Indica an Important Marine Bio-Resource along Southwest Coast of India

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Perna indica the Indian brown mussel has a very restricted distribution along the southwest coast from Quilon to Cape Comorin. A traditional sustenance fishery exists for the brown mussel off south west coast of Kerala and west coast of Tamil Nadu. Considering the growing demand for mussel in Kerala, it has become a necessity to monitor and manage this resource. Mussel data was collected from the Vizhinjam, Pulinkudi and Mulloor along the south west cost of India by fortnightly visits to mussel landing centres during 2008-15. The average landing of brown mussel at Vizhinjam during 2008-15 was 713t, ranging from 490 t in 2008 to 1,181 t in 2012. Fishing was observed year-round off Vizhinjam-Kovalam beds, whereas, in Pulinkudi-Mulloor stretch, mussel fishery was only during the post-monsoon and pre-monsoon periods. The peak-fishing period was observed during October to November in the region. Fully mature specimens of *P. indica* were observed from May to November and peak spawning period was May – June. The main landing centres of Mussel along west coast of Tamilnadu are Kadiayapattanam, Kolachal and Enayam. In all these landing centres mussel fishery starts from October middle peaks in November to January. Total catch was 265 t. After the peak season some fishermen migrate to malpe for mussel picking. Kadiayapatanam about 300 persons are engaged in mussel picking, Kolachal 120 and at Enayam about 200. The Kadiayapatanam contributed about 50% of the total catch followed by Kulachal and Enayam.

Keywords: Indian brown mussel, *Perna indica*, Fishery, Biology

1701 (P-92)

Ichthyofaunal biodiversity of Wular Lake - A Ramsar site in Kashmir Himalayas

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The abundance and distribution of fishes in an ecosystem is regarded as an indicator of water quality and ecosystem health. The aquatic ecosystems in the Himalayas are facing an ever increasing threat from anthropogenic activities which necessitate better understanding of the freshwater biodiversity. In order to assess the diversity of fish species, an investigation was carried out at five different sites of Wular Lake, for a period of one year from December, 2014 to November, 2015. Sampling was done on a monthly basis using cast net with the help of local skilled fishermen. During the entire study period, a total of 738 fishes were sampled. These fishes represented 2 orders, 2 families, 4 sub-families and 6 genera. Cyprinidae was observed to be the most dominant family followed by Cobitidae. The study revealed that there was a drastic decline in the native Schizothorax due to the introduction of exotic common carp, pollution and other anthropogenic disturbances. Many fish species that had been reported in the lake in the earlier studies were not reported in this study, indicating their disappearance from the lake. Keeping in view the progressively worse situation, there is an urgent need to take remedial steps to conserve the endangered native fish fauna of the lake in order to preserve its biodiversity from further ecological degradation.

Keywords: Anthropogenic, Ecosystem, Endangered, Himalayas, Wular Lake.

1709 (P-93)

Captive Rearing and Nutrition of Schizothorax Richardsonii: First Observations

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Schizothorax richardsonii is considered as one of the most promising candidates for species diversification in hill aquaculture. However, the domestication process is incomplete, partially due to poor understanding of their nutritional needs under captive conditions. The reported study therefore aimed to adapt wild snow trout to a captive feeding regime and investigate the impact of different nutritional conditions on growth performance. 1500 snow trout were collected from Chaffi stretch of river Gola. As this fish inhabit rocky crevices in stream bottoms, the catch per unit effort in electro-fishing was considerably higher than cast netting. In representative catch cohorts, the average condition factor was estimated to be 1.5-1.7. In captive conditions, fishes were well adapted to purified diet containing 35% protein, 6% lipid and 38% carbohydrate. Feed acceptance was good. To explicate the effect of nutritional status on growth, a 6 week feeding trial was conducted using 5 g size fishes. The treatment group was starved for the first 21 days and refed the remaining period, whereas the control group was continuously fed. Regardless of the nutritional state, there was no mortality. The starved group lost weight (-5.4%) during the first phase, but showed compensatory growth (24.8%) in the final phase. Weight gain in the control group was 16.8 and 9.6% in the first and second phase, respectively. Moreover, remarkable changes in the viscera-somatic index of the treatment group indicated distinct metabolic changes due to feed availability. Overall, the effect of nutritional status on growth and metabolism of S. richardsonii was elucidated.

Keywords: Domestication, Feed, Growth, Metabolism, Snow trout

1726 (P-94)

Biodiversity Assessment of Sea Cage Farming Sites in Gulf of Mannar, Tamilnadu, India

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The biodiversity of sea cage farm at Mandapam (9.2770° N, 79.1252° E) in Gulf of Mannar, south-east coast of India was studied during 2009-2011. The cage farm had broodstock cages for Rachycentron canadum and Trachinotus blochii, besides, rearing cages for Lates calcarifer. A rich aggregation of more than 30 species of fishes was noticed in the cage farm site. The entrant animals into the cages include silver bellies, lion fish and banner fish, lobsters and shrimps. The crabs commonly found in the cage nets include Plagusia squamosa, Hyastenus diacanthus, Nanopilumnus rouxi and some Porcellanid crabs. The barnacles often form a very thick mat on the cage nets the density of which attained a maximum of 915 nos./sq.m. The other major fouling organisms include oysters, sponges, seaweeds, Ascidians and Modiolus sp. The rate of fouling was high compelling periodic cleaning and net exchange to facilitate good water exchange. A rich assemblage of thirty nine genera of phytoplankters and twenty zooplankton groups were identified during the study. Four groups of macrobenthos namely, bivalves, gastropods, foraminiferans and polychaetes were commonly found. The diversity and monthwise distribution of plankters and benthos in the cage and reference sites are described and discussed.

Keywords: Biodiversity, Cage farm, Gulf of Mannar

1727 (P-95)

Biodiversity Assessment Along the Coast of Central Kerala, India in Relation to Ecosystem Services

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Rapid Biodiversity Assessment Survey (RBAS) was conducted in 2015-16 along the coastal districts of Alapuzha, Ernakulam and Thrissur of central Kerala to ascertain the provisional, regulatory, supporting and cultural services provided by the coastal and marine ecosystems. Coastal fisheries, ecosystems such as mangroves, estuaries and beaches, avifauna, conservation of endangered animals and factors impacting biodiversity such as habitat loss, coastal erosion, pollution and tourism were assessed. The area from Thottapally N 9°18'17.8" E 76°23'05.6" to Purakad N 9°21'34.7" E 76°21'40.2" (6.5 km) in Alapuzha district followed by Chettuva 10°30'13.0" E 76° 02'31.0" to Periambalam 10°41'15.5" E 75°57' 20.4" (22.2 km) in Thrissur district and Kuzhupilly N 10°5'56.2" E 76°11'22.3" to Cherai 10° 10'08.7" E 76°10'05.3" (8.4 km) in Ernakulam district obtained maximum scores in the RBAS. Mangrove areas of Vypin of Ernakulam district lie within the most ecologically sensitive areas suffering from habitat loss followed by Chettuva region in Thrissur. Response from 111 stakeholders from 58 locations indicated that decline in fish catch was the major concern with populations of catfish, small sharks, rays, threadfins and false trevally showing marked declines as compared to thirty years previously. Sea turtle conservation as a participatory public initiative has seen several success stories at Thottapally, Kuzhupilly, Palapetty and Papally areas. Barmouths at Cochin as well as Azhikode have resident pods of the Indo-Pacific humpbacked dolphin Sousa chinensis. The beach and ecotone at Thottapally and adjoining beaches northwards upto Purakkad in Alapuzha are recommended for inclusion as an Ecological and Biologically Sensitive Area.

Keywords: Coastal Biodiversity Assessment, Central Kerala

1735 (P-96)

Breeding and Seed Production of *Chagunius Chagunio* (Hamilton-Buchanan, 1822) in Captivity for Aquaculture Diversification

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Chagunius chagunio, commonly known as "Chaguni" belongs to family cyprinidae is one of the economically important indigenous fish of Himalayan region. An attempt was made to standardize the breeding protocol of this species under captivity in coldwater condition. Wild stock was collected from the Kosi River, Ramnagar, Uttarakhand and reared at ICAR- DCFR. Fish were periodically checked for maturity status and bred through dry stripping method without using any inducing hormone. Results indicate that fish can achieve gonadal maturity in confinement and there are two distinct breeding seasons of C. chagunio (During May- June and August – September). Estimated batch fecundity was 1186 to 1706 hydrated eggs for the fishes of weight 74.30 g to 98.70 g. Unfertilized eggs were bright orange in colour with an average diameter of 1.1±0.13 mm while fertilized eggs were transparent, demersal and semi adhesive with a mean diameter of 1.42±0.17 mm. Incubation period was recorded 96-134 hours post fertilization and yolksac absorption time was 9-11 days post hatch (at incubation temperature 19-22°C) with overall survival of 83-85% from eggs to spawn. Average length and weight of larva, having completely absorbed yolksac were 8.1±0.17mm and 0.007±0.03 g, respectively. The present study is the first report of successful breeding of C. chagunio in captivity and would be undoubtedly torch light for the academicians and researchers. This will pave the path of species diversification in coldwater aquaculture.

Keywords: Breeding, Chagunius chagunio, Dry stripping, Species diversification

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1741 (P-97)

Studies on Fish Genetic Diversity of Ull River and Sharda River in Lakhimpur Khiri of Uttar Pradesh - A Measure towards Conservation

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The challenges associated with natural genetic resources, including fishes is undergoing paradigm shift. The growing population of the world needs to be not only fed, but should be nutritionally secured and conserve our resource also. In this context, agro-biodiversity for food and agriculture take the center stage. As the fish genetic resources are basic component for enhancing nutritional supplements, sustainable production and conservation of fish species is vital. In this context, exploratory survey has been conducted at the natural water bodies ,fish market and interactions with the fisherman of nearby areas of Ull and Sarda river of Lakhimpur khiri District, Uttar Pradesh which is connected with Dudhwa reserve forest to find out the occurrence of fishery resources of this region. The exploration survey was mainly targeted at the Sharda river and its tributaries. Cirrhinus reba, , Labeo calbasu, Ompak pabda, Xexentodon cancila, Labeo rohita and Puntius species are the dominant fishes while Labeo gonius L. dyocheilus, L. dero, Puntius sarana, X. cancila and O. pabda were noticed with limited numbers. Followed, the exploration was done at Ull River, which is the tributary of Sharda river and L. gonius population was noticed as dominant . Besides, few P. sarana, Notopterus notopterus, L. dyocheillus X. cancila were also found. The collected information from the water bodies and the interaction made with the fishermen are revealed that the fish populations of the said regions have declined. This may be due to overexploitation and anthropogenic activities of this region. There is a need for replenish and enhance population of fish species through stock specific breeding and ranching programmes.

Keywords: Fish, diversity, Sharda river, Lakhimpur khiri, Conservation

1760 (P-98)

Assessment of Marine Genetic Resources of Gulf of Mannar Biosphere Reserve-Tamil Nadu, India

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The Gulf of Mannar Biosphere Reserve (GOMBR) including the Gulf of Mannar (GOM) National Park is considered as ‘Biological Paradise’ because of the diverse ecological niches like coral islands, estuaries, seagrass beds, pearl paars, chank beds, mangroves forests and beaches. The GOMBR harbours numerous marine flora and fauna of global significance and considered as one of the world’s richest region in marine biodiversity perspective. It helps the livelihood of fisherman population inhabiting along the coastline. The methodology for the assessment of the marine genetic resources involves the weekly observations on 14 different fish landing centres during the period 2012 to 2016 and also from the published literatures. The GOMBR comprises of about 4223 floral and faunal species like mangroves (11 species), seagrasses (15 species), seaweeds (181 species), corals (145 species), echinoderms (153 species), crustaceans (206 species), crabs (210 species), molluscs (856 species), fishes (1147 species), sponges (280 species), marine reptiles (18 species), marine mammals including dugong, etc. The sacred chank is exploited at the rate of 15 lakhs of chanks per year and the fossilised chanks are being exploited in higher intensity. Recently, a new fish species Bleekeri murtii has been described along GOM with several new records from this area adds the biological diversity. Furthermore, a range of steps has been taken by various national/ international organisations to sustain and manage the marine biological resources of the GOMBR.

Keywords: Biodiversity, Biosphere Reserve, Endemic, Gulf of Mannar

Technical Session 2-A :

Conservation Strategies and Methodologies

Concurrent Session :

Seed Genebanks

1623 (O-9)

Low Carbon Footprint Seed Conservation Technique: The Desiccated-Ambient Storage System Using Zeolite Beads

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Informal seed system fulfils 70% of total seed requirement in India. Farmers use seed produced in their own field, exchange or sell among themselves when unable to access commercial seeds. India is a tropical country and on-farm conditions do not allow storing seed even for a year. Higher temperature accompanied with high relative humidity deteriorates seed quality rapidly and make them prone to insects and diseases. In gene banks, long or medium term conservation is done under sub-zero temperatures which is totally dependent on electricity and also produce a big carbon footprint. Different studies have reported that seed longevity can be enhanced similar to medium term storage (10-20 years) by storing dried seeds up to 3-5%. Sun-drying cannot bring down the seed moisture content of seeds less than 10% under normal conditions. A novel technique has been proposed where seed moisture content is brought down by using Zeolite beads and subsequently the reduced moisture is maintained by storing the dried seed in air-tight containers. Zeolite beads adsorb moisture from the surroundings and lower down the RH of the air to >1%, in-turn reducing the seed moisture content of the seeds being kept adjacent hermetically. These beads can adsorb moisture about 20-25% of its own weight. The beads are rechargeable and can be reused thousand times by heating them in an oven at 200-2500C for 3 hours. The technique is easy to use, farmer friendly and doesn't require a strong expertise with seed storage being possible under ambient temperatures.

Keywords: Zeolite beads, Seed storage, Seed longevity

1835 (O-10)

Conservation of Forest Genetic Resources: Need and Challenges

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Loss of forests around the world is widely deplored for many reasons. The obvious consequence of deforestation is the loss of valuable germplasm that could be used in artificial regeneration and the future breeding programmes. Threats to Forest Genetic Resources (FGRs) continue at an unprecedented rate and almost 20% of the FGRs are facing different categories of threats to their existence. There is an urgent need to address the issue to arrest degradation of natural populations of forestry species and improve status of regeneration from continuously increasing biotic pressure, assess conservation status of FGRs and develop a prioritized action plan as well as to prepare an elaborate inventory of the wild populations of FGR. Before embarking on a comprehensive programme for conservation of FGRs, there are many issues that need to be addressed, like inadequate knowledge about the genetic diversity of priority forest species; limited knowledge about conservation biology, population dynamics, reproductive biology and fruit/seed production; irregularity in flowering and fruiting schedules; variability in seed production among species and regions- the causes of these variations are often uncertain; determining the seed storage behaviour of a species; devising appropriate methods of conservation for species producing intermediate and recalcitrant seeds, etc. Under a programme for conservation of FGRs of Uttarakhand, *ex situ* conservation of valuable germplasm of economically important forestry species as well as the ones facing threats to their existence, is envisaged. The paper presents the entire programme and the approaches to successfully conserve the precious genetic resources through seeds.

Keywords: Conservation, Forest Genetic Resources, Seeds, Storage physiology

1845 (O-11)

Phyto-Diversity and Its Conservation Strategies in Permafrost Conditions at Extreme Altitude of Trans Himalaya in Leh-Ladakh (India)

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The Ladakh located in Trans Himalaya, is one such geographical entity having unique culture and the customary practice of indigenous knowledge to sustain man and animal life in harsh cold climatic condition. The vegetation of the cold desert supports temperate, sub-alpine and alpine vegetation comprises of herbs, shrubs and few species of trees which are of economically importance mainly in the form of food, fodder, medicine, fuel and ornamental purpose. To collect the germplasm of wild edibles and to record the uses of traditional vegetables and healthcare remedies practiced by the local inhabitants and Amchis (local herbal doctor), the survey was carried out in the three valleys of Ladakh viz., Nubra, Indus and Suru. Since the dawn of history, in the barren land of Ladakh, where otherwise the existence of life has been questionable; the indigenous people have been using wild plants as only source of their food, fodder and medicines. Of the known wild edibles plant species and varieties including, *Atriplex hortensis*, C*apparis spinosa, Nepta floccose, Allium carolinianum, Rheum spiciforme, Rhodiola tibetica, Rhodiola imbricate, Arnebia euchroma, Carum carvi, Teraxicum officinale, Lepidium latifolium, Potentill anserine, Hippophae rhamnoides* etc., constitute a small number of the imperative and nutritious un-trapped plants consumed in different areas across Ladakh. The present study was undertaken to evaluate the potential germplasm of indigenous vegetables through agro-morphological characterization, genetic diversity studies in order to study cultivation and conservation strategies for PGR including rare endangered wild relative plants species at Permafrost facility situated at extreme high altitude, Changla (17,600 ft amsl) in Leh-Ladakh (J&K).

Keywords: Conservation Strategies, Extreme Altitude, Permafrost Conditions, Phyto-Diversity, Trans Himalaya

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1922 (P-99)

Improved Facilities and Methodologies for Regenerating Unadapted and Wild Groundnut Germplasm at ICRISAT Genebank

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Germplasm seed accessions require frequent regeneration for continued conservation and utilization. Regeneration of diverse crop germplasm accessions is a challenging task for large genebanks. The problem is severe especially with the wild relatives because of adaptation problems, lack of facilities and seasonal constraints where genebanks are located. Special facilities were created at ICRISAT Genebank for regenerating all the seed producing wild species of genus *Arachis* and unadapted *Arachis hypogaea* accessions. A total of 304 accessions represented by 41 wild species and 290 accessions of six botanical varieties of cultivated groundnut were successfully regenerated using these facilities. Much of the problems encountered during field regeneration especially with the wild species were overcome. Regeneration was possible round the year with minimum operational interference. The seedling establishment, plant growth and pod yields per cycle were significantly higher in these facilities. Establishing such facilities by genebanks could be advantages in efficient regeneration of problem accessions on a long-run for conservation and continued availability of diverse germplasm for utilization in crop improvement programs.

Keywords: Germplasm, Regeneration, *Arachis,* Wild species

243 (P-100)

Assessment of Recalcitrance in Forestry

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Recalcitrant seed instinctively shed from the tree/plant at higher moisture contents, metabolically active, desiccation sensitive and so have limited life span. The loss of viability at low moisture content makes the seeds unsuitable for orthodox storage conditions; the cause of which is yet to be truly understood. However, the presence or absence a specific set of proteins (dehydrins) and appropriate sugars, which prevent cellular damage during desiccation by binding to macromolecular structures and formation of effective protectants, could be implicated in the acquisition of desiccation tolerance in seeds. Probably, the immediate ancestors of the land plants being aquatic were desiccation sensitive and nobody knows at what stage of succession to the land habitat, desiccation tolerance arose. Recalcitrant seeds are common in mesic tropical forests where conditions are favourable for germination and seedling establishment, hence, no pressure of driving the evolution of desiccation tolerance or the instinct has been lost in the course of evolution. The seeds of climax species in an ecosystem generally show no dormancy, germinate rapidly, are absent from soil seed banks and rely more on seedling bank for survival, whereas seeds of gap specialists are well represented in soil seed banks. Even though recalcitrant seeds are common in mesic forests but also do occur in more seasonal habitats and evolved a number of strategies to have successful seedling establishment like those of recalcitrant species of temperate regions which are generally more desiccation tolerant and have little more life span than those arose in tropical regions. Desiccation sensitivity of seeds poses difficulties on regeneration biology of forest plants, and species producing recalcitrant seeds are generally confined to habitats continuously conducive for germination and seedling establishment, presumably because having seedlings on the forest floor may be more advantageous with respect to predation of seeds thereof.

Keywords: Desiccation tolerance, Recalcitrant seeds, Seedlings, Tropical.

361 (P-101)

Ex situ Conservation of Genetic Variability of Food Legumes in National Genebank

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Grain legume improvement requires genetic variability to cater for a wide range of needs regarding quality, productivity and both biotic and abiotic stresses to adapt to climate changes. These groups of crops have faced serious genetic erosion in their past evolutionary history since a large part of their genetic variability has been lost in the process of their adaptation to stressful environments of marginal lands characterized by moisture, temperature and fertility stress. The Indian gene center has rich diversity in genetic resources of pulse crops native to India viz., pigeonpea, mung bean, urd bean, horse gram as well as several others for which India is known as secondary centre of diversity e.g., chickpea and cowpea and in introduced crops like French bean. The National Bureau of Plant Genetic Resources, in collaboration with crop-based institutes, has made considerable efforts in conserving the pulse crop germplasm resources to strengthen the National Crop Improvement Programmes. The National Genebank holds 64,418 accessions of pulse crops belonging to about 80 species, which are stored at 180 C in its long-term conservation facility. These comprise mainly, chickpea (14,632), pigeonpea (11,240), green gram (4,153), urd bean (3,191), lentil (2,761), pea (4,168), cowpea (3,790), French bean (3,724), Lathyrus (2,646), moth bean (1,488), horse gram (3,035), guar (4,312), faba bean (905), rice bean (2,072) and lablab bean (1,665). The collection includes about 55,150 indigenous and 9,250 exotic accessions. The status of ex situ genetic resources collections, especially, of trait specific accessions in major pulse crops is presented.

Keywords: *Ex situ* conservation, Genetic resources, Pulses

367 (P-102)

Physiological Manifestations During Accelerated Ageing in *Phaseolus vulgaris* Germplasm

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French bean is a nutritionally rich legume which is highly important as a vegetable crop. Accelerated ageing is a vigour test that can be used to estimate field emergence as well as to predict the storability of seeds thereby facilitating the ranking of seed lots/genotypes as good, medium or poor storers. With the objective to assess the storability, 50 genotypes of French bean seeds procured from different locations within India, were subjected to Accelerated ageing (AA) test at 45^{0}C and 100% RH for 4 days. Seed quality was assessed using the physiological parameters such as per cent germination, speed of germination, seedling vigour (root and shoot vigour) and seedling vigour index. Seeds subjected to accelerated aging for a period of 2 days maintained vigour and viability closer to the initial but increase in ageing duration reduced the viability and vigour progressively and significantly. Ageing beyond 2 days resulted in loss of seed vigour, as evidenced by decreased number of vigorous seedlings and several fold increase in the abnormal seedlings. The AA test could thus delineate 17 genotypes as distinctly different from others in their storability and could be ranked as good storers. These were IC-328372, IC-258365, IC-361547, IC-415517, IC-258395, EC-500577, IC-047655, BASPA, EC-500275, EC-500336, EC-500528, IC-037138, EC-398536, EC-100098, EC-500522, EC-398563 and EC-500250.

Keywords: Accelerated ageing, Physiology, Seed deterioration, Storage and Seed quality

491 (P-103)

Identification Key for Identification of *Brassica* species and its Related Genera

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The seed gene banks contain large number of conserved collections with specific genera or of individual species where species are generally identified by collector. India possesses rich diversity of oilseed brassicas of which toria, brown sarson and *juncea* are considered to be native to Indian gene centre. Rapeseed- mustard crop group which is one of the largest oil producing crop and resilience to grow under diverse agro-climatic conditions often face problem in accurate identification of species and their related genera. The National Genebank houses 11,000 accessions of *Brassica* species and their related genera. As a curator, it becomes very difficult to store the seeds without proper identification/ wrong identification. Such seeds are identified by plant taxonomist or are grown in the field for further evaluation which is labour intensive, time consuming and expensive. Understanding the basis of particular crop morphotypes within species would assist the breeders for better utilization. Therefore an attempt has been made under the present investigation to evaluate the seeds of *Brassica* species and related genera (10 species, and 3-5 cultivars under each species) based on seed characteristics (size, length, diameter, perimeter and roundness by Grain size and shape properties software, seedling characteristics (7-20 days old seedlings raised in pots at 23°C and 70% RH, by recording observation on cotyledonary and first leaf size, shape, colour (RHS colour chart) and seed surface scanning studies (High resolution microscope, Nikon, Model SMZ1500 at 20X) to develop an identification key for their correct identification for proper utilization.

Keywords: *Brassica*, Rapeseed-mustard, Seed and Seedling characteristics

498 (P-104)

Seed Maturation, Germination and Vigour in Rice Genotypes and Parental Lines Varying in Crop Maturity Period

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Eighty-eight rice (Oryza sativa L.) genotypes were analysed for seed maturation and germination during different developmental stages starting from 10 to15-d after completion of anthesis i.e., dough stage (stage 1) until harvest maturity (stage 6), at 3-d intervals. Average seed filling rate (dry mass assimilation) ranged between 0.407 at stage 1 and 0.573 g/25 at stage 6. Among genotypes it was higher in Pusa Sugandh 3 (0.654 at stage 1 and 0.776 g at stage 6) while Samba Mahsuri exhibited lower (0.188 at stage 1 and 0.553 g at stage 6). Average seed moisture content (mc), however, ranged between 38.8 and 16.1 at stage 1 and stage 6, respectively, and loss of mc was inversely associated with seed dry mass assimilation. Speed of germination (SG) and germination percentage (G) was higher in Pusa 6A as compared to Pusa 6B and PRR78, while among cultivars Makom (60%), Ravi and VL Dhan 81 (both 50%) exhibited higher germination and SG, at stage 1. At this stage seed of most of the genotypes showed no radical protrusion even after 6-d of imbibition. Also, onset of germination was much early in these lines. Only, 10 cultivars and all parental lines (A, B and R) exhibited â‰¥80% germination at stage 5, while it increased to 33 with â‰¥80%, and seven genotypes showed <10% germination, at harvest maturity (stage 6). In conclusion, wide genotypic variability was recorded in seed filling rate, seed vigour at physiological maturity and harvest maturity, post harvest germination and its speed.

Keywords: Developmental stages, Dry mass assimilation, Genotypic variability, Seed germination, Seed vigour

521 (P-105)

Strategies for Conservation of Horticultural Genetic Resources at ICAR IIHR, Bengaluru

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Horticultural crops includes fruits vegetables, ornamentals, root, tubers, spices, condiments, plantation, medicinal and aromatic crops. The species diversity in horticultural crops is much higher than in agricultural (field) crops. This high species diversity may lead to operational constraints if the gene-bank format is followed, due to lack of expertise and adequately established procedures, besides suitable infrastructure. Being the nodal center for genetic resources of horticultural crops ICAR-IIHR, Bangaluru has to coordinate all activities related to management of Horticultural PGR. Conservation of biodiversity in horticulture is an important component of sustainable agriculture and of late attracted international attention. *Ex-situ* conservation in gene banks has been a dominant strategy. This form of conservation includes gene bank storage (seed and field), in-vitro storage, pollen storage, and DNA storage. Seed gene banks are the most common storage practice in field crops. Generally, ex-situ management of PGR for plant breeding involves exploration collection, characterization evaluation for use in pre-breeding of genetic stocks. Genetic Resources Management is a gigantic task particularly in the context of richness of genetic resources in horticulture, considering the agro-ecological diversity of the country. In case of vegetatively propagated and recalcitrant seed producing species, the gene bank management is inadequate, which require more attention. Recently, in-situ conservation has been advocated as a complementary strategy. The changing scenario in horticulture calls for more emphasis on in situ on farm conservation with incentives to custodian farmers to keep the process of evolution, with genetic diversity responding to changing environment. Crucial concerns associated with in situ and on farm conservation through participatory approaches involving local communities develop appropriate regeneration systems, maintenance and continuous cultivation in farmers field to provide adequate incentives to farmers. Thus, PGR management of horticulture crops indicates that complementary strategies are relevant for more effective and sustainable conservation of maximum usable genetic diversity.

Keywords: *Ex-situ* conservation ,PGR management of horticulture crops

552 (P-106)

Conservation Gaps in Crop Wild Relatives at Indian National Genebank

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CWRs are important resource but despite their recognised value their conservation has been largely neglected. To achieve the objective of effective conservation there is a need to priortise the crops for conservation.The total number species of CWRs in the genebank is 1,247, including both indigenous as well as exotic species. Among the 1,073 indigenous species the maximun number of species conserved belong to medicinal and aromatic plants followed by fodder crops, agroforestry, ornamental and vegetables, refelecting the similar trend as per their occurrence in Indian sub-continent, albiet a very small number of species conserved in NGB. In the exotic CWRs species the maximum number of species conserved belongs to medicinal and aromatic group followed by cereals and vegetables. Taking into consideration only native status, economic value, national distribution and *ex situ* conservation status of indigenous CWR germplasm in NGB, 238 species were identified for gap analysis. Initial results of gap analysis highlight that out of 238 CWRs species, 210 were ranked as high priority CWRs species as they are either not present in the genebank or are represented by less than 20 accessions, 14 species each were ranked as medium priority (with 20-40 accessions are conserved in the genebank) and low priority (> 40 accessions are conserved in genebank). Further analysis of various agro-biodiversity zones and occurrence of the these species Western Himalayan region, North-eastern hill region, Deccan plateau, Konkan and Malabar regions are the highly targeted areas for future collections and subsequently for long term conservation.

Keywords: Conservation, Crop Wild Relatives, Future thrusts

559 (P-107)

Seed Health Status of Plant Genetic Resources for Pest-free Conservation in the National Genebank, India

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Conservation of plant genetic resources (PGR) in National Gene Bank (NGB) for long-term storage is one of the mandates of ICAR-NBPGR, New Delhi for their utilization towards food security and sustainability. Seed health testing (SHT) has major application in conservation of PGR for long-term storage in the National Gene Bank by detecting and identifying seed-borne pests. Hence, SHT with specialized tests are essential undershot for long-term conservation of PGR free from pests. During 2011 to 2015, a total of 67,279 samples of indigenous PGR samples have been processed for SHT and observations of incubated seeds resulted in detection of a large number of economically important fungal pathogens from 5,922 samples (8.8%), X-ray radiography revealed hidden infestation of insects in 4,673 samples (6.9%) and nematode infestation in 175 samples out of 1,874 paddy samples (9.3%) with varying infection/ infestation level. Based on morphological characteristics, some of the important pathogens identified were *Alternaria brassisicola, A. brassicae*, *Botrytis cinerea, Fusarium oxysporum, F. solani*, *Lasiodiplodia theobromae*, *Verticillium albo-atrum*, etc. Apart from immature stages of bruchid, some insect species such as *Callosobruchus chinensis, Pectinophora gossypiella*, *Tribolium castaneum*, *Rhizopertha dominica*, *Sitotroga cerealella*, *Sitophilus oryzae*, etc. were identified. A predominant nematode, *Aphelenchoides besseyi* was identified in paddy samples. A total of 72 samples (0.1%) due to heavy fungal infection and 1,816 samples (2.7%) due to heavy insect infestation were rejected. Therefore, SHT plays a unique role in conserving pest-free material for long-term storage of PGR and also in minimizing the risk of spreading pests and diseases.

Keywords: PGR, Seed-borne Pests, Seed Health Testing

673 (P-108)

Weedy Rice: An Unexplored Gene Pool for Rice Improvement

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Weedy rice is an introgressed form between wild and cultivated species and appears as hybrid swarm. In Asian rice, it is known as *Oryza spontanea* whereas in African context it is *O. stapfii,* both the species not being distinct taxonomically. The weedy rice usually grows faster, produces more tillers, panicles and biomass, having better nitrogen use efficiency, shatters early, better resistance to adverse conditions, and possesses longer dormancy in soil. Because of its high competitive ability, it becomes threat to rice growers worldwide. Great morphological variability, similar growth behaviour and high biological affinity with cultivated varieties make its control difficult. No single management technique can effectively control weedy rice. Therefore, an appropriate combination of preventive, cultural, mechanical and chemical control measures is essential. Explorations were conducted from different parts of eastern India mainly Odisha, Assam, Chhattisgarh and Jharkhand to collect, characterize and conserve these invaluable genetic resources, which were hitherto neglected due to their tremendous within line variations. About 283 accessions of wild and weedy rice germplasm were collected during last four years and they have been characterized as per the descriptors. The weedy rice collections showed wider variations than the wild rices, however, some collections were found to be uniform which may indicate about its stability and may emerge as a landrace in future if left undisturbed in nature.

Keywords: Characterization, Exploration, Weedy rice

680 (P-109)

Storability of Soybean Seeds in Genebank under Long-Term Storage Conditions

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Soybean is one of the most widely grown and consumed oilseed in the world. The Indian National Genebank at ICAR-NBPGR, the second largest in the world holds ~3,700 soybean accessions. The seeds are processed and conserved under long-term storage conditions adhering to the standards set by Food and Agricultural Organization (FAO, 2014) to minimize deterioration in quality. Regular monitoring of seed viability by germination testing revealed a reduction in the viability over the years. An investigation was undertaken where, 100 germplasm accessions stored at -20°C for more than 30 years, showing diverse seed vigour and viability, were compared for seed traits with the freshly harvested regenerated seeds of the same accessions. Overnight humidification was found to significantly increase vigour and viability of stored seeds. It was observed that the longevity is influenced by initial seed quality and moisture content at storage, relative humidity, gaseous exchange under storage and the genotype. We observed that the germination was good both in fresh and stored samples while vigour reduced in accessions stored for 30 years. Few accessions (3%) in the (30-year) stored seed accessions showed better germination over the fresh. Relationship of seed storability with geographical origin, seed morphological characteristics, seed biochemical constituents, moisture content, seed coat type, seed treatments (hydrated/non-hydrated) were also examined. The present study has implications on improving the standards for long-term conservation of soybean germplasm.

Keywords: Long-term storage, Soybean germplasm, Seed viability, Seed longevity

709 (P-110)

Exploration, Collection and Conservation of Rice Genetic Resources: A Historical Perspective

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There are 24 species in genus-*Oryza*, two of which man has domesticated, one in Asia known as Oryza sativa and the other *O. glaberrima* as the African cultivated rice. The diversity within the Asian cultivated rice (O. sativa) is vast and enormous compared to the African cultivated species. The breeding work started at Paddy Breeding Station, Coimbatore in 1911-12 mainly through pure line selection and subsequently rice research stations were established in different regions of the country. The introduction of exotic rice germplasm started with the inter-racial hybridization between japonicas and indicas during 1950-1964 being operated at CRRI. The F1 seeds were distributed to many countries for further crop improvement programme. Limited success was achieved in this project, four varieties were released; Malinja and Mahsuri released in Malaysia, ADT 27 in Tamil Nadu, India and Circna in Australia. During the early part of the 20th century i.e. between 1910 and 1920, Parnell, Hector and Graham collected germplasm from the Madras Presidency, Bengal and Central provinces, respectively. The first systematic rice germplasm diversity collection was undertaken by the CRRI from the Jeypore tract during 1955-59, popularly known as Jeypore Botanical Survey (JBS). During 1967-72, IARI explored and collected rice germplasm from Northeast India and is popularly known as Assam Rice Collection (ARC). During 1970-79, Richharia explored 42 districts of MP and collected 19,226 accessions which is so far the largest collection from any region. The need for conservation is now felt as the paddy cultivation affected by rapid climate change.

Keywords: Germplasm, Rice, *Oryza sativa*, Collection, Conservation

727 (P-111)

Effect of Storage Conditions and Packaging Material on Maintenance of Seed Quality of Onion Seeds

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Onion seeds are short-lived and deteriorate faster during storage. Packaging material greatly influence the storability of crop seeds. The objective of present study was to determine the effect of packaging material during storage of onion seeds conditioned to different moisture contents at different temperatures on the viability and vigour of two cultivars of onion namely AFLR and N-53 with 90 and 92 per cent initial germination respectively. Seeds conditioned to 4, 6, 8, 10 and 12% were packed in Plastic bags (250 gauge) and trilayered aluminum foil packets and stored at three different temperatures *i.e.* 4˚C, 20˚C and ambient condition for 24 months and observations were recorded at six months interval. For seeds conditioned to 4, 6 and 8% moisture content, the germination percent and seedling vigor were higher in aluminum foil packets than plastic bags at all storage temperatures. At 10 and 12% moisture contents, these parameters were higher for seeds stored in plastic bags. Throughout the storage period, seeds stored at low temperature (4˚C) irrespective of moisture or container maintained better viability (>80%). Seeds stored with higher moisture content at ambient temperature deteriorated faster in both varieties irrespective of containers. However in seeds with moisture contents between 4-8%, packaging in aluminium foil packets was superior. Results clearly indicate that medium/ short term storage of registered varieties/ DUS test samples of onion seeds in the PPV&FRA genebank can be best accomplished by reducing the moisture content to less than 10% and storing at 4 and 20˚C respectively.

Keywords: Deterioration, Germination, Viability, Vigour

734 (P-112)

Occurrence of Dormancy and Methods to Enhance Seed Germination in Wild Rice Accessions

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Seed dormancy in rice is a genetically controlled complex trait. It is considered to be an economically important trait preventing the premature germination of seeds when rainfall occurs during harvest. On the contrary, dormancy interferes in the handling of seeds for genebank storage. Seeds received for long-term storage are tested for initial germination and accessions registering more than 85% only are conserved in the genebank. Presence of dormancy necessitates the confirmation of viability through the tetrazolium test which is laborious and time consuming besides requiring special skills in evaluation. The present study was envisaged to understand the dormancy behavior of 30 wild rice accessions (28, *Oryza nivara* and 2, *Oryza rufipogon*) received for long-term conservation in the genebank which failed to germinate under normal test conditions. Tetrazolium test results indicated high initial viability (80-100%) confirming the existence of dormancy in all the accessions. Therefore these were subjected to various treatments such as exposure to 50 °C for 7 days, hotwater treatment at 50 °C for 15-30 minutes, manual removal of seed covering structures, afterripening of seeds at room temperature for 90 days and coapplication of GA_3 (0.03M) to decoated seeds. Among these treatments, co-application of GA_3 and afterripening were highly effective in alleviating the dormancy of various accessions leading to 50-100% germination. This implies the need for periodical germination tests during afterripening at room conditions until complete germination is achieved which is cost effective and will help to avoid unnecessary dis-qualification of valuable germplasm received for genebank conservation.

Keywords: Dormancy, Germination, Tetrazolium test

736 (P-113)

Oilseed Germplasm Collection in the Indian Genebank: Current Status and Future Concerns

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Oilseeds are next to food grains in cultivated area, production and value in India. Indian National Genebank at ICAR-NBPGR, the second largest in the world holds about 0.4 million accessions of various agri-horticultural crops 14% of which is comprised of the oilseed collection (42,279 indigenous and 14,545 exotic accessions). The success of a genebank depends on the extent to which the conserved diversity is linked to end-use. The collection passport and genebank management data are invaluable in planning for intended conservation and utilization. The current oilseed collection in the Natural Genebank includes traditional varieties/landraces (~20,000 accessions), released cultivars/hybrids (790), registered germplasm (154) and wild species (832 accessions representing 37 species), trait-specific germplasm (~3,000) and core/minicore sets of groundnut, safflower, sunflower and sesame. Abundance of diverse and locally adaptive traditional cultivars/landraces and wild species in the collection offers a valuable reservoir of desirable traits to the breeders including those climate change readiness. About 1,98,104 accessions of oilseeds including wild species are available globally, which can be used to enrich the national genebank particularly with respect to trait-specific accessions. Formerly about 5,000 groundnut accessions of Indian origin and trait-specific nature have been repatriated from ICRISAT. The genetic base of the currently cultivated oilseed varieties is narrow which can be further broadened by utilization of diverse germplasm in the national genebank. Post-collection care in oilseeds needs to be strengthened as the oil content has implications on seed moisture content and thereby on seed longevity.

Keywords: Long-term storage, Oilseeds, Seed gene bank

783 (P-114)

Seed Quality Enhancement through Seed Priming in Paddy (*Oryza sativa* L.)

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Seed germination is an important and crucial factor for good crop stand. Low germination and poor seedling growth can lead to large economic losses. This problem can be minimized by seed priming which is a sustainable method to enhance crop establishment, uniform emergence, and growth of plant on the field. Seed priming is a low-cost less cumbersome technology and does not need expensive chemicals and sophisticated equipments. The purpose of this study was to evaluate the effects of various methods of priming of seven rice genotypes received for long -term storage registering less than 85% germination which is the threshold level for acceptance of seed for genebank conservation in accordance to genebank standards. Seeds were subjected to nine priming treatments *viz*. hydropriming for 24 and 48 hr, osmopriming with PEG 6000 (1.5 MPa) for 24 and 48 hr, halopriming in 2.2% solution of Calcium chloride, Potassium chloride and Sodium dihydrogen phosphate for 24 hr and hormonal priming in 100 ppm of GA_3 for 24 hr. Non-primed seeds served as control. Results revealed that priming with GA_3 was the best among all the treatments for all the genotypes where significant enhancement of vigour index was observed (1162-2010.83) as compared to the control (763.7-1278.32). All other treatments enhanced the vigour index to various extents and also were genotype-specific. This implies that paddy seeds positively respond to several priming methods which can be applied as pre -sowing treatment before regeneration in order to enhance seedling vigour leading to better crop stand and yield.

Keywords: Germination, Halopriming, Osmopriming, Vigour index

803 (P-115)

Germplasm Handling for Long- and Medium-Term Conservation of Plant Germplasm at National Gene Bank in India

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Conservation and sustainable management of plant genetic resources (PGR) is a cooperative endeavour and requires active collaboration between genebanks and all crop-based donor organizations/institutes, both within and outside the country. With a view to conserving the varied PGR in the National Genebank (NGB), the Germplasm Handling Unit (GHU) has played a sheet anchor role in segregation, visual inspection, seed health testing and documentation of the accessions received for conservation. A study of the flow of unique germplasm during the last 15 years for conservation under medium- or long-term storage condition has revealed that out of a total of 2,15,737 accessions processed by GHU, 1,99,294 accessions (92.5%) have been found suitable for long-term storage based on their germination and viability. During the seed health testing, 5.43 % of the accessions were not found suitable as per genebank standards. Remaining accessions with less seed quantity or poor quality of germplasm could not qualify for conservation as per genebank standards. With the inception of National Agricultural Technology Project, the inflow of germplasm in NGB enhanced significantly. We analyse the trend of inflow of germplasm state-wise received during the past 15 years. It revealed that maximum number of accessions (17,575) of various crops were received from Andhra Pradesh followed by Uttar Pradesh (12,193) and with a minimum (175) from Goa state. The study is useful to further prioritize the states having rich genetic diversity from which the germplasm of a particular crop to be collected for long-term conservation in NGB.

Keywords: Conservation, Germplasm Handling, Plant Genetic Resources

856 (P-116)

Status of Rice Germplasm in the National Genebank, ICAR-National Bureau of Plant Genetic Resources, New Delhi, India

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Rice (*Oryza sativa* L.) is one of the most important dietary staples and is consumed by almost two thirds of the global population. The need for effective conservation of rice diversity for maintaining sustainable increase in productivity and climate resilience is a major global concern. Over 5,00,000 accessions of rice genetic resources are conserved in about 1,750 international and national genebanks around the world. The holding of rice germplasm in National Genebank of ICAR-National Bureau of Plant Genetic Resources (NBPGR) is the 2nd largest globally with 1,06,105 accessions (including 10,049 exotic accessions) after IRRI, Philippines (1,27,168 accessions). India is also the highest contributor of rice germplasm (13.49%) to the genebank of International Rice Research Institute, Philippines followed by Lao PDR (12.20%). The 96,056 indigenous rice accessions conserved in the National Genebank of ICAR-NBPGR include landraces (81,001 from 2 cultivated species), wild rice (1,426 from 18 wild species), genetic stocks (281 including 122 registered germplasm lines), released varieties/hybrid (1,226), breeding lines (1,582) and others (10,540). Though, this collection includes accessions from all the Indian states and union territories however, the major representation is from Odisha (26,107), Chhattisgarh (20,828), Andhra Pradesh (7,900), Madhya Pradesh (5,636), Kerala (3,683) and states of North-Eastern India (10,062). Trait-specific germplasm, such as for drought tolerance (21), tolerance to saline-alkaline soil (11) and resistant to many biotic stresses viz., bacterial leaf blight (110), rice gall midge (45), rice tungro virus disease (57), brown plant hopper (33) and rice blast disease (20) are also available in National Genebank.

Keywords: Conservation, National Genebank, Rice

Technical Session 2-B :

Conservation Strategies and Methodologies

Concurrent Session :

In-situ and On-farm Conservation

1477 (O-12)

The Role of Monastic Gardens in Sustainable Conservation of Grape (*Vitis vinifera* L.) Genetic Diversity in Armenia

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Having centuries of old tradition in viticulture Armenia characterized with high diversity of grape autochthonous varieties. There are more than 400 native varieties of which only 17.5 % are preserved ex situ. The ampelographic descriptions of most varieties are available. Historical data prove that in medieval Armenia the Monasteries were playing important role by developing the viticulture, as well as grape breeding, which means that the old vineyards of the Monasteries can be considered as possible places of rich genetic diversity of grapevine resources. Archaeological and ampleography data allowed to choose the old vineyards of the Noravank Monastery (13th-century) and Gndevank Monastery (10th-century) (Vayots Dzor), Haghpat Monastery (10th-century) (Lori), Vorotnavank Monastery (10th-century) and Tatev Monastery (11-17th centuries) (Syunik region) as possible habitants of old authochtonous varieties. From each vineyard the samples were collected and characterized morphologically (OIV 24 descriptors) and genetically (23 SSR markers). Unique genotypes with very high level genetic diversity were identified. The levels of observed and expected heterozygosity and PCoA were calculated. The neighbour-joining analyses were conducted. 10 varieties were re-discovered and considered for the conservation *ex situ* and *in situ*. The Monastic old vineyards are becoming an important source for identification of lost genetic diversity, which has not only scientific, but also economic and cultural importance. The Monasteries are becoming a natural environments for the effective preservation of the grape genetic resources in situ. The approach chosen became the useful model for lants which are possibly preserved in the Monastic vineyards.

Keywords: Grape, Authochtonous, *In situ*, SSR markers, Ampelography

1819 (O-13)

On-farm Conservation of Mango Diversity through Community Based Organization - A Case Study

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Malihabad is well known for its quality fruits and unique mango varieties. Numerous mango varieties in Malihabad existed as a result of selections from seedling mango plantings. Farmers are the custodian of these varieties in orchards over several generations. Number of seedling varieties and farmers varieties are decreasing because orchards planted with commercial variety grafts. Community efforts for successful and profitable production, linking suitable markets with producers and value addition of non commercial mango varieties gave birth to community based organization: The Society for Conservation of Mango Diversity (SMDC) established in 2009. Community members of four villages volunteered for developing CBO for managing farmers varieties 500 mango farmers are associated with SCMD. The SCMD aims to strengthen capacity of community farmers on the conservation of mango varieties by linking suitable markets with producers. The activities of the SCMD resulted: (i) assessed genetic diversity within community and prepared farmers catalogue, (ii) organized mango diversity fairs (>15); (iii) identified and multiplied elite materials for table and pickling purposes; (iv) developed community nursery and linked up with existing nurseries; (v) helped in registration process of 37 farmers and community varieties with PPV&FRA and (vi) improved livelihoods through better marketing of traditional and non-commercial varieties. We analysed experiences since creation of community based organization and on farm conservation initiatives taken by SCMD. Local community efforts of SCMD helped to achieved dual goals of supporting livelihood of mango growers of non-commercial varieties and on-farm conservation of mango diversity sustainably.

Keywords: Community Based Organization, Diversity Fair, Documentation, Non-Commercial Varieties

1786 (O-14)

'*Kulagar*' – A Potential System to Conserve the Crop Diversity

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Goa and the konkan region of Maharashtra are blessed with the diversity of tropical flora and fauna due to the nearness to the Western Ghats. The hot humid climate and the presence of heavy monsoon have made this region a biodiversity hotspot with beautiful landscape. Rural Goa and Konkan region farmers have a conventional homestead system of gardening transmitted from their ancestors called '*Kulagar*' to cultivate and conserve the local of crop plants near their household. It is an integrated system which includes cash crops, plantation crops, spices, fruits, local vegetables, medicinal and aromatic plants and flower crops. Some of the '*Kulagars*' includes animal components to make the system economic and complete. The cash crop component in a '*Kulagar*' can be arecanut, coconut, cashew nut, betel vine etc. In Goa, mostly areca nut based (rarely coconut based) '*Kulagars*' are common. The important local coconut landraces' Benaulim' and 'Calangute' and areca nut palms are trailed with black pepper and the interspaces are effectively utilized for the cultivation of pineapple, banana, shade tolerant vegetables and tuber crops like elephant foot yam. 'Mankurad' and 'Hilario' are two local Goan mango varieties with sweet relishing flavor and enormous diversity in size, shape and quality. In Goa, seven important varieties of banana *viz.,* Saldatti (AAB), Savarboni (ABB), Amti (AAB), Raspali (AAB), Velchi (AB), Myndoli (AAB), Sugandi (AAB) are cultivated in the interspaces of palms. Spice crops like nutmeg, cinnamon and underutilized fruit crops like Kokum, Jack fruit, Acid lime, Bread fruit, Karonda, Sapota., flower crops like Hibiscus, Jasmine(four different species), Marigold, Crossandra (Ratan aboli-unique with dark red petals) and medicinal plants like Tulsi are always a part of this system. Crop diversification, recycling of the resources, value addition and processing and byproduct utilization are important features of a '*Kulagar*'. Advanced crop production technologies are being incorporated in '*Kulagar*' by the new generation farmers to make it sustainable and economically viable.

Keywords: *Kulagar*, Goa, Konkan, Crop diversity, Conservation

148 (O-15)

Farmers' Participatory Conservation of Rice Landrace Champakali

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The rice landrace Champakali grown in the Ajara and Chandgad tehsils of Maharashtra is distinguished for its aroma and peculiarity. The variety is popular among urban areas and gains significant demand. However, the local farmers are reluctant about its cultivation due to low productivity. In this context, Farmers Participatory Variety Selection (PVS) was carried out with the objectives of varietal purification and conservation of the landrace. The individual progenies generated from local selections were evaluated through farmers' selection criteria for seed characteristics *viz*., grain length, grain breadth, Length: Breadth ratio. The consumption qualities refined the selection. Other factors are secondary for the farmers. Present work increased farmers' awareness and their access to improved variety. This PVS should supplement the formal breeding system to further improve product quality. To accelerate seed dissemination farmer-to-farmer exchange mechanisms was followed. A faster, more efficient and reliable pure-seed supply system than the traditional mechanism is required for proper maintenance of pure seed of the landraces like Ghansal, which can be better achieved through small-scale commercial producers and/or cooperatives.

Keywords: Champakali, Farmers Participatory Variety Selection, Rice landrace

379 (P-117)

Aegilops Spp. (Triticeae, Poaceae) in India- Identification of Species

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Aegilops (Triticeae) is a diverse genus that includes progenitor species and others used in breeding of wheat as a source of resistance to biotic and abiotic stresses. Several species are a part of germplasm under exchange for use in breeding programmes and genomic study and hence are represented in genebanks and herbaria worldwide to a greater or lesser extent. Species studied were represented as plant and seed samples belonging to 15 species (44 accessions) collected or introduced into the Indian region. Species-specific data on taxonomy, classification, distribution, habitat features, diversity, flowering/fruiting and genepool were delineated, and distinguishing characters were worked out and used to check species identity. *Aegilops tauschii* is the only species represented as collections from the south Asian and adjoining regions; other species were introduced. Characters important for establishing the correct identity of species pertained to differences in spikelets at the apex and base of the spike, in terms of relative sizes of awns, grains, presence and number of rudimentary spikelets, spikelets at a node, and nature of awns on glumes and lemma. These were used for establishing the correct identity of the morphologically close species, *A. geniculata*, *A. neglecta* and *A. triaristata*, and germplasm with confusion in identity- *A. vavilovii*, *A. peregrina*, *A. kotschyi* and *A. uniaristata*. Identification resource was developed with digital images for use in authentication of species/ materials. Key characters of young and mature spikes and spikelets, represented in plant specimens, were useful for identification of plant specimens, as well as fruits and grains.

Keywords: Aegilops identification key characters

1516 (P-118)

Community Seed Banks to Conserve Local Crop Diversity and Ensure Resilience against Climate Change

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India is known for the rich source of Agrobiodiversity with great scope of agriculture cropdiversity conservation, owing to the presence of 13 agro climatic zones, 2 global biodiversity hotspots and being the Centre of origin of major cereal, pulse, vegetable and fruit crops. Climate change is having a big impact on farming, growing diverse crops and varieties are very important because cropdiversity will have the capacity to withstand environmental stresses. Moreover, farmers should cultivate old traditional varieties that have evolved in a certain region and had more adaptability compared to conventional varieties. The informal seed systems are to be encouraged and local seed production of these diverse crops and varieties are to be encouraged. Traditional varieties can also possess some special traits which have good price in the market, thus improving farm income. The Community Seed bank (CSB) will help farmers to conserve existing indigenous crop diversity in a region, maintaining the availability which is normally unavailable in the formal seed systems. With this the seed supply within a community can be streamlined and a big diversity of seeds of various crops can be made available to the farmers. The CSBs can serve as the Centre of activity where women can be engaged in its maintenance and operation in conservation work. So a self-sustaining cycle can be established which consists of selection of different crops/varieties, their seed production, conservation in CSBs and cultivation.

Keywords: Climate change, Community Seed Bank, Crop Diversity.

424 (P-119)

Assessment of Loss of On-farm Diversity of Traditional Crops in Earthquake Affected Mountain Regions of Nepal

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The devastating earthquake that hit Nepal on 25 April 2015 was most severe in rural farm households particularly in remote and risk-prone mountainous regions where farmers' dependence on food security was high from self-saved and locally exchanged seeds of traditional crops and varieties. Aftermath of the earthquake, various national government and international relief agencies made efforts to rescue human beings, livestock and valuable assets but no immediate initiatives were made to rescue endangered seeds and native crop varieties. Considering the critical role of local crop diversity in the livelihood of smallholder farmers in remote and risk-prone mountainous regions, Bioversity International and National Gene bank of Nepal jointly initiated a study on rescue seed collection, conservation and repatriation of local crop genetic resources that are endangered from disasters. The main objective of the study was to assess and measure loss of on-farm diversity of traditional crops in earthquake affected areas. Rescue seed collection missions and information collection on seed losses were carried out in most severely affected villages of 10 earthquake affected districts. The collected information was analysed for diversity assessment, regeneration and processing for their safe storage in national gene bank. The most endangered and valuable local diversity based on farmers' demand are planned for repatriation to same communities and community seed banks for on-farm conservation and strengthening local seed system. This strategy will be useful to promote both ex situ and in situ conservation and help to safeguard native crop diversity for future generation in disaster affected areas.

Keywords: Diversity assessment, Local diversity, Traditional crops, Rescue collection, Repatriation

531 (P-120)

On farm Conservation of Shrubs as Provider of Ecosystem Services in Hot Arid Region

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Shrubs are an important element of arid vegetation and an integral component of the traditional farming system. They provide ecosystem services and support the livelihood of inhabitants/farmers during normal and drought period by providing a variety of economic products e.g. food, fodder, fibre, fuelwood, medicine, gum etc. Recent studies on germplasm collection, evaluation and conservation of shrubs in western Rajasthan revealed the existing diversity and utilization of key arid shrub species viz., *Acacia jacquemontii, Calligonum polygonoides, Haloxylon recurvum* and *H. salicornicum* etc. in the region. Most of these shrub species are traditionally utilized by the farmers as per habitat and suitability of species However, the population of many of these species has decreased to a great extant in the crop fields due to changes in land use pattern and mechanization. Various studies indicate that shrubs will be very important vegetation component in future climate change scenario, thus emphasizing the conservation of existing diversity of shrubs. Utilizing the hot arid shrub diversity as live hedge system in crop fields has prime and yet unrealized role. The live-hedge system also changes the microclimate by moderating the extreme temperatures and decreasing the adverse effects of high wind velocity in crop field. Many of these species also support number of faunal and floral species particularly climbing ones, resulting in improvement in the overall agro biodiversity. Thus, there is a need to promote on farm *in situ* conservation of key arid shrubs for providing ecosystem services in the hot arid region.

Keywords: Shrubs, Live hedge, Germplasm, *In situ* conservation, Agro biodiversity

639 (P-121)

Indigenous Rice Germplasms (Locals) of West Bengal: The Status and Conservation strategy

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To assemble and preserve rich rice germplasms field collections are conducted and a total of 126 local rice types are collected from ten districts of West Bengal grown under different land situations and climatic conditions. As many as 41 locals are collected from the district Purulia, 32 from Midnapur, 20 from Burdwan and 11from Bankura district. The collections are limited by 1 to 6 for other districts (Jalpaiguri, Nadia, Hoogly, 24 Parganas, Dinajpur and Howrah). They are evaluated for different plant characters including panicles, grain, kernel characters, grain protein content and cooking quality through amylose estimate. As many as 19 promising locals, both aromatic and non-aromatic from different ecosystems are identified, of which 8 are from laterite rain-fed, 9 from coastal rain-fed, 2 from old alluvial rain-fed. Of which 5 scented, 4 from lowland (up to 30cm water) of coastal rain-fed and only one from old alluvial rain-fed. Scented rices are poor yielder with low grain density. The promising types under low land (up to 30cm water) and shallow deep (up to 70cm water) record in general 26 to 32 g yield/plant with grain density ranging from 40 to 70. The district Purulia records almost half the rice productivity of that of district Burdwan. Maximum indigenous germplasms are collected from Purulia where locals continue to dominate under limited rainfall and poor soil nutrition of laterite soil. Locals are replaced by high yielders in district Burdwan with high input agriculture. A strategy has been suggested to explore and conserve traditional rice through active participation of Panchayet with Centre State responsibility allocation.

Keywords: Collection, Conservation strategy, Ecosystem, Evaluation, Indigenous germplasms

650 (P-122)

Diversity of Native Orchids in Bangladesh

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Due to diverse agro-ecological conditions, Bangladesh flora is richly endowed with orchids, with an estimated 50 genera and more than 200 species. Orchids are found in all parts of Bangladesh but mostly available in the hilly areas of the country. Their elegance, exotic shapes, and wild colours give them a haunting beauty. Native orchids are not only important for their natural beauty but also important for medicinal properties, ecological diversity and reproductive complexity. In Bangladesh, orchids are used as cut flowers and pot plants though it's commercial orientation is not given so much emphasis like other flowers. Moreover, those orchids considered threatened due to destruction of their natural habitat. So, there is an urgent need for collection, characterization, documentation and conservation of these orchids including geographical variations which could be used for future improvement of that crop. Floriculture Division of Bangladesh Agricultural Research Institute is collecting the orchids from natural sources since 2002. Till now 44 orchid species under 27 genera have been collected those showed a large variations in collection sources, nature of habitats, flower colour, shape, blooming period and duration etc. Maximum orchids are suitable for pot plants but some of them such as *Phaius tankervilliae, Calathe sp* and *Eulophia andamanensis* are considered as cut flowers. Among the collected germplasms, 10 were on the verge of extinction. This paper broadly focuses on the variability of native orchids in Bangladesh. The findings of the paper are expected to arouse interest to the breeder for further improvement in this field.

Keywords: Native Orchids, Variability, Conservation

934 (P-123)

Madhuca indica j.f Gmel. (Mahua) Candidate Tree Selection Based on the Perception of Tribal Community and Scientific Validation

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Madhuca indica commonly known as mahua belongs to family Sapotaceae. Mahua is believed to be back bone for livelihood and cultural prospective of tribal community. The variation within the species with respect to morphology, flower and seed are well recognized by the tribal communities. Considering the tribal needs and their perceptions towards selection of best Mahua tree, a pilot study was undertaken by BAIF Development Research Foundation, under Maharashtra Gene Bank project covering three agro climatic zones of Maharshtra. Through active involvement of peoples participation, totally, 58 Mahua candidate trees were selected and scientifically validated at various levels.The study revealed that, the highly significant differences were observed with flower dropping period (29.71±0.12), fresh flower yield (342.42± 24.30), flower dry matter (94.93± 0.24), seed oil (39.69±2.14), dry matter in seeds (94.80±0.23) at Dhadagaon over Ettapalli and Jawahr clusters and flower moisture (93.62±0.46), dry flower (7.99±0.16), Zn (4.42± 0.16) at Ettapalli (Gadchiroli Dist) cluster over Jawhar (Palghar Dist) and Dhadagaon (Nandurbar Dist) clusters. The only maximum mean value of crude protein (5.33±0.18) was recorded at Jawhar cluster. Similarly, the significant difference was recorded with respective tree canopy (127.32± 16.76) and Fe contain in flower (81.48± 13.07) at Ettapalli and Dadagaon cluster respectively. The maximum potential of seed oil from selected candidate tree was 50.47 %.This study also revealed that, mass multiplication of Mahua trees having specific characters like high flower and seed yield, protein, taste, moisture, Fe, Mn could be under taken for conservation of best candidate Mahvua tree.

Keywords: Agro climatic zones, Candidate tree, Perception, Variation

1089 (P-124)

Methods and Best Practices for enhancing the use of Nutritious Small Millets in India

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Despite significant progress in its Gross Domestic Product, India is among the countries with the most malnourished children, thus facing a significant nutrition challenge. Micro-nutrient deficiency in infants and young children can lead to impaired psychomotor development, coordination and scholastic achievement, as well as reduced physical activity. Small millets (Eleusine, Setaria, Panicum, Paspalum) are sources of micro nutrients such as calcium, iron, and folic acid, in addition to being climate hardy crops. The most popular minor millet across India is finger millet, which is cultivated over nearly 1.6 million hectares with annual production of 2.4 million tonnes and productivity of around 1,534 kg/ha. The area under other minor millets is slightly smaller (1.1 million ha) with notably lower productivity (635 kg/ha; 0.7 million tonnes/year). The area under minor millet cultivation in India has significantly decreased since the 1950s, which is ascribed to a number of agronomic and socio-economic aspects: Lack of suitable improved varieties and cultivation practices, poor extension systems for yield enhancement and crop promotion, lack of specific post-harvest and processing technologies for small users, low economic competiveness, poorly organized value chains, lack of attractive, modern food recipes, and insufficient awareness of nutritional value and income opportunities. With the support of IFAD and Bioversity International, these challenges were addressed in a holistic 7C approach over the last decade, involving custodian farmer communities, State government, research and development institutions, and the private sector. This presentation shares experience of applying 7C holistic approach: Chronicling, Conservation, Cultivation, Consumption, Commerce, Collectives and Communication.

Keywords: Small millet diversity, Stakeholders, Value chain development, Holistic approach

1888 (P-125)

Incentives, Innovations and Institutions for *in situ* Conservation: A 30-Year-Long Perspective On Community Based Climate Change Adaptation

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Building upon a study by CMA, IIMA started in 1988-89 in the flood prone regions of eastern India, I have analysed the plot wise varietal choice to cope with edaphic and climate change effects. The plot-wise maps of the three study villages were monitored in 1988-89, 2002-2004 and 2013-14. The incentives preferred by communities for in situ conservation were studied from gender and wealth perspectives. Decadal surveys showed a steep decline and almost complete erosion of diversity of traditional paddy varieties. Even among the new varieties and hybrids, dominance of a couple of varieties was found. Although a traditional improved variety still dominated the high risk flood prone lowlands. The role of women in coping through exchange of information, companion plants/weeds, seeds, nursery and labour was also studied. The implications are: the community level coping strategies need strengthening through public as well as collective management of nurseries of diverse varieties. Cultivation of traditional varieties on common lands and/or by bigger farmers. Insurance, compensation of yield differences with modern varieties, procurement at competitive price for PDS and food processing industry may be encouraged. Potential for market mediated instruments for in situ conservation thus remains to be properly exploited. Cultural mechanisms of coping need a virtual as well as proximal platform of exchange of agro-biodiversity resources and associate knowledge. Given the erosion of specific characters useful for coping with stress under ex situ conditions, the case for in situ conservation deserves much more focused attention than has been the case so far.

Keywords: Agro-Biodiversity, Consumer Preference, In Situ Conservation

Technical Session 2-C :

Conservation Strategies and Methodologies

Concurrent Session :

In vitro, Cryo, and DNA Banking

1305 (O-16)

Success Story of Rejuvenation of Near Extinct Fragrant Banana, cv. Manoranjitham through Inter Institutional and Public Private Partnership

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Kolli Hills in Tamil Nadu is the home for fragrant banana landrace Manoranjitham protected by the 'Malyali Tribes' for religious preference and economic security. Hexanol, limonene and eugenol based compounds in pulp and skin contribute for the fragrance which lingers over a week's time. Screening at NRCB has identified cv. Manoranjitham as one of the tolerance gene sources to Eumusae leaf spot disease (*Mycosphaerella eumusae*) apart from its possible exploitation in improving Cavendish clones (AAA) due to seed fertile nature. But a survey indicated it's near extinction due to rampant Fusarium wilt caused by *Fusarium oxysporum fsp. cubense* viral diseases like Bunchy Top and pseudostem weevil (*Odioporus longicollis*). Through a DBT supported programme, NRCB demonstrated that public private partnership could successfully rejuvenate a crop landrace. The programme involved collection of few existing planting materials, virus indexing, large scale multiplication through tissue culture and reintroduction into their natural habitat achieved through adoption of villages, beneficiaries, training on production and protection technologies, market support and overall technical back stopping. NRCB has successfully rejuvenated an important banana landrace with breeding potential and extended area under cultivation in its natural habitat for the economical, food and nutritional security of the tribal farmers of the Kolli Hills. Inter institutional collaboration has resulted in safe conservation at NBPGR both under *in-vitro* and cryobanks.

Keywords: Cryobanks, Fragrant Banana, Kolli Hills, Landrace

298 (O-17)

Pollen Cryopreservation in Aid to Conservation of Potato Genetic Resources

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Pollen grains are a rich source for diverse alleles in any genepool, holding large genetic diversity in small sample size, offering an effective propagule for germplasm conservation. Its inherent ability of hardiness and stability in harsh conditions enables its long-term cryogenic storage. Cryopreservation was used to conserve pollens of six potato varieties Kufri Girdhari, Kufri Himalini, Kufri Himsona, Kufri Jyoti, Kufri Kanchan and Kufri Shailja at Central Potato Research Institute Shimla. Pollen collected were packed in gelusil capsules, kept in cryo-vials, immersed in liquid nitrogen cryocan. A single lot was tested after 24-hrs of cryopreservation using pollen germination and double staining with Alexanders stain, containing malachite green for pollen cell wall staining (indigo-blue colour) and acid fuschine for pollen protoplasm (purple). Under similar conditions, the germination response for fresh and cryopreserved varieties was observed to be statistically at par, with heat-killed pollen as negative control showing nil germination. The germination response among varieties varied from 4.6% (Kufri Jyoti) to 24.6% (Kufri Himalini). Low germination response was mainly attributable to pollen grains showing no protoplasms and having only indigo-blue staining walls, this may reportedly be due to abnormal meiotic segregation producing inviable pollen in potato. The pollen tube lengths varied from 10 μm to 500 μM after 3 hrs of incubation in medium, indicative of differences in pollen vigour. The positive germination response after 24-hrs cryogenic treatment is a direct indicative of its prognostic long-term storage, for potato germplasm conservation, directly channelled into breeding programmes, also offering ease of transport and germplasm exchange.

Keywords: Conservation, Cryopreservation, Germplasm, Pollen

1325 (O-18)

Cryopreservation of *Allium* Germplasm Resources at ICAR-NBPGR-Achievements and Challenges

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Most of the *Allium* species, selectively or exclusively vegetatively propagated, are maintained in the field genebank which is not only labour intensive but also suffer from disease outbreak and climatic vagaries. *In vitro* conservation though promising, requires periodic subculture, constant monitoring and is also challenged with accumulation of endophytes particularly in case of garlic (*A. sativum*). Cryopreservation is the preferred choice for safe and secure, long-term conservation of *Allium* germplasm resources owing to aforementioned problems. In recent years, vitrification-based cryopreservation techniques have been successfully applied to many vegetatively propagated crops including alliums. These comprise species which are not only used as a vegetable or a spice but to some extent, as a medicinal plant also. Though garlic is more popular and widely cultivated, species like *A. chinense, A. hookeri* and *A. tuberosum* hold potential as under-utilized, commercial crops. Several exotic species (*A. fistulosum, A. ramosum* and *A. scorodoprasum*) along with above mentioned *Allium* species are being maintained in the field genebank and *in vitro* genebank at ICAR-NBPGR. Shoot tips, excised from cloves (in garlic) or from *in vitro* plantlets (in other *Allium* species) served as the explants for cryopreservation. Three cryopreservation techniques, namely, vitrification (V), droplet vitrification (DV) and encapsulation-dehydration (ED) were tested. Depending on the species/genotype, varying degree of success (10-60%) was achieved, with shoots regenerating without intermediary callus. Cryobanking has been initiated in some *Allium* species. Present findings will focus on achievements and challenges with respect to *Allium* germplasm cryopreservation at ICAR-NBPGR.

Keywords: *Allium* germplasm conservation, Cryopreservation, Droplet vitrification, Encapsulation-dehydration, Vitrification

876 (P-126)

Cistanche Tubulosa - An Endangered Flora with Rich Medicinal Value Endemic to Sand Dunes of Rajasthan, India

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Cistanche tubulosa (Schenk) R. Wight of the family Orobanchaceae has been found growing as a parasite on *Calotropis, Tamarix* and *Lantana* species in Beechwal village of Bikaner, Rajasthan. *Cistanche* is all flower bearing parasite grows on roots of desert shrubs due to absence of chlorophyllus leaves. This rare species produce dense pyramid spike of bright yellow flowers topped by maroon tinted buds. The seed germinates on the host root near the soil surface and penetrates haustoria into the deeper layers of the root, *i.e.* to the centre of metaxylem to tap the nutrition from the host. It is a powerhouse herb and its use has evolved over nearly 2000 years. The dried succulent stem is used as a potential food ingredient to prevent hyperglycemia and hyperlipidemia in Chinese medicine. Active compounds such as echinoside, acetoside and kankanoside of *C. tubulosa* are used for its multifaceted restorative effects, increasing the hyaluronic acid and improving immune function. Clinical research has shown that it increases the levels of free testosterone and have strong age related neuro protective properties. In the current world, it is at the brink of extinction due to severe exploitation for its high medicinal value as it is primary source material in the official pharmacopoeia. The population of the species has notably decreased and it was placed on CITES which requires monitoring. While the situation with *C. tubulosa* continues to be a serious problem, use of alternative species, avoiding over collection, artificial propagation along with its hosts and conservatory measures are increasingly important to protect these desert plants from the endangered species list.

Keywords: *Cistanche tubulosa*, medicinal value and endangered species

1193 (P-127)

Evaluation of Germplasm of and Standardization of Propagation Techniques of *Inula Racemosa* Hook.F. : An Endangered Medicinal Crop of North Western Himalayas

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Inula racemosa commonly known as *Pushkarmool* is an endangered medicinal plant of Himalayas is highly valued for its roots and is a source of raw material for pharmaceutical industries. Current work has been carried out on the basis of field trials conducted in the Department of Forest Products, Dr YS Parmar University of Horticulture & Forestry, Nauni, Solan, (HP). Observations on morphological and quantitative characteristics were observed from eight different sites *i.e*. Keylong (G_1), Kardang (G_2), Dalang (G_3), Sissu (G_4), Udaipur (G_5) and Kukumseri (G_6) from Himachal Pradesh (Lahaul & Spiti) and Tangmerg (G_7) and Shopian (G_8) from Jammu & Kashmir (Kashmir valley). The results of morphological and quantitative parameters indicated that maximum plant height, maximum leaf size, number of stems, fresh root weight and essential oil (%) was recorded from germplasm collection sites G_5 and $G_{6.}$ For seed characteristics maximum seed weight, moisture content, seed viability and germination (%) was also registered for sites collection G_5 and G_6. The maximum collar diameter and seedling vigour index was recorded in pre-sowing treatment 150 ppm $GA_{3,}$ whereas maximum fresh shoot weight, root weight, dry shoot weight, dry root weight and maximum root length was also recorded in treatment GA_3 150 ppm. The effect of location site on the germination and growth at two different location sites was found to be significant and the maximum sprouting per cent,, number of shoots, number of leaves, number of flower heads maximum primary root length, fresh root weight and dry root weight was observed from germplasm collection site G_5 and G_6.

Keywords: Germplasm, Propagation, Treatments

1285 (P-128)

Application of *In vitro* techniques for Conservation of Indian Medicinal Plants – A Case Study

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Medicinal plants play a critical role in the health care provision of all sections of the world's population either directly as folk remedies or indirectly in the preparation of modern pharmaceuticals. Last three decades have witnessed increased application of *in vitro* techniques for rapid multiplication and medium-term conservation of medicinal plants. In India, *Bacopa monnieri* L. has been used for a variety of ailments in traditional as well as modern medicine system due to its rich secondary metabolites of pharmaceutical importance. Primarily only wild populations serve the source of raw material which will be a limiting factor for its use due to indiscriminate collection, unless safeguarded. In the *in vitro* gene bank at ICAR-NBPGR, *in vitro* multiplication, an essential prerequisite for *in vitro* conservation programme, has been standardized and applied to *Bacopa* germplasm collected from different agro-ecological regions. Amongst several slow growth strategies experimented for medium-term conservation, subculture duration could be enhanced to 14 months with mannitol, 12 months with sucrose, 15 months with minimal media and 24 months with mineral oil overlay, using polypropylene caps as closures under culture room conditions. For long term-conservation, cryopreservation is the only option in vogue. Shoot tips were successfully cryopreserved with low recovery and the regenerated plantlets were successfully transferred to pots. The protocol standardized thus far has the potential application in bulking up the material for pharmaceutical purposes for now as well as its availability for future.

Keywords: *Bacopa monnieri,* Cryopreservation, *In vitro* conservation, *In vitro* gene bank

1316 (P-129)

Vapour Phase Storage – Potential Technique for Extra Long Term Seeds Conservation

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Plant Genetic Resources contributed enormously for global food security, poverty alleviation and most significantly for sustainable development of agrobiodiversity. Seed being a form of genetic resources serves as the starting point in agriculture. This has to be perpetuated and maintained in its original state. With the success in seed conservation in *in vitro* gene banks *viz.,* long term storage or at 5°C medium term storage, germplasm still necessitated with storage condition where it can be kept viable for indefinite period and minimum requirement of regeneration which is considered to be more labour intensive in the field of seed conservation. This can easily resolved by the use of the modern technology called 'cryopreservation (-196°C)'. Further the use of vapour phase temperature (-150°C) rather utilizing -196°C as a storage temperature found to reduce the cost per accession storage at gene banks along with the thriving seed recovery. This was conceptualized during 2014-2015 in the Department of Plant Genetic Resources, TNAU, Coimbatore through the study of few major vegetable seeds with the morphometric methods as a parameters for investigation and found its relative amenability under sub zero vapour phase storage condition (-150°C) exposing it fitness towards extra long term conservation.

Keywords: Seeds, Vapour phase temperature (-150°C), Extra longterm storage

1320 (P-130)

Development of Cryopreservation Protocol in Dahlia Germplasm

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Possessing brilliantly coloured flowers, dahlias are a favourite amongst decorators, exhibitionists and wedding planners coupled with their usefulness for garden display. Crop improvement in dahlia relies heavily on availability of a wide genetic base of promising genotypes. Though representing one of the most popular ornamental crops not only in India but the world over, their maintenance in field genebanks is fraught with challenges including safety from disease outbreak/climatic perturbances. Plant tissue culture techniques offer great promise for conservation of dahlia germplasm by eliminating the above risks along with faster multiplication of elite clones. Long term conservation by cryopreservation offers a feasible option for maintaining important cultivars of clonally-propagated ornamental plants including dahlias. Research on cryopreservation of dahlia is very limited and needs further attention. At ICAR-NBPGR, both vitrifictaion (V) and droplet vitrification (DV) methods were used for cryopreservation of cultures of dahlia germplasm using shoot tip and nodal segment explants. Explants, isolated from mother cultures maintained on shoot multiplication medium and also pre-grown on the same medium, failed to survive LN freezing irrespective of using V or DV method. Inclusion of high sucrose (10%) in the pre-growth medium was conducive for regeneration after LN freezing. Depending on the cryopreservation method used (DV *vs* V), there was better regeneration of shoot tips (20% *vs* 10%) and nodal segments (20% *vs* 0%) following LN freezing. Present findings on cryopreservation of dahlia germplasm are very important as they offer the feasibility of cryopreserving the germplasm for long term conservation.

Keywords: Cryopreservation, Dahlia cultures, Droplet vitrification, Vitrification

1589 (P-131)

Germplasm Conservation Via Encapsulating *In Vitro* Generated Shoot Tips and Nodal Segment of *Capparis Decidua*

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A methodical procedure for conservation of *Capparis decidua* explant was estabilished employing *in vitro* generated shoot tips and nodal segments for encapsulation and complexation in 3% alginate solution and 100mM calcium chloride .Shoot tips and nodal segments were encapsulated and stored at 4^{o}c and 8^{o}c temperature whereas immediate cultured synthetic beads kept as control. Seed longivity was investigated by storing synthetic seed at 4^{o}c and 8^{o}c for 20, 30 and 40 days respectively. The viability/ germination was depicted 80 %(maximum) in the seeds stored at 4^{o}c and 8^{o}c respectively for 30 days on MS Media MS 1, MS2, MSA AND MSB. The time taken for germination was comparatively swift on MSA containing 1mg/l BAP+1mg/l NAA+ 0.2% charcoal, Media MSB containing 1/2MS+0.1mg/l BAP+0.7mg/l IBA+ 2.5gm phytagel, responded good in case of nodal segments. Based on the results of the moisture content percentage, synthetic seeds stored for 30 days at 4^{o}c and 8^{o}c respectively manifested moisture content 69.7% and 50.9% , which shows highest germination (90% on MSA &80% ON MSB). The encapsulated shoot tips of *capparis decidua* responded 100% conversion to plantlets as compared to nodal segment.Intact plant regeneration was attained from the synthetic seeds of shoot tips .The present experiment could effectively be used for estabilishing a certain system for conservation, short term storage and production of synthetic seed to be released for commercial purposes.

Keywords: *Capparis decidua*, Encapsulation, MS Media, Regeneration, Synthetic seed.

1640 (P-132)

Application of Cryotherapy for Eradication of Banana Viruses in *In Vitro* Conserved Germplasm - A Preliminary Study

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The present work was undertaken to study the efficacy of cryotherapy on nine accessions of *in vitro* conserved *Musa* germplasm out of 50, for generating virus-free material. All accessions were indexed for two viruses, namely, *Banana bunchy top virus* (BBTV) and *Banana bract mosaic virus* (BBrMV) using polyclonal antisera kits by DAS ELISA, and five were subjected to PCR/RT-PCR for BSV and CMV viruses and viewed under TEM to visualize virus particles. The germplasm accessions were cryopreserved using droplet-vitrification protocol on proliferating meristems. Post-cryotherapy, all samples were retested for virus, as before. Out of the nine banana samples tested for the BBTV and BBrMV, 100% were free from *BBTV* whereas only one was infected with BBrMV, based on DAS-ELISA test. Cryopreservation of nine accessions yielded mean shoot regeneration rate from 3.3 to 38.9%, depending on genotype. The accession IC250618 (Dwarf Cavendish, AAA) was found free from all the four viruses. Similarly accessions IC250708 (Kottavazhai, AAB) and IC250585 (Boothi Bale, ABB) were found free from BBTV and BBrMV in both pre and post-cryotherapy tissue, based on DAS ELISA test. A success rate of cryotherapy of 25% for BSV elimination and 33% for BBrMV was achieved in the accession IC250618 (Dwarf Cavendish, AAA). Present study demonstrated that cryotherapy is a potential technique for virus elimination. Specific virus(es) can be detected in plants regenerated after cryotherapy, using appropriate reliable methods such as ELISA for virus coat protein, RT-PCR for RNA virus, PCR for DNA markers and TEM for visualization of virus particles.

Keywords: Cryotherapy, ELISA, PCR, RT-PCR, Virus eradication

1647 (P-133)

Virus-indexing of *In Vitro* Conserved Strawberry Germplasm in *In Vitro Gene Bank*, India

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Strawberry accessions (69) conserved in In Vitro Gene Bank (IVGB) of ICAR-NBPGR, New Delhi were virus-indexed during 2009 to 2014 using commercially available antiserum kits against seven strawberry viruses viz., *Arabis mosaic virus* (ArMV), *Raspberry bushy dwarf virus* (RBDV), *Raspberry ring spot virus* (RpRSV), *Strawberry latent ring spot virus* (SLRSV), *Strawberry mild yellow edge virus* (SMYEV), *Tobacco streak virus* (TSV) and *Tobacco necrosis virus* (TNV). DAS-ELISA and electron microscopy (EM) technique was employed to detect viruses in *in vitro* accessions and results revealed presence of ArMV (1), RBDV (29), RpRSV(9), SLRSV (11), SMYEV(34) and TSV(20). Accession F-50 was infected with six viruses except TSV and accessions F-2, F-36, F-42, F-44, F-45, F-46, F-51, FS-5, FS-6, FS-7, FS-8, FS-11, FS-14, FS-22, FS-23, FS-25, FS-27, FS-31and FS-34 were found free from the seven viruses tested. SLRSV was detected in known infected *in vitro* accession (F2V) confirming the sensitivity of Agdia Kits uses for detecting strawberry viruses. However, no virus was detected by EM when leaf-dip method was used. The aim of virus-indexing in *in vitro* conserved germplasm at IVGB was to generate passport data for the germplasm accessions conserved and identify virus-free accessions.

Keywords: Conservation, Detection, Strawberry

1832 (P-134)

Conservation of Fragaria Germplasm at ICAR-NBPGR

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Strawberry cultivation is gaining importance in Indian agriculture. Farmers are interested in good quality fruiting varieties while breeders require quality germplasm for crop improvement purposes. Since, Fragaria spp. (family Rosaceae) is a vegetatively propagated crop, the germplasm is conventionally maintained in the field genebanks in the Regional Station of ICAR-NBPGR, Bhowali. However, the field-grown plants are exposed to pest-pathogen and natural vagaries including climate change. Therefore, in vitro conservation of germplasm is necessary as complementary method to the field genebank. ICAR-NBPGR, New Delhi, is actively involved in the in vitro conservation of strawberry germplasm. The protocols have been developed using slow growth methods at low temperature storage. Cultures are raised from shoot tips and runners from field genebank-grown plants to have true-to-type accessions. More than eighty accessions are being maintained in the In Vitro Genebank of ICAR-NBPGR including many exotic accessions. The average subculture period ranges from 6-8 months. About 60 accessions have been virus indexed against seven viruses. The cultures are also being conserved at normal growth conditions. Cryopreservation of in vitro- grown shoot tips of strawberry using vitrification based techniques, viz., encapsulation-dehydration and vitrification have been attempted for long-term conservation.

Keywords: *Ex situ* conservation, Tissue culture, Strawberry, Slow growth, Cryopreservation

1841 (P-135)

Influence of Preculture Conditions and Dehydration Temperature on Cryopreservation of *Elettaria Cardamomum* Shoot Tips

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Cryopreservation is the most suitable long-term storage method for genetic resources of vegetatively propagated crops like *Elettaria*. At NBPGR, New Delhi efforts are being made to develop an efficient cryopreservation technique for *in vitro* grown shoot tips of *E. cardamomum* using vitrification method. Standardization of preculture duration and sucrose concentration is needed to obtain the best regrowth for all techniques. The influence of preculture medium on the shoot tips was studied using –Murashige and Skoog medium containing three concentrations of sucrose (0.3M, 0.4 M and 0.75M) for three incubation periods (24, 48 and 72 h) at 25ºC temperature, 16/8 h day/night photoperiod. *In vitro* grown shoot tip explants of *E. cardamomum*, exhibited 60% regrowth after 48 hrs of preculturing in 0.4M sucrose at 25^{0}C. In the vitrification procedure, precultured shoot tips were osmoprotected with Loading solution, LS (A mixture of 2M glycerol and 0.4 M sucrose) for 20 min; before being dehydrated with a highly concentrated vitrification solution (PVS_2) for 30 to 90 min at 25ºC. The dehydrated explants were then transferred to 2 ml cryotubes, suspended in 1 ml PVS_2 and plunged directly into liquid nitrogen. After 1hr LN exposure cryovials were thawed for 2-3 min. at 40^{0}C. Added unloading solution (MS + 1.2M sucrose) to the cryovials and incubated for 10 min twice at RT. 30 to 50% pre-freezing regrowth was recorded in the explants exposed to LS for 20 min. followed by 30 to 90 min PVS_2 dehydration. After 4 weeks of LN freezing inspite of 100% survival of explants, no regrowth was noted. For better recovery growth, the influence of sucrose concentrations, duration period for preculturing, duration of dehydration and suitable regrowth medium for cryoprotected shoot tips is under progress.

Keywords: *Elettaria*, Cryopreservation, Vitrification, Preculture

Technical Session 2-D :

Conservation Strategies and Methodologies

Concurrent Session :

Animal and Aquatic Genetic Resources

39 (O-19)

Impact of Structured Breed Improvement Programmes on Genetic Improvement and Conservation of Indian

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The All India Coordinated Research Project (AICRP) on Goat Improvement is a long term, in-situ based, mega conservation and genetic evaluation programme involving animals from institutional farms as well as from traditional goat keepers. Presently, 13 goat breeds and two lesser known genetic resources, stationed at 18 centers, located across various agro climatic zones of the country are under animal identification and field performance recording for genetic evaluations. The breeds covered are Barbari, Jamunapari under semi-intensive farming system and Assam Hill goat, Black Bengal at Kolkata and Ranchi, Gaddi, Marwari, Osmanabadi, Pantja, Sangamneri, Sirohi, Ganjam, Surti and Malabari under in-situ conditions. Conservation of Barbari, Jamunapari, Surti, and Sangamneri threatened goat breeds are simultaneously taken care of. Presently, India is facing scarcity of true to the breed type bucks for future breeding and conservation. In the project, for each of 14 breeds covered, 30-150 genetically superior bucks every year are produced for conservation and breed improvement in their home tract.

Keywords: Goat management, Genetic improvement, Impact

675 (O-20)

Germ Cell Transplantation into Adult Recipient Fish for Speedy Propagation of Endangered Germlines

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Germ Cell (GC) Transplantation (GCT) is a powerful assisted reproductive technology consists on the transplantation of donor GCs into the gonads of a sterile recipient animal for rapid and unlimited production of donor-origin gametes. Here we describe the establishment of a working model for xenogeneic GCT in sexually competent adult fish. The spermatogonial cells isolated from the prepubertal goldfish *Carassius auratus* (Cyprinidae), were transplanted into the gonads of sexually mature adult common carp *Cyprinus carpio* through genital papilla, which have been prior depleted of endogenous GCs by a combination of cytotoxic drug Busulfan (40 mg/kg; total 5 dosages) and elevated water temperature (38°C) treatments. The observation of the donor cells' behaviour showed that transplanted goldfish-origin spermatogonial cells were able to recolonize the recipient common carp gonads and resume spermatogenesis within 4 months from the GCT. The presence of donor-derived gametes was confirmed by molecular tools using species-specific marker in the surrogate parents and crosses (artificial insemination) with pure goldfish parents produced hybrids and pure goldfish offspring, with donor-derived germline transmission rates of 45.5–60%. These findings indicate that transplantation of spermatogonial cells into sexually competent adult fish, devoid of endogenous GCs, can considerably shorten the production time of donor-derived gametes and offspring and could play a vital role in germline conservation and propagation of commercially valued and/or endangered fish species.

Keywords: Conservation, Fish, Germ cell transplantation, Surrogate gametes, Spermatogonial cell

1890 (O-21)

Options and Strategies for the Conservation of Sheep and Goat Genetic Resources for Food Security

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Sheep and goats were domesticated about 10,000 years ago and are disseminated all over the world because of their great adaptability to varying environmental conditions and the different nutritional regimes under which they were evolved and subsequently maintained. They proved useful to human community due to their productivity, small size and non-competiveness with him for food. There are about 900 million goat and 1100 million sheep around the world with the ratio of 1:1.25 and the ratios varied among the different parts of the world. It ranged between one goat to 0.8 sheep in the Caribbean to one goat to 119.2 sheep in Oceania. The percentage of sheep present in Asian and African continent is 42.0 and 26.7 per cent respectively and the corresponding values of goats is 59.7 and 33.8 per cent respectively. There are about 1,350 sheep and 600 goat breeds available around the world. However, these genetic resources are being eroded as a result of changing agricultural practices and economic, environmental and other factors. The percentage of sheep and goat breeds that are extinct today are about 12 and 3 per cent respectively. Sustainable management of sheep and goat biodiversity is vital to rural development, food security and the environment. Hence, a range of policy instruments could be applied to address these issues. These includes developing procedures for access and benefit sharing, regulation of export and import of animal genetic resources (AnGR) and support for both conservation (*in vivo and in vitro*) and improvement of indigenous AnGR.

Keywords: Sheep, Goat, Conservation, Strategies

239 (P-136)

Setting Conservation Priorities: A Case Study of Indian Sheep

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The question of which breeds to conserve is important in conservation of livestock breeds. Conservation decisions can be based on a number of different considerations. In India, these decisions are primarily based on the degree of endangerment. Combined use of genetic (microsatellite based diversity) and non-genetic (present-day utility) factors is fully lacking in setting conservation priorities. Our study decides conservation priorities by combining contributions to genetic diversity, breed merits and threat status. Four hundred fifty six animals, belonging to five sheep ecotypes viz. Kolhapuri, Lonand, Madgyal, Solapuri and Sangamneri of Maharashtra (India), were genotyped for 25 microsatellite markers to measure the genetic diversity existing among them. Weitzman approach was used to estimate contribution of the ecotypes to genetic diversity. Contribution of non–genetic factors was assessed based on the opinion of the farmers (21-40) and field survey. These included economic, ecological and cultural importance of the ecotypes indicating their present day utility and threats including population size, average no of rams per flock, indiscriminate cross breeding, maintenance of pure flock and farmer's opinion towards the ecotype. Extinction probabilities were estimated using threat data. Total utility of an ecotype was the sum of twice the product of extinction probability and marginal diversity, and its current average utility. The findings gave highest conservation priority to Lonand and least to Solapuri ecotypes. These results are useful for implementing conservation plans for Indian sheep as well as other livestock breeds based on their ranking on regional or national level.

Keywords: Breed utility, Conservation priority, Marginal diversity, Sheep ecotype, Threat status

383 (P-137)

Ex Situ Conservation of Indigenous Caprine Genetic Biodiversity Utilizing Cauda Epididymal Sperms

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Collection of cauda epididymal sperms from slaughtered animals, for conservation of goat genetic resources, could be a rapid and economical alternative as epididymal semen provides a high enough number of viable spermatozoa for genetic stocks. The epididymal sperm freezing and their subsequent fertility potential in goats was evaluated in the present study. The testis of slaughtered bucks were procured, their epididymis removed and washed with normal saline. The caudal region of epididymis was cut and kept in a buffer solution, so as to allow the sperms to swim out. The isolated sperms were diluted in seven different extenders containing varying proportion of different constituents like buffer, sugar, cryoprotectant, egg yolk and antibiotics. The sperms were evaluated for their motility, viability, acrosomal and membrane integrity during storage at room temperature. The extended sperms were frozen using gradient cooling in a programmable freezer and evaluated after 30 days of storage in liquid nitrogen. The fertilizing ability of frozen sperms was evaluated through *in vitro* and *in vivo* procedures. The motility of extracted sperms from cut cauda epididymis was around 75% and live sperm proportion was 90%. The sperms extended in different extenders showed varied levels of motility, viability, acrosomal and memberane integrity during storage at room temperature. The frozen sperms after 30 days of storage in liquid nitrogen showed maximum post thaw motility as 55%. In vitro incubation of frozen sperms with goat mature oocytes resulted in successful zygote formation. The artificial insemination of does also resulted in successful kidding. The observation of this study supports utility of epididymal sperms for conservation purpose.

Keywords: Conservation, Goats, Sperms

565 (P-138)

Strategies for Conservation of Domestic Animal Diversity in India

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The genetic resources of farm animals in India are represented by a broad spectrum of native breeds of cattle, buffaloes, goat, sheep, swine, equines, camels and poultry. The genetic biodiversity among this livestock needs to be conserved. Conservation is effective management of genetic resources for human use and it is always better to keep the live populations of animals or in situ conservation, which may go on improving not only in production potentials but also in their adaptation to the changing environment. In situ conservation of Beetal goat and Kilakarsal sheep breeds has been successfully undertaken in their native tract, which resulted in addition of animals to their dwindling population. In another approach of conservation, different forms of germplasm has been cryopreserved, which offers great advantage for conserving large livestock biodiversity. Frozen Semen is ideal for genetic resources utilization activities and NBAGR stores semen doses of 44 indigenous livestock breeds belonging to 7 species in its repository. Cauda epididymal sperms banking has been started for conservation of caprine and ovine genetic resources. The somatic cells are being conserved for species like camel, where conventional semen freezing and artificial insemination is not well characterized. Considering the large breeds of livestock to be conserved, many agencies are planned to be involved for participation in this venture and exchange of germplasm among them.

Keywords: Livestock, Biodiversity, Conservation

789 (P-139)

Prioritized Management Strategies for Conservation of Endangered Mahseer, *Tor putitora* in Mid Himalayan region, India

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Golden mahseer, *Tor putitora* is most important game fish of coldwaters of India. It has been observed that the population of mashseer has been declined due to a combination of factor including loss of breeding area, rearing habitat, over exploitation and low recovery rates of fishes, result in poor record of sustainability of *Tor putitora* . This papers reviews the problem faced in sustainability of mahseer in natural waters and to draw a comprehensive set of prioritized management strategies to facilitate the sustainable management. It is needed to incorporate different management strategies relevant to local socio- economic agenda. The management recommendation deal with method to improve the regulation of fishing, ways to improve conservation ethics and encourage active public participation for drawing specific management strategies. In this endeavor, the need is to conserve and propagate the mahseer fishery resources together with establishing of fish parks, fish reserves and conservation efforts of natural resources that would facilitate faster action towards enhancing the stock. Under this perspective, we have conceived an agro-climatic zones wise multifarious programme concept to establish of "Germplasm repository" and "Self sustained mahseer conservation model Interlinking ecotourism" as a tool for *in- situ* and *ex- situ* conservation.

Keywords: Fish conservation, Tor putitora, conservation.

807 (P-140)

Conservation of Nicobari Pig, an Indigenous Pig Germplasm of Nicobar Group of Islands, India under Intensive System of Rearing

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An indigenous pig germplasm is available in the Nicobar group of Island, India locally known as Ha-un. Genetic diversity of this pig breed was very high compared to Large White Yorkshire and other European pig breeds. The population of this breed has been reduced drastically after tsunami. The pigs are reared in a free-range system. Survey based data indicate that the pig is well accepted by the Nicobari community. No systematic data is available to explore the potentiality of the precious pig germplasm. Understanding the factors that drive breed richness and turnover across ecological gradients is important for breed conservation planning. Productive and reproductive data are important to explore the potentiality of the breed. Hence this study was designed to record the productive data in a scientific way. Six Nicobari pigs were procured from the breeding tract of the pig and reared in the institute farm. It was found that the Nicobari pigs are well adapted in the intensive system of rearing. Reproductive performances are good in terms of numbers of farrowing per year and higher litter weight at birth showed better survivability rate at weaning.

Keywords: Indigenous pig rearing, Nicobari pig, Reproductive Performances

872 (P-141)

In Silico Mining of Conserved miRNAs from the Contigs, ESTS and BAC End Sequences of *Clarias batrachus* (Linnaeus, 1758)

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MicroRNAs are a class of small, non-coding RNAs that serve as main players in RNA interference. The present work is a maiden attempt in *Clarias batrachus* to mine the conserved miRNA and their target genes from the assembled contigs, ESTs and BAC end sequences. A total of 138, 1 and 1 pre-miRNA, which were highly conserved with miRBase, were found in the assembled contigs, ESTs and BAC end sequences of *C. batrachus*, respectively. Family analyses of the conserved pre-miRNA revealed conservation of the mir-430 family that has been reported to be fish specific along with other important pre-miRNA families, such as mir-455, let-7, mir-133 and mir-137. The mir-455 is involved in hypoxia signalling, let-7 family represents potential anti-tumor molecules involved in human cancer therapy, mir-133 and mir-137 has high therapeutic potentials. *In silico* mining of mature miRNAs, using an alternate computational approach, resulted in identification of 210, 1, 2 and 2 mature miRNA from the assembled contigs, EST, forward as well as reverse BAC end sequences, respectively. Target prediction of these putative miRNA resulted in the identification of 66,758 and 18,747 target genes being regulated in *C. batrachus* and *Danio rerio*, respectively. Functional annotation of these miRNA showed their involvement in diverse biological functions. The findings of the present study can serve as a valuable resource for functional genomics studies in *C. batrachus*.

Keywords: *Clarias batrachus*, Fish, Genome, miRNA

946 (P-142)

An Attempt to Rehabilitate Giant Freshwater Prawn, *Macrobrachium rosenbergii* (de Man) in Valapattanam River of Kannur District of Kerala (South India)

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Valapatanam River is the largest river in Kannur distict of Kerala (South India). The river originates from the Brahmagiri reserve forest in Karnataka (South India), at an altitude of 900-1350 m above mean sea level and drains into the Arabian Sea after travelling a distance of 110 km. The river supports a sizeable fishery and is one of the principal sources of inland fishes in North Kerala. The giant freshwater prawn. *Macrobrachium rosenbergii* (de Man) had been contributing to the commercial fishery of the river system till 1970s. However the species has since then become extinct and has not been reflected in commercial catches during the last four decades. The disappearance of the species from the river system was reported to be due to a number of reasons like obstruction of breeding migration owing to the construction of Katampalli barrage, environmental pollution, loss of habitats etc. In the context, an attempt was made to rehabilitate the species by regular river ranching. A total of 1750154 hatchery produced healthy seeds of the prawn were stocked in the river at four pre- selected locations between 10-10-2014 and 14-10-2015. Fish catch data were collected every month from major fish landing centres for 31 months viz., one year prior to the first stocking and seven months after the date of last stocking. Analysis of the catch data reveals the success of the rehabilitation programme. The prawn started appearing in commercial catches in substantial quantities and the contribution of the species was estimated to be 5.36 tonnes, during the twelve month period ending 15th May 2016. Presence of berried females and juveniles of *M. rosenbergii* indicates the success in recruitment of the species in the river system.

Keywords: *Macrobrachium rosenbergii*, Rehabilitation, Valapatanam River

993 (P-143)

Combination of Culture Media for Enriched Fibroblast Generation from Buffalo Skin Explant

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Skin explants are preferred for generating fibroblast cells for cell banking, especially when dealing with endangered animals due to least adverse effect on the animal. Here, we describe a method for growing fibroblast from bubaline skin explants that increases the efficiency of generating the cultured cells by several folds. Different media (Human fibroblast specific media- HifibroXL^{TM}, DMEM and DMEM+Ham's F12) were tested for their growth potential on buffalo skin explants as well as fibroblast cells. All the adhered tissues showed outgrowth in HifibroXL^{TM} with cells having enlarged cytoplasmic extensions and faster increase in cell numbers. Increased number of fibroblast cells and reduced number of epithelial cells were observed in case of HifibroXL^{TM} media as compared to DMEM+Ham's F12 media. Thus HifibroXL^{TM} is a better option during primary cell culture. All the three media were compared to test their efficacy for fibroblast growth potential during subsequent passaging. Total cell count with same seeding and under similar culture conditions was highest (2.4 times) in DMEM+Ham's F12 followed by DMEM (1.9 times) as compared to fibroblast specific media. Lowest population doubling time (27hrs) with highest number of population doublings (11) was recorded for DMEM+Ham's F12 indicating that DMEM+Ham's F12 (1:1) was most efficient for bubaline fibroblast growth in later passages. Here we described selection of fibroblast specific media in combination with DMEM+Ham's F12 (1:1) media for growing fibroblast from bubaline skin explants that maximizes the number of cells obtained, thus increasing the amount of material available for conservation and research purposes.

Keywords: Explant culture, Genebank, Skin fibroblasts

1588 (P-144)

Studies on Flatfishes of India as a Step Towards Conservation of Resources

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Landing of flatfishes has been on the decline especially along the southwest coast of India. The major species contributing to the fishery is *Cynoglossus macrostomus*. The present study was undertaken to study the flatfish diversity of India and document the possibilities of finding out new species to be protected if any as well to examine the possibility of any ornamental and cultivable species. Results indicate the presence of 63 species of flatfishes in 8 families and 26 genera from south India including the islands of Andaman and Nicobar. The most speciose family was Soleidae with 9 genera and 17 species, followed by Bothidae with 9 genera and 14 species and Cynoglossidae with 2 genera and 13 species. The disappearance of the halibut *Psettodes erumei* from the fishery calls for stringent conservation measures as well as conservation mariculture. The Malabar sole, *Cynoglossus macrostomus*, endemic to Malabar Coast from Mulki to Quilon on the southwest coast of India has also shown considerable decline during the last five years; these features call for strict measures to continuously monitor the resource and its stock position. The hydrography of the Indian Ocean and the interconnecting patterns of water bodies in it could be the reason for maximum common diversity of flatfishes within the region. Appropriate conservation strategies for the flatfishes available in the Indian waters is integral to any approach in preserving biodiversity since greater species diversity ensures natural sustainability for all life forms.

Keywords: Bothids, Conservation, Flatfish, Psettodes

1609 (P-145)

Salinity Tolerance of Endangered Canara Peralspot, *Etroplus canarensis* with Respect to Captive Breeding Programs

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India is a major biodiversity hot spot, with its vast and varied fish germplasm resources contributing to about 11.72% of global fish biodiversity. Around 3231 species of freshwater and marine fish genetic resources have been recorded in India. Due to natural and anthropogenic stress, India's germplasm is getting depleted and many freshwater species have been threatened. *Etroplus canarensis*, commonly known as Canara Pearlspot, is an important ornamental fish species listed as Endangered in the IUCN Red list Threatened species 2013.2. This is mainly due to natural & anthropogenic stress and its restricted distributions (Netravathi & Kumardhara river) in Karnataka, India. This fish has more export ornamental values (35-40£) in USA and European Unions and fetches Rs.150-250/fish in local ornamental fish markets in India. Central Institute of Brackishwater Aquaculture; (ICAR-CIBA) Chennai has initiated conservation programs for this endangered species through induced breeding trials by simulating natural environmental parameters. This programs has been started due to its export ornamental values and CIBA's success in breeding *Etroplus maculatus* which is the closely related species of same family of Cichlidae which grows in both brackishwater and freshwater. Studies were undertaken to analyze the salinity tolerance of *Etroplus canarensis* in brackishwater environment which would give an opportunity to breed the species and thus contributing towards the conservation and also in promotion as a candidate species for brackishwater aquaculture. Fishes (n=100, average length & average weight, was 8.89 ± 0.89cm, 18.26 ± 6.79g respectively) were collected from Karnataka transported to MES Hatchery, acclimatized for one month to the hatchery conditions (Salinity: 5-8 ppt, Temp.: 26-28^{oC} & pH-7.5-8.2) fed with commercial diet. Matured ova (~ 430 micron sizes) were observed in females maintained at Muttukadu Experimental Station, (MES), Muttukadu. Though, this species is basically of stenohaline in nature, the detailed study on the salinity tolerance has not been reported in *E.canarensis.* Acute salinity stress experiments were conducted by direct transfer of freshwater acclimatized fish to low saline water (5, 10, 15 & 20 ppt) and were observed for survival at 24 hr and 96 hr of post salinity stress. The results obtained indicated 100% survival in 5, 10, &15 ppt treatments however 100% mortality was observed in 20 ppt. The result suggested that the Canara Pearlspot can tolerate low salinity range from 5-15 ppt and thereby indicating its habitat suitability of low saline brackishwater ecosystems.

Keywords: Endangered, Canara Pearlspots, *Etroplus canarensis*, Brackishwater ecosystems.

1650 (P-146)

Traditional Community Fishing Festival in Himalayan River Aglar: Biodiversity Conservation and Governance Issues

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Traditional Knowledge (TK) related to Biological Resources (BR) has found its way in the Convention on Biological Diversity (CBD) that obliges a Nation to respect maintain, preserve and promote traditional knowledge with approval of holders of knowledge. The appreciation of traditional knowledge is growing and as it has been used and reused by traditional communities through years. A documentation was done for traditional community fishing festival called practiced in the Himalayan region, in a river stream Aglar using traditional Ichthyotoxic powder that contains saponin and cardiac glycosides, made from the bark of a local medicinal plant, Timru (*Zanthoxylum armatum*) stunning fishes. With CBD in place for conservation and sustainable utilization of genetic resources, the rampant destruction of ecology of the area poses a threat to BR through negative use of TK. The living stream dies, as insects, frogs, snakes and fish species are destroyed include *Schizothorax* spp., *Tor* spp., *Glyptothorax* spp. and *Garra* spp. disturbing the ecological food chain. Government intervention is needed for conservation of the river ecosystem harbouring wild species. when TK and culture practice of community becomes destructive for an ecosystem, it is time for the government machinery to intervene. The mass destruction of fishes and other biological beings is an example of negative traditional knowledge that can be given a positive dimension by turning destruction towards conservation with the help of local people who are members of Biological Management Committee to make best use of traditional practices to help community and conserving ecosystem for sustainability.

Keywords: CBD, Biological Resources, Traditional Knowledge

1669 (P-147)

Sex Ratio, Length-weight Relationship and Condition Factor as Indicators of Health of a Snow Trout, *Schizothorax labiatus* McClelland in River Jhelum, Kashmir

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Schizothoracids (snow trouts) being commercially important food fishes of Kashmir valley, are exploited in one-way or the other and are facing immense pressure due to various reasons. Pollution, destruction of breeding ground and Overexploitation are the main reasons of their decline. *Schizothorax labiatus* McClelland is one of the commercially important Schizothoracid and the present study was undertaken to study the health of this fish in river Jehlum. The results indicated the dominance of males over females with mean sex ratio as 1:0.41, the length-weight relationship established indicated negative allometric growth i.e. b> 3, the value of 'b' being equal to 2.578 for combined data of both males and females. The condition factor (Kn) which is used as an index for monitoring of feeding intensity, age and growth rate of fish was recorded with a mean value of 1.5 in case of females and 1.4 in case of males.

Keywords: Condition factor, Health*,* Length-Weight, *Schizothorax labiatus*, Sex ratio.

1692 (P-148)

Signs of Panmixia in the Scalloped Spiny Lobster *Panulirus homarus* (Linnaeus, 1758) along the Indian Coast

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The scalloped spiny lobster *Panulirus homarus* (Linnaeus, 1758) is one of the most important species in lobster fishery of India. The declining trend in catches of lobsters in general and lack of larval rearing technologies in particular demands for urgent conservation measures for the species. Demography and assessment of larval connectivity pattern are of primary importance in management and conservation of *P. homarus* population. Genetic stock structure assessment of the species was carried out using molecular markers like RAPD and partial sequences of Cytochrome Oxidase I/ COI gene for samples from three major sites of its fishery along Indian coast. RAPD markers showed moderate genetic variability with an overall G_{ST} value of 0.0136 indicative of low genetic differentiation among local populations. Analysis of COI sequences revealed high genetic similarity among groups with values of high mean haplotype diversity (0.9226) and low nucleotide diversity (0.0089), characteristic of expanding populations with an initial low effective population size. Mismatch distribution analysis, neutrality tests and the star-like median joining network also indicated demographic expansion. The low level of genetic differentiation (F_{ST} - 0.0169) in the population which was not significant may be attributed to panmixia resultant of the lengthy planktonic larval duration in wild and larval transportation via the coastal and monsoon currents of Northern Indian Ocean. The random mating homogenous stock of this species requires management and conservation efforts, which must be coordinated at the national level.

Keywords: COI gene, *Panulirus homarus*, Population genetic structure, RAPD

1769 (P-149)

Derivation, Characterization and Cryostorage of Continuous Cell Lines from Threatened Species of Groupers (Serranidae), *Cromileptes altivelis* and *Epinephelus bleekeri*

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Globally aquatic ecosystems experience serious threats to both biodiversity and ecosystem stability. Overfishing, pollution and climate changes are the major factors that impact marine fish biodiversity. Several conservation strategies have been developed to overcome the crisis. Cryobanking of fish cell lines is recognized as an important tool for conservation of fish germplasm. The advantage of preserving cell lines lies in their ability to provide a source of renewable material that can be cultured for long periods. Somatic cell line banking provides valuable information in the genetic management and biodiversity conservation of declining species as well as aid as an indispensable tool providing genetic and cellular resource material for scientific study. The present study envisaged to develop continuous cell lines from two species of groupers (Family: Serranidae) *viz., Cromileptes altivelis* and *Epinephelus bleekeri* which are categorized as vulnerable and near threatened in the IUCN Red list. Cell lines have been developed from brain, fin, gill, caudal peduncle, heart and spleen tissues employing explantation/trypsinization methods. Successful monolayers obtained in primary cultures were passaged to develop continuous cell lines. The growth media and culture conditions for the cell lines have been optimised. The established cell lines were characterized by karyotyping, immunophenotyping and authenticated by sequencing mitochondrial CO1 gene. The cell lines have been successfully cryopreserved and the viability of cells were found to be >80% when revived from liquid nitrogen.

Keywords: Cryobanking, Fish cell lines, Germplasm conservation

1818 (P-150)

Development and Standardization of Induced Breeding Technique of the Mahanadi Rita, Rita Chrysea in Captivity

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Rita chrysea is an indigenous catfish, endemic to Mahanadi river of Odisha and Chhattisgarh region. Popularly called as Mahanadi Rita, it has good consumer preference and market demand fetching Rs. 250-300/kg. Captive breeding and seed production technique of R. chrysea has been developed and standardized at ICAR-Central Institute of Freshwater Aquaculture, Bhubaneswar, Odisha. The wild brood fishes were collected from Munduli, Cuttack and Dalei Ghai, Jagatsinghpur, Odisha. The brood fishes of 130-150 g were selected for induced breeding and injected with commercially available synthetic hormone, Ovatide at the rate of 1.0 ml kg-1 body weight of fish. Female fish was stripped after 13-15 h (latency period) of hormonal injection. Male was sacrificed for the collection of testis and preparation of sperm suspension for fertilization. The ovulated eggs are demersal, non-adhesive and transparent, with 1.1-1.3 mm in diameter and weighing 1.2- 1.4 mg. Fecundity of female of 90-120 g body weight ranged between 9,000 and 12,000 eggs. Fertilized eggs were placed in glass jar hatchery with gentle water flow in order to make egg circulation. The larvae hatched out after 24-26 h of incubation at 26-28 Â°C. Fertilization and hatching rates were 70-80 % and 60-70 % respectively. Hatchlings measured 3.5 to 4.5 mm in total length and weighed 0.8 to 1.2 mg. They had transparent body, were demersal, photonegative, and preferred shelter.

Keywords: Bagrid catfish, Breeding, Hatchling

Technical Session 2-E :

Conservation Strategies and Methodologies

Concurrent Session :

Microbial and Insect Genetic Resources

700 (O-22)

Reviving Tradintional Bee Keeping Practices and Restoration of Landscape for Sustainable Agriculture in Indian Himalaya

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Bee keeping practices have been prevalent in the Indian Himalayan Region (IHR) since ages. People had their own sustainable ways of bee keeping like wall hives and log hives. However, traditional bee keeping was not meant to enhance the pollination services, but to produce honey which by default supported the ecosystem services to a great extent. Though these practices can still be seen in the remote villages of Himalaya, they are dying a slow death owing to modern housing. Depletion of forage attributing to mono cropping, changing climate, indiscriminate use of insecticides and pesticides are the other major factors responsible for the loss of native bee species *Apis cerana* and habitat of wild pollinators in the IHR. Due to the decline of bees, apple farmers are feeling the pinch for the reduced yield. Realizing the urgent need, farmers have started to supplement their orchards with rented bees brought from the adjoining state of Punjab. Earthwatch Institute India in collaboration with G.B. Pant Institute of Himalayan Environment & Development are focusing on revival of traditional bee keeping practices and restoration of landscape for sustainable pollination services for sustaining agriculture in IHR. Pollinator diversity, abundance and their preferential flora is being monitored through citizen science approach. This is a first of its kind effort to revive traditional bee keeping practices for pollination and restoration of landscape for improving pollinator diversity in the region, using the citizen science and experiential learning methods.

Keywords: Himalaya, Pollination, Ecosystem services, Restoration, Landscape, Diversity, Citizen science and Experiential learning.

1524 (O-23)

Natural Habitats Support Benefits of Organic Farming for Rich Wild Bee Diversity

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We explore, how alternative farming such as organic behave similar to natural habitats, and promote ecosystems that support healthier bee communities than conventional farms (monoculture). We tested our hypothesis if natural and semi-natural habitats act as refuges to bee communities then agroecosystems near these habitats should display greater bee diversity than those further away. Furthermore, if organic farms in our study area behave similar to natural habitats, they should support diverse bee communities in comparison to the conventional (monocultures) systems. We conducted the study over a period of three years (2012 to 2014) in the peak flowering season of spring (January to April) in the Doon Valley Landscape, Uttarakhand, India. We sampled for bees in organic and conventional agroecosystems using passive and active methods at a gradient of increasing distance from the forest (from 0 m to 700 m). A linear regression model run on our data demonstrated higher bee diversity in agroecosystems in close proximity to forests (H' for <200 m = 1.60) compared to those further away (H' for >600 m <700 m = 0.56) (R2 = 0.81, SE = .152, p value = 0.006). We tested weather organic farms behaved similar to natural habitats. A comparison between farm ecosystems demonstrated that organic agroecosystems supported significantly higher species richness than the conventional (Mann Whitney U test, n1 = 33, n2 = 35; P = 0.001). The findings of our investigation emphasizes the importance of natural habitats as potential refuge (provide nesting, off seasonal foraging and breeding sites) for bee pollinators. Crop mixes behave similar to the diverse natural habitats that support healthy bee communities. On the contrary, monocultures consist of stretches of single crop that not only promises little to attract bees but also cause reduction of corridors such as hedges that provide refuge to bees locally.

Keywords: Bees, Diversity, Conventional agroecosystems, Natural habitats, Organic farming

655 (P-151)

Isolation and Purification of Multiple Viruses from Mixed Viral Infections: Viral Interference, Persistence and Exclusion

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In this study, we investigated peste des petits ruminants virus (PPRV) and foot-and-mouth disease virus (FMDV) mixed infection in goats. Rather than in a single cell type, cytopathic effect (CPE) of the virus was observed in cocultured Vero/BHK-21 cells at 6th blind passage (BP). PPRV, but not FMDV could be purified from the virus mixture by plaque assay. Viral RNA (mixture) transfection in BHK-21 cells produced FMDV but not PPRV virions, a strategy which we have successfully employed for the first time to eliminate the negative-stranded RNA virus from the virus mixture. FMDV phenotypes, such as replication competent but noncytolytic, cytolytic but defective in plaque formation and, cytolytic but defective in both plaque formation and standard FMDV genome were observed respectively, at passage level BP8, BP15 and BP19 and hence complicated virus isolation in the cell culture system. Further, we for the first time demonstrated the viral interference between PPRV and FMDV. Prior transfection of PPRV RNA, but not Newcastle disease virus (NDV) and rotavirus RNA resulted in reduced FMDV replication in BHK-21 cells suggesting that the PPRV RNA-induced interference was specifically directed against FMDV. To the best of our knowledge, this is the first documented evidence describing a natural mixed infection of FMDV and PPRV. The study not only provides simple and reliable methodologies for isolation and purification of two epidemiologically and economically important groups of viruses, but could also help in establishing better guidelines for trading animals that could transmit further infections and epidemics in disease free nations.

Keywords: Mixed infection, PPRV, FMDV, Defective interfering particles

1203 (P-152)

Diversity of Arthropod Fauna in Flue cured Virginia Tobacco

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Flue cured Virginia tobacco is cultivated extensively in India as monoculture. Use of chemical inputs for higher yields adversely affects the arthropod community balance in tobacco. The current studies were aimed at studying the composition and structure of the arthropod populations in FCV tobacco. Field experiments were conducted to understand the diversity of arthropods on plants and soil in fallow-tobacco, maize-tobacco and soybean-tobacco rotation following minimum tillage for all the crops and compared with recommended tillage. The biodiversity indices were calculated using Shannon-Wiener index. In maize the Shannon-Wiener index (H) for different arthropods was 0.99 in minimum tillage plots and 0.88 in recommended tillage plots. In soybean, the diversity index varied from 0.8 to 1.19. Higher indices were observed in recommended tillage plots. In case of fallow-tobacco, in the minimum tillage plots, the H index varied by two percent among different insect orders inhabiting tobacco and it was 18 per cent higher in maize-tobacco rotation. The diversity was 12 per cent lesser in soybean-tobacco with minimum tillage than in the recommended tillage plots. In soybean minimum tillage plots, 4.2 per cent higher H value was recorded than in recommended tillage. It was observed that in soybean-tobacco rotation, minimum tillage plots had 8.70 per cent higher H value in contrast with recommended tillage; however the reverse was true in case of maize-tobacco rotation. Minimum tillage practices in maize improved diversity of insect fauna. The insect diversity in tobacco under maize-tobacco and fallow tobacco with minimum tillage showed higher H values. The studies indicated that maize-tobacco as well as fallow-tobacco with minimum tillage can be advantageous in bringing out a mosaic, of insect communities in tobacco.

Keywords: Arthropod diversity, Shannon-Wiener index, Tobacco

Technical Session 3 :

Adaptation and Mitigation to Climate Change

Common Session

1055 (O-24)

Germplasm Enhancement for Increasing Groundnut Productivity and Production in West and Central Africa

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West and Central Africa (WCA) account for almost 70% of groundnut production in Africa playing an important role to farmers' livelihood and significantly contributes to the export sector of the countries in the region. However, the productivity in the region is limited due to many factors including biotic and abiotic constraints. The gap between potential and realized yield is large in subsistence farming. To address these issues, ICRISAT has been working with national partners in the region to improve productivity of groundnut with the Tropical Legumes project support. ICRISAT has supplied more than 2,500 trait-specific advanced breeding lines (resistance to foliar diseases, rosette, aflatoxin contamination, early and medium maturing, confectionery types and tolerant to drought) to the national programs in WCA for genetic enhancement of groundnut. Based on the NPT and PVS trials, the national programs in Niger released four varieties (RRB, ICG 9346, J11 and Fleur 11). In Nigeria, three short-duration, rosette resistant varieties (Samnut-24, Samnut-25 and Samnut-26) were released. In Mali, eight varieties including ICGV 86015 and ICGV 86124 were selected by farmers. While six and four varieties were released in Senegal and Ghana respectively. Most of these varieties were preferred by farmers for their high yield, disease resistance, drought tolerance, short duration, seed size, suitability for home consumption, seed color and market demand and had yield advantage of up to 42% over the local varieties grown by farmers. The current efforts to deploy modern breeding approaches and tools to enhance genetic gains are discussed.

Keywords: Genetic Enhancement, Groundnut, Productivity, Trait specific breeding lines, West and Central Africa

1434 (O-25)

Increasing Resilience to Climate Change in Rural Livelihoods: to Diversify or Not?

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Climate change causes unpredictable weather patterns in tropical rural landscapes that may lead to harvest failure which can threaten food security, farmers' income loss, and livelihood vulnerability. High agrobiodiversity in agroforestry (AF) systems provides functional diversity (product variety) that may increase the resilience of farmers. AF system practices also help conserving land sustainability and maintaining diverse habitat to counter climate change. This study aims to determine whether farmers' decision over land allocations are made to maximize their resilience to climate change. We conducted household interviews with 30 random households in Bantaeng, South Sulawesi. On the 133 land parcels owned by those households, we used nested plot method for vegetation analysis with every woody and other utilized species enumerated, and the origins of every individual documented. We grouped the land use management into: (1) complex AF; (2) simple AF; and (3) annual cropland. Household plant functional diversity index are also calculated. The study shows that 67 (50%) land parcels are complex AF, 51 (41%) are simple AF, and 15 (9%) are annual cropland. 63% of species in annual cropland are commodities, while in simple AF and complex AF commodities represent 54% and 50%, respectively. In annual cropland systems, 13% of species are used as wood, while in simple AF and complex AF 17% and 19%, respectively. Other plants are grouped as staple food, medicinal, fodder, and fibre. Although farmers' decisions over land allocations vary, most of them practice the system which maximizes resilience to climate change. Policy guide approaches can be used to enhance integration between agrobiodiversity, resilience, and economy.

Keywords: Resilience, Agroforestry, Agrobiodiversity, Functional Diversity

1641 (O-26)

Effective Utilization of Local Genetic Diversity of Pigeonpea, Sorghum and Finger Millet in Eastern and Southern Africa: Impacts and Prospects

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Eastern and Southern Africa (ESA) is the centre of genetic diversity for pigeonpea, sorghum and

Finger millet. ICRISAT regional bank located in Nairobi-Kenya maintains about 6000 germplasm accessions that are of greater use in ESA. ICRISAT-Nairobi is regularly collecting local diversity existing in the region and thus collected germplasm characterized/evaluated to identify locally adapted germpalsm with highly desirable traits. Local diversity captured in ESA has unique traits with respect to local agro-ecological adaptation, farmer and consumer preferred grain traits, tolerance to drought and region specific diseases. ESA regional germplasm also contributed to global genetic diversity maintained ICRISAT-Patancheru in several ways. During recent years 30 new varieties of pigeonpea (8), sorghum (10) and Finger millet (12) were released in eight ESA countries and occupying huge area in respective countries. Pigeonpea is an example crop with great success recorded during last 15 years when breeding program started using local germplasm. Pigeonpea improvement in ESA started in 1992 by mostly relying on native germplasm and through this 33 high yielding varieties that are belonging to short(8), medium(13) and long(12) maturity group were released. A strong region specific genetic enhancement program is in operation with major breeding thrust on high grain yield, inter-cropping compatibility, photo-period insensitivity, grain quality, resistance and/or tolerance to *Fusarium* wilt and *Helicoverpa* pod borer and resilience to climate change. Most of the cultivated germplasm is susceptible to insects but regional germplasm contributed develop that are insect-cum-drought tolerant, high yielding and big seeded (28 g/100 seed mass). ESA region has huge untapped potential with respect to genetic diversity and its use in genetic enhancement.

Keywords: Eastern and Southern Africa, Genetic diversity, Genetic enhancement

1720 (O-27)

Indian Edible Oyster, a Promising Bivalve for Aquaculture amidst the Challenges of Climate Change as Revealed Through Thermo Tolerance Studies

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Temperature tolerance of a species is an indicator which determines its potential to persist or become extinct in response to climate change and related environmental challenges. Aquaculture of the Indian edible oyster (*Crassostrea madrasensis*) is becoming more popular along the Indian coasts. Hence, knowledge on the level of thermo tolerance and the molecular mechanism behind it shall be of immense use for the scientific management of the system to ensure sustainable production. The oysters collected from the oyster farm were acclimated in aerated sea water. Sub lethal temperature (SLT) and lethal temperature (LT) were determined as 44˚C and 47˚C respectively by exposing the acclimated oysters to temperatures ranging from 37˚C to 47˚C and monitoring the survival in normal temperature (28˚C). Transcriptomic analysis of oysters recovering from SLT has shown a statistically significant up regulation of genes coding for heat shock protein 70 (Hsp70) and super oxide dismutase (Cu/Zn SOD). The oysters recovering from sub lethal shock (SLT) were found to be resistant to the subsequent lethal temperature (LT) shock while the control animals not exposed to SLT succumbed to death. The phenomenon of induced tolerance was evident and the oysters survived LT up to of 26 days which stands as record duration ever reported. The study has revealed the special potential of Indian edible oyster in thermo tolerance over its western counter parts Thus the Indian edible oyster could be projected as a winner species with the ability to survive the challenges posed by climate change.

Keywords: Oyster, Thermo Tolerance, Winner Species

1742 (O-28)

Abiotic Stresses Tolerance and Nutrients Contents in Groundnut, Pearl Millet and Sorghum Mini Core Collections for Food and Nutrition Security

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Food and nutrition security still require new sources of tolerance to major abiotic stresses and high nutritional quality. Groundnut, pearl millet and sorghum mini core collections are representing diversity of global collections but few studies investigated the nutrients contents and the tolerance to low phosphorus (LP) and drought stress (WS). Under lysimetre and pots conditions, subsets of these mini core collections were used to assess genotypic variation in nutrients contents and identify new sources of tolerance to WS and LP. In a randomized completely block design with 5 replications, water regimes and phosphorus treatments were imposed. Agromorphological and nutrients contents parameters were investigated. ANOVA were performed to assess the genotype and treatments effects. WS decreased the transpiration efficiency (47%), yield and its components (68%) in groundnut. Combined WS-LP reduced pods weight (83%). ICG3312, ICG81, ICG13395 and ICG467 revealed tolerant to WS/LP. In Pearl millet, LP decreased 100 seeds weight (14%), panicle and shoot biomass weight (25%), the booting date delayed except on IP1060, IP5869, IP9000, IP17532 and IP17775. WS-LP decreased total biomass (35%) while LP reduced total N(4.5%), P(20%), K(23%), Fe(25%) and Zn(3%). IP17532, IP 5153 and IP 5581 revealed highest Fe content (524mgkg^{-1}). In sorghum, LP delayed the booting date, decreased biomass (32%) and WS-LP reduced biomass (74%). ISS2151, ISS705 and ISS862 revealed tolerant to WS-LP. LP decreased total N(11%), P(32%), K(13%), Fe(13%) and Zn(11%). IS1412, IS311 and IS376 showed high Fe content (515mgKg^{-1}). Selected genotypes and traits might be useful in crops improvement for more adaptation and productivity.

Keywords: Mini core collections, Drought stress tolerance, Low phosphorus, Nutrients contents, Crop improvement

1773 (O-29)

Exploiting Genetic Diversity for Adaptation and Mitigation of Climate Change: A Case of Finger Millet in East Africa

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With the reality of global climate change there is a need to exploit the variation in the germplasm in order to develop genotypes adapted to these changes. This requires breeding and selection of crops at strategically selected locations along a rainfall/temperature gradient to enable farmers select desired cultivars. Eighty one finger millet germplasm lines from East Africa were evaluated in eight environments spread across Kenya, Tanzania and Uganda for adaptation, grain yield stability using the additive main effects and multiplicative interaction (AMMI) ANOVA and Genotype and Genotype x Environment (GGE) models and blast reaction under artificial and natural inoculation. Lanet 2012 long rains, Serere 2012 long rains and Miwaleni 2012 long rains were found to be the most discriminating environments for the low temperature, sub-humid mid-altitude and dry lowland areas, respectively. Alupe 2012 long rains was the ideal environment for blast selection. Seven genotypes were identified for yield stability across the eight environments whereas nine genotypes had specific adaptation. Nine genotypes were identified with resistance to three blast types. However, one and two genotypes had high resistance only to leaf and neck blast, respectively. Two resistant and 12 moderately resistant genotypes to blast attained the highest grain yields and had varied maturity, plant heights and grain colour. This will provide farmers the opportunity to select genotypes appropriate to their target agro-ecologies with desired end-uses. The East African finger millet germplasm has high potential as a source of climate smart high yielding and blast resistant genotypes for direct production and/or breeding.

Keywords: Genetic Diversity, Finger Millet, GGE, Yield Stability

1846 (O-30)

Crop Interdependence, Adaptation to Climate Change and the Multilateral Systems of Access and Benefit Sharing: The Case of Nepal

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Improving farmers' access to more plant diversity is expected to be an effective strategy to respond to climate changes. Degrees of current crop interdependency were estimated based on the origin and pedigree analysis of modern varieties of rice, wheat and potato cultivated in Nepal. Geographical information system (GIS) was applied to identify germplasm from the global and national gene pool with respect to current and future climate analogue sites. Among the total 275 released varieties in Nepal, 76% of them originated outside Nepal. Forty seven landraces originating in 12 countries were used to develop 20 mid- and high-hills rice cultivars and 35 landraces originating in 11 countries were used to develop 28 Tarai rice cultivars. Only exotic parents were used to develop 35 modern wheat varieties; 89 ancestors originated in 22 countries, mostly from the United States (13%), India (13%), France (12%), Argentina (6%), and Italy (6%). Only exotic parents were used to develop eight modern varieties of potato in Nepal. Nepal is 95–100% dependent on foreign germplasm for varietal development. Using the Climate Analogue Tool (CAT), the analysis identified current, future, and past analogue sites within and outside Nepal, suggesting that there might be useful genetic materials that could be exchanged between such regions. To do so, Nepal has to be capable to make better use of the MLS/ITPGRFA. Right now more than 2500 genotypes of rice, wheat and potato are introduced annually for field evaluation in Nepal. This number could be increased with a fully operational MLS.

Keywords: Analogue sites, Genebank, Origin, Pedigree

16 (P-153)

Impact Assessment of Broad Bed and Furrow System in Tsunami Affected Water Logged Saline Areas for Agrobiodiversity in Island Agro-Ecosystem of India: A Case Study

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In 2004, Tsunami caused a great loss to agrobiodiversity and farmlands became waterlogged saline soil in Island agro ecosystem. Keeping this view, an investigation was carried out to assess the impact of the most viable Broad Bed and Furrow (BBF) technology implemented by government for upgrading farming community and maintaining agrobiodiversity of Andaman Island. Totally 50 respondents from selected five villages were interviewed for the study of BBF and assessed variation in salinity. Results of study showed that excavated depressed area is used for paddy-fish cultivation and the raised broad bed area which is above the water level of the paddy fields are used for cultivating seasonal vegetables or fodder crops during monsoon period. The suitable size of beds 4-5 m width, furrows 5-6 m width and 1-1.2 m depth was observed for this system of cultivation. The initial expenditure of about Rs. 1,00000 ha^{-1} incurred on land shaping is easily returned back by vegetables produced during season. The income received by farmers amounted to approximately Rs. 62,000 during first year, which was increased to Rs. 1,17000 ha^{-1} in subsequent years by cultivating vegetables, paddy and fish. Due to technological interventions the water stored in furrows to a depth of 0.50 m (±0.20 m) in BBF resulted in reduction of ECe 6.5-10.12 dSm^{-1} to 1.89-2.0 in April 2013. The BBF technology helps in enhancing the income of farmers in water logged saline soil areas by diversified farming viz. vegetables, fish, paddy and fodder throughout the year.

Keywords: Agrobiodiversity, Broad Bed and Furrow, Vegetables

26 (P-154)

Introduction of Plant Genetic Resources for Climate Resilient Agriculture

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Climate change is a serious threat, which may result in multiple stresses and reduction in present crop production. To develop climate-change-resistant crop varieties, such as those resistant to biotic and abiotic stress conditions, it is critical to maintain agro-biodiversity and to ensure the continued survival of crop wild relatives. Crop wild relatives can be used to breed new varieties that can cope with the changing climatic conditions. The increased need for consolidating collections of crop wild relatives, newly adapted commercial species or varieties is due to the increased likelihood and extinction for narrowly adapted and endemic species. A large number of crop wild relatives contribute as a source of resistance for pests & disease resistance, abiotic stress etc. There is a need to target of diverse plant genetic resources from different agro-climatic zones of world. Utilization of germplasm in crop improvement from the centres of crop diversity, such as maize in Mexico and Guatemala, potatoes in the Andes, durum wheat and sorghum in Ethiopia, cassava in Amazon basin, Banana and plantains in Papuasia and millets in India. Incorporation of exotic germplasm is the best means to enhance the genetic base of modern crops. Landraces grown in extreme areas like semi-arid to arid regions in Asia and Africa, can represent important plant genetic resources (PGR) in breeding for specific adaptation. Use of diverse PGR in response to climate change is an important element for an option-rich agriculture would be a critical component of agricultural sustainability, adaptation and resilience through crop diversity.

Keywords: Abiotic and Biotic Stress, Crop wild relatives, Plant Genetic Resources

191 (P-155)

Utilizing Maize Genetic Resources towards Enhanced Resilience in Diverse Ecosystems

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The base germplasm provides foundation for genetic improvement of any species. With this backdrop, maize genetic resources housed in the National Gene Bank (NGB) at NBPGR, New Delhi are being characterized and regenerated in a phased manner under the Consortium Research Platform (CRP)-Agrobiodiversity in India, as per the common set of descriptors and are being distributed to breeders of maize improvement programme of country. The majority of germplasm comprises of the landraces, native cultivars collected over a period of time from diverse ecologies, and elite parental lines of released and commercial hybrids. We organized two field days during Rabi seasons of 2013-14 and 2014-15. A total of 1870 accessions were showcased during the two field days for the benefit of the breeders from the All India Coordinated Research Project on maize and other institutes. The objectives were to i) subject the germplasm sets for selection by scientists and ii) make the selected germplasm available to the breeders for broadening the genetic base of future maize hybrids/cultivars and thereby enhancing the resilience of maize cultivation. We discuss here the extent of diversity among the genetic resources showcased during the field days; synthesis of deliberations by the group at the time of field days and also analyze the selections made by the breeders for different production ecologies.

Keywords: Genetic resources, Resilience, Landraces, Diversity, Field day, Maize

206 (P-156)

Status of Inbreeding in a Closed Flock of Marwari Sheep at Arid Region of Rajasthan

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Marwari is an important carpet wool producing sheep breed of North Western arid and semi arid region of India having medium and coarse wool. Inbreeding in the flock was calculated by Wright's formula, and was computed from pedigrees traced in 4964 animals by path coefficient analysis using PEDIGREE VIEWER V6.5b computer package. The rate of inbreeding was calculated as $\Delta F_t = (F_t - F_{t-1}) X100/(100-F_{t-1})$. Average inbreeding coefficient was also studied sex wise and in 6 classified periods spread from 1998 to 2015. The incidence of mean inbreeding for a period of 18 years was 0.47%, which was in normal limits. During the first period of three years the F value was 0.0%, and it was 0.92% in the sixth period (2013-15). Out of 4964 animals, 35.11% were found to be inbred. Overall mean inbreeding in inbred animals was 1.83%. Only 97 animals have inbreeding level more than 6.25%. There is increase in number of inbred individuals which rises from zero inbred animals in first period to 698 inbred animals in period of 2013-15 which are 66 percent of total individuals in this period however there was considerable downfall in mean inbreeding level of inbred animals from first to sixth period. It is difficult to avoid inbreeding completely in the closed flock mating system. However, level of inbreeding was in normal limits in flock indicating careful breeding practices. There is need of introducing novel germplasm of Marwari animals from field to avoid the risk of increase of inbreeding.

Keywords: Closed flock, Inbreeding, Marwari sheep

214 (P-157)

Sugarbeet–Germplasm Evaluation, Seed Production and Agro-Techniques for Sub Tropical India

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Sugarbeet has economic potential in Indian agriculture by supplementing sugar production. The changing bio-fuel scenario in the country has started looking at sugarbeet with ethanol as the end product. In this view, more than four hundred germplasm comprising of *Beta vulgaris,* fodder beets, CMS lines, Inbred lines and diploid, anisoploid and hybrid varieties from public research institutes and private seed companies from different countries were evaluated for root crop performance at IISR farm, Lucknow. Over 25 lines have shown potential for high sugar, while, 14 varieties showed adaptability to high temperature tolerance and IISR Comp-1, Pant Comp-3, Ramonskaya, CIR pb II/79, M.R. Poly, Virtus and Solid for salinity tolerance. Genetic improvement efforts & germplasm maintenance activities is going on at Lucknow and Mukteswar. Meanwhile, standardization of sugarbeet seed production was done at altitudes above 5000' for the diploid Russian Variety R-06. Other varieties *viz*., IISR Comp-1 and LS-6 developed by Lucknow and Pant S-10 by Pantnagar were also tried in a limited way. Indigenous diploid varieties recommended for cultivation in India with high temperature (40-45^0) tolerance varieties maintained. The work done at Maharashtra showed that sugar beet could be grown successfully from October to May. The package of practices along with the suitable varieties was developed by AP Cess Network project in 2004. The potential for root yield was observed to be 60-80 t ha^{-1} with sugar content of 13-15 per cent. IISR, Lucknow has developed tools for sowing of sugarbeet, inter-culture and harvesting of the crop.

Keywords: Bio-Fuel, High Temperature & Salinity Tolerance, Package & Practice, Seed Production, Sugar Beet

244 (P-158)

Impact of White Fly on the Yield of Cotton in District Bathinda, Punjab

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Weekly data corresponding to the Standard Meteorological Week (25th to 42nd) were taken for analysis. Maximum temperature & minimum temperature both showed negative correlation from 2012 to 2015 but in 2015 minimum temperature showed a positive correlation with white fly population. Relative Humidity both for morning and evening showed a significant positive correlation with white fly population. Rainfall showed negative correlation for 2012 & 2013 and positive for 2014 & 2015 with white fly population. Baring 2015, the maximum temperatures were on the higher side and minimum temperatures were on the lower side. The white fly population peaked during the 35th week in 2015, in 42nd week in 2014, 37th week in 2013 & 42nd week in 2012.Scatter plot of yield of cotton and average white fly numbers showed a negative linear relationship. Correlation co-efficient between yield and average white fly numbers was -0.27.The present analysis enables scientists to devise a system to monitor and develop management strategies for the control of white fly.

Keywords: Cotton, Correlation Coefficient, Standard Meteorological Week, Weather factors, Model.

302 (P-159)

Disease Index Variations of Cotton Leaf Curl Virus Disease in Relation to Weather in Punjab

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Cotton crop is sensitive to Cotton leaf curl virus disease (CLCuD) during the cropping season but it faces great set back if the incidences or its high severity noticed at initial phenological stages. The Percent Diseases Index (PDI) of CLCuD is also varied with weather parameters temperature, relative humidity and erratic monsoon patterns. To know the variations of the severity or PDI of the CLCuD in relations to variable weather parameters, a survey for the CLCuD infected cotton crop in the farmer's field of villages of Bathinda, Mansa and Mukstar district since last three consecutive years i.e. 2013,2014 and 2015. The PDI was found to be the maximum (2.16 - 41.50, 12.67 - 56.00 and 25.33 – 72.67) in the district Bathinda followed by Mansa (5.66 – 32.50, 16.67 – 50.67 and 16.67-51.33) and Mukstar district (7.33 – 31.83, 14.00 and 31.33-56.67) for the last three year. PDI of CLCuD was found to be higher in 2015. The PDI of CLCuD has been increasing continuously from 2013 to 2015 in respect of all the districts due to higher seasonal mean relative humidity and improper distribution of rainfall, although, the seasonal mean temperature was lesser in the year 2015 than 2014 and 2013. Moreover, the PDI of CLCuD was found to be the maximum in the Bathinda as compared to Mansa and Muktsar due to higher seasonal mean temperature and relative humidity in all the three years.

Keywords: Cotton, Cotton Leaf Curl Virus disease (CLCuD), Percent Diseases Index (PDI), Temperature, Relative humidity and Rainfall

418 (P-160)

Characterization of Vegetable Crops Germplasm in Relation to Drought Tolerance

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Vegetables are best resources for overcoming micronutrient deficiency and provide farmers high income and jobs than other crops. Drought is the most important factor affecting world food security and the catalyst of the great famines of the past. Vegetables, being succulent products by definition, generally consist of greater than 90% water. Vegetables are generally sensitive to limited soil moisture than many other crops. Therefore, it is the major causes of low yields in vegetable crops worldwide and will be further increase by climate change scenario. Plant responses to drought stress are very complex as stress itself involves various climatic, soil and agronomic factors, frequently complicated by substantial variation in timing of occurrence, duration and intensity. This high variation in the nature of drought stress and an insufficient understanding of its complexity, have made it difficult to identify and screening of specific physiological traits required for improved vegetable crop performance under drought, consequently limiting plant breeding efforts to enhance crop drought tolerance. It is highly probable that optimal drought-adaptation requires the combination of several morphological, physiological, and phonological processes, which depend on a multitude of genes and varies within each target environment. Hence, it is challenge in front of breeder to identify and develop more productive drought tolerant genotypes in less favorable environments. An attempt has been made in this review to inheritance of drought tolerance, methods of screening, parameters, genetics and breeding approaches for drought tolerance. The literature summarized in this paper may serve as important guideline in vegetable crops.

Keywords: Breeding approaches, Characterization, Drought tolerance, Screening and Vegetables

452 (P-161)

Genetic Diversity Studies on Kalabhatt (*Glycine max* (L.) Merrill) landraces - A Potential Phytonutrient Crop of Uttarakhand

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The black-seeded soybean landraces, also known as kalabhatt in hilly terrains of Uttarakhand, are grown since ancient time in North Western Indian Himalayas and occupied a significant place in staple food diet. Black soybeans and its products are the richest sources of isoflavones which are good for bone health. Owing to the economic importance of the kalabhatt, a study was initiated to know the genetic variability of black soybean land races cultivated in the Uttarakhand state. Seventy-five land races of kalabhatt originating from different districts of Uttarakhand were collected and molecular genetic diversity was done using twenty one SSR primers. A total of 60 alleles were amplified with an average of 2.85 alleles per locus. Cluster analysis was done using Neighbor Joining (NJ) method to classify soybean landraces in to different groups. The unrooted phylogentic tree grouped soybean genotypes into three major clusters, where, yellow seed coat (improved varieties) genotypes were grouped in one cluster, while reddish brown (improved varieties) and Kalabhatt showed intermixing. Population structure divided the soybean genotypes into six different populations. AMOVA analysis showed 12% variance among population, 66% variance among individual and 22% variance was observed within individuals. Principal Coordinate Analysis (PCoA) also showed that yellow seed coat genotypes were grouped in one cluster, whereas, the Kalabhatt showed scattered distribution and few genotypes of Kalabhatt showed grouping with red and yellow genotypes. The different genetic parameters used in the present study indicate that Kalabhatt genotypes are more diverse than the yellow seed coat and brown seed coat genotypes. Therefore, Kalabhatt genotypes can act as a good source of genetic diversity in soybean breeding programme.

Keywords: Soybean, SSR, Molecular Diversity, Population Structure, AMOVA, PCA

466 (P-162)

Graphical Analysis of Genotype by Environment Interaction of Finger millet Grain Yield in India

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Identification of wide adaptable stable cultivars with low Genotype by Environment interaction (GEI) is the major aim of all crop breeding programmes. This study was aimed at applying AMMI and GGE biplot techniques for the assessment of stability and patterns of GEI in 13 elite finger millet genotypes of different origin in multi-location trial in four diverse locations of the country. The combined ANOVA for grain yield showed that Environments (E), Genotypes (G) and GEI were highly significant ($P<0.01$). The partitioning of GEI sum of squares showed that first IPCA axis accounted for 72.2% and 64.1% and second IPCA axis accounted for 23.2% and 28.1% of the interaction sum of squares for AMMI and GGE analysis, respectively. Both AMMI 1 and GGE biplot indicated the general adaptation of genotype VL 368 across the environments. In GGE biplot analysis, the four environments were grouped into two mega environments with VL 368 and VR 988 as winning genotypes. The results suggest inclusion of afore-mentioned high yielding wide adaptable genotypes in finger millet breeding programme for yield improvement in the country.

Keywords: AMMI, Finger millet, GGE, Stability

489 (P-163)

Association of HSP-90 and HSP70 gene Polymorphism with Physio-Biochemical Parameters in Indian Sheep Breeds

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Heat is one of the main sources of stress which has an important impact on production and reproduction of livestock species. HSP genes are candidate genes for heat stress resistance and few studies have shown association between Single Nucleotide Polymorphism in HSP genes and heat stress. Fifty ewes of about one and half year of age from each sheep breed (Chokla, Magra, Marwari and Madras Red) were used for the estimation of hematological and physio-biochemical parameters under normal and heat stress condition. Least square analysis was carried using SPSS software. Season and breed had significant effect ($P<0.05$) on all the physiological parameters ie temperature, respiratory rate and pulse rate (AM & PM) as well as haematological parameters (Hb, PCV, TEC, TLC). For biochemical parameters, glucose, SGOT, Phosphorous, Triglycerides and albumin had significant effect ($P<0.05$) on breed. Genomic DNA was isolated, different primer sets were designed and representative samples were sequenced for HSP-90 and HSP-70 gene. Four amplicon each of HSP-70 and HSP90 genes were successfully generated. Genotyping protocols were developed by TETRA-ARMS PCR, PCR-RFLP and allele specific PCR for the 4 SNPs ie SNP01 (HSP90 exon6-7 390T>G, 490bp), SNP02 (HSP70 set2 459A>G, 609 bp), SNP03 (HSP90 exon9 180C>T, 354 bp) and SNP04 (HSP90AA1 112 G> C, 499bp). Least square analysis revealed a significant difference ($P<0.05$) of rectal temperature (AM), albumin (gm/dL) and pulse rate (AM) at SNP01, SNP02 and SNP03; respectively. SNPs with significant effect might be useful for the development of the DNA markers for selection of thermo-tolerant sheep.

Keywords: Heat stress protein genes, Sheep Thermo-tolerance

560 (P-164)

Crucial Reproductive Traits as Screening of Tomato Genotypes under High Temperature Stress

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Twenty one tomato lines were evaluated under summer seasons in field conditions (average day and night temperature of 38.4 and 19.7°C, respectively). Several floral and fruit traits were adversely affected due to high temperature stress clearly indicating high sensitivity of specific physiological processes in floral development to high temperature stress resulting in limited fruit set. A significant increase in flower drop (19.30% to 74.36%), styler exertion (20.37% to 83.72%), decrease in pollen viability (14.78-74.55%) and fruit set truss-1 (15.45 to 75.37) were noted among genotypes. On the basis of initial screening with respect to fruit set at high temperature stress, three lines i.e. CLN-2026, EC-538439 and EC-538148 emerged as high temperature tolerant genotypes, which can be used as a source of high temperature tolerance genes for further breeding programs. These lines, along with highly susceptible varieties i.e. Arka vikas, were critically observed for the stress tolerance traits. Most of the genotypes showed stigma exertion or tip burn under high temperature condition. Fruit number and fruit weight were the important yield components, which were severely affected under high temperature stress and as a result, the yield was markedly reduced. Yield potential of the genotypes, which was dependent on fruit set and fruit weight was severely reduced under high temperature stress and yield varied from 386 g plant^{-1} (EC-538380) to 1832 g plant^{-1} (CLN-2026). It was concluded that the traits like fruit setting, pollen and yield attributes traits could be used in selection of high temperature tolerant genotypes for better fruit setting.

Keywords: Floral traits, High temperature, Pollen traits, Stigma exertion, Yield attributes traits

579 (P-165)

Adaptive Fitness of Vechur and Kasargode (Dwarf *Bos Taurus Indicus*) Cattle Over Crossbred Cattle During Acute Heat Stress in a Field Environment

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From production loss to heat stress mortality, global warming is pushing animal agriculture to extreme unsustainability. The dwarf breeds of cattle are better known for their tolerance to different forms of stress. An experiment was designed to analyse the comparative heat stress response among Vechur, Kasargode (dwarf *Bos taurus indicus)* and crossbred (*Bos taurus indicus* x *Bos taurus taurus*) cattle (n=30) in a field environment. They were allowed to graze in the field on a hot summer day. The physiological, biochemical and molecular responses were assessed in response to stress. The results showed superior thermotolerance of dwarf Vechur and Kasargode animals while crossbred cattle were sensitive to stress. As per the present findings, the production loss among crossbred cattle under tropical conditions may partly be explained on the basis of their poor thermotolerance. The crossbred cattle were found to be reaching their tolerance limit even at the prevailing climatic conditions. The findings are important in designing appropriate animal breeding and selection strategies to alleviate the adverse effect of souring heat.

Keywords: Climate Change, Heat Stress, Adaptation, Dwarf Cattle, Vechur

594 (P-166)

Genetic Variation in Morpho-Physiological Discriminators for Cold Tolerance in Maize

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The development of genetic resources more tolerant to rapidly changing environment is an important aspect of crop adaptation to climate change. In India, variation in temperature during winter months in changing climate has challenged winter season maize crop from seedling to grain filling stage. Adaptation of maize in seedling stage in winter season requires genetic improvement for cold tolerance, which implies vigorous seedling growth with less cold injuries. To evaluate the effect of low temperature on early growth stages and to assess the secondary traits for cold tolerance, study was conducted during *Rabi* 2013-14, 2014-15 and 2015-16. A total of 80 inbred lines (S_4–Sn), evaluated in replicated trials at IARI farms, New Delhi where critical period of vegetative growth was exposed to <10°C temperature. Data on various growth and developmental traits were recorded. Results of low temperature during December-February were expressed as stunted plants, altered plant type and changes in leaf colour (chlorosis, chlorotic bands, burning and drying).Genotypes with high leaf appearance, early vigour and less injury to leaves showed better cold tolerance and eventually grain yield under cold stress. Low temperature greatly influenced Anthesis silking interval (ASI), days to flowering and its duration. Identified resistant genotypes EC-655724, Z172-110, Z172-166, Z172-91, Z172-24, Z172-340, Z172-473, Z172-221, A2-86, A2-89 and A8-9-1 can be utilized in breeding programmes. Our findings suggest that screening of genotypes using traits such as leaf characters, early vigour and visual cold rating could be used as selection index for improvement of cold tolerance in tropical maize.

Keywords: Maize, Cold tolerance

666 (P-167)

Interventions for the Management of Cotton Leaf Curl Virus Disease in the South Western Region of Punjab

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Cotton, an important Kharif crop known as the “White Gold”. The major constraint is the Cotton leaf curl virus disease (CLCuD).The trial was conducted against CLCuD in the hybrid NCS 855 BG II(RAGHAV) in Kharif 2015 at the Regional Research Station, Bathinda(PAU). The interventions i.e. Botanical extract and Homeopathic medicine have been taken for its management. The interventions i.e. Butter Milk @ 5%, Cow Urine @ 6.6%, Neem Oil @ 1%, Mustard Oil @ 3%, Calcium Nitrate @ 0.5%, Cow Urine @ 6.6% + Calcium Nitrate @ 0.5%, Cow Urine @ 6.6% + Butter Milk @ 5%, Butter Milk @ 5%+ Calcium Nitrate @ 0.5%, *Lachesis* 30 @ 0.1%, *Digitalis* 30 @ 0.1%, *Apis Mallifera* 30@ 0.1%, *Bryonia* 30 @ 0.1%, *Natrum Mure* 30 @ 0.1% and Polo @ 0.1%.The foliar spray was done after 30 days of sowing and followed at fortnight interval. The total 5 spray was done. Percent Disease incidence(%), Percent Disease index(PDI) and Average grade at pre-spray, 7 and 15 days after spray was recorded as per CLCuD scale(0-6).After 30 days of sowing, no incidence of CLCuD recorded and after 45 days, incidence of CLCuD recorded. Butter Milk, Neem Oil, Cow Urine + Calcium Nitrate and *Natrum Mure* 30 have shown the PDI at lower range as per the data 7 DAS. Later on, all the interventions shows the susceptible reaction to CLCuD. It can be concluded that above interventions can be applied in the initial stages followed by the chemical sprays against CLCuD.

Keywords: Average Grade, Cotton, Cotton Leaf Curl Virus disease (CLCuD), Percent Diseases Index (PDI), Percent Disease incidence(%)

716 (P-168)

Agro-biotechnological Practices for Agricultural Sustainability under Warming Climate

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Managing soil carbon pool is a major step towards improving soil fertility, sustainable agriculture and climate change mitigation. Temperature is a key regulatory factor to soil carbon stock and atmospheric CO_2 concentration feedback. Therefore the present article was aimed to test the hypothesis that temperature variation will alter the nutrient dynamics in above and belowground parts, soil CO_2 efflux, microbial community and other soil biodiversity. In this context, *Brassica juncea, Zea mays and Vigna mungo* crops were grown with various agro-biotechnological practices at three different agroecosystems of Uttar Pradesh, India. Soil sampling were done from amended and control plot at each experimental sites and mesocosm experiments were performed at +2 and +5ºC compare to ambient temperature under plant growth chamber. Soil physicochemical, biological and enzymatic analyses were done at regular interval and data were correlated with the ambient and elevated temperature. Diurnal variation in the microbial CO_2 efflux was monitored continuously in each amended and control plot under mesocosm experiment. Our results showed significant difference ($p<0.05$) in soil organic carbon, soil microbial biomass and soil enzymes at elevated temperature compared to the ambient. Also the incubated soil from conventional plot showed significant ($p<0.05$) increased rate of microbial CO_2 efflux (from 97.19±13.17 to 101.35±16.64 mg m^{-2} hrs^{-1}) than the biological inoculum and organic amended plots (84.60±11.78 to 92.05± 16.22 mg m^{-2} hrs^{-1}) at elevated temperature. In conclusion adoption of above mentioned agro-biotechnological practices may reduce the CO_2 mediated warming, improve soil quality, crop stress tolerance and nutritional quality under warming climate.

Keywords: Agricultural Sustainability, Microbial CO_2 efflux, Warming climate

786 (P-169)

Development of Reference Set for Terminal Heat Stress Tolerance in Wheat Germplasm Conserved in National Genebank of India

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High temperature stress reduces both grain yield and quality of wheat crop globally. The progress in genetic improvement of wheat for terminal heat tolerance (THT) related traits have been slow due to lack of donors for associated component traits. This problem can be circumvented by evaluating the uncharacterized wheat gene pool available in the genebank and developing the reference set for terminal heat stress. It will identify trait specific donors as well as novel alleles for utilization in crop improvement programme. We took a challenging task of screening the entire cultivated wheat germplasm (~22,000) conserved in National Genebank of India against terminal heat stress tolerance at NBPGR Research Farm, Issapur under heat stress as well as non-stress condition. Based on preliminary screening, a diverse set of ~3000 wheat accessions was selected and re-evaluated during *Rabi* 2012-13 for seventeen morpho-physiological traits. A reference set of about ten percent (316 accessions) were identified based on heat susceptibility index (HSI) for yield components and proportional sampling. This trait specific reference set comprised of 210 *Triticum aestivum*, 103 *T. durum* and 3 *T. dicoccum* wheat germpalsm and was phenotyped subsequently for two years at Issapur farm. Out of these accessions, a total of 42 lines were identified promising against terminal heat tolerance. Few of them were IC290080, EC445377, EC445114 for grains per spike and IC539261, IC539287 for 1000 grain weight and, may be utilized as donors in the wheat breeding programme for development of climate resilient cultivar.

Keywords: Germplasm, Heat tolerance, Reference set, Wheat

799 (P-170)

Characterization of Rhizospheric Bacterial Community from Mangrove Plants of Sunderban as Potential Antagonist of *Macrophomina phaseolina* [(Tassi) Goid.]

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Mangrove forest in Sunderban region of India is the most diverse and productive ecosystem. Unique environmental conditions make mangroves a microbial diversity hotspot that plays an important role to the overall sustainability of this ecosystem. In recent years, there has been an increasing interest in utilization of metabolically diverse microorganisms in climate resilient agriculture that are isolated from specific ecosystem particularly mangrove forest of Sunderban. *Macrophomina phaseolina* is a soil borne fungus that causes charcoal rot and dry root rot in many economically important crop plants. In this study, a total of 156 bacterial isolates recovered from the rhizosphere of *Rhizophora mucronata* L., *Exoecaria agallocho* L. and *Heritiera fomes* Buch.-Ham. from different locations of Sundarban mangrove forest of West Bengal, India, were screened for their antagonistic activity against *M. phaseolina.* Of 156 isolates, 23 isolates showed antagonistic activity against test pathogen. These isolates grew well at pH ranging from 5 to 11 and showed growth on medium supplemented with 5% NaCl. In addition, they were also screened for plant growth promoting activities such as IAA, siderophore production and phosphate solubilization. The isolate Gw-25 was found positive for production of IAA, siderophore and phosphate solubilization. Cultural and molecular characterization is underway for deciphering identity of these microorganisms. Further characterization of the antagonistic isolates for detection of metabolites under *in vitro* and *in vivo* condition will facilitate understanding the mechanisms of biocontrol potential. Such biocontrol agents may be useful in managing diseases in crops cultivated in salt affected soil.

Keywords: Sunderban, Mangrove forest, Rhizosphere, *Macrophomina phaseolina*

829 (P-171)

Morpho-physiological Evaluation of Maize *(Zea Mays L.)* Accessions for Moisture Stress Condition under Rainout Shelter.

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Maize (*Zea mays* L.) is one of the most important, emerging crop having wide adaptability under varied agro-climatic conditions. Major abiotic stresses in maize are moisture, temperature, salt and nutrient stresses. Moisture stress is one of major constraints in maize production as its production and yield is greatly affected by drought and high temperature. An experiment was conducted with 34 selected maize accessions grown under rainout shelter for accessing the drought tolerance in Augmented Block Design at NBPGR Farm, IARI, New Delhi during *Kharif* 2014. Accessions were evaluated for different morpho-physiological traits i.e., days to 50% tasseling, days to 50% silking, days to physiological maturity, plant height, chlorophyll content index (CCI %), canopy temperature, leaf length, leaf breadth, chlorophyll fluorescence, membrane stability index (MSI %), relative water content (RWC %), cob width, cob length, cob height, No. of row/cob, No. of grain / row, 100 seed weight under irrigated and unirrigated conditions. The values of all traits under unirrigated conditions were lower due to moisture stress. The water stress during reproductive period induced early senescence and shortened the grain-filling period. On the basis of earliness, canopy temperature, CCI, MSI, RWC and No. of rows/cob IC541056, IC333084, EC639189 and EC639310 were found promising growing under moisture stress condition. Accessions IC541056, IC333084 promising for earliness and canopy temperature and accession EC639189 promising for membrane stability index, chlorophyll content index and chlorophyll fluorescence under irrigated and moisture stress conditions.

Keywords: Canopy Temperature, Chlorophyll Fluorescence, Maize, Moisture stress, MSI

832 (P-172)

Identification of Molecular Markers to Screen for Heat Tolerant Wheat (*Triticum* sp.) Genotypes

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Identification of functional markers or gene specific markers that are directly associated with phenotypic variations are expected to facilitate screening of germplasm accessions and expediting identification of trait specific germplasm. An exhaustive mining of published literature to list transcription factors, genes, proteins, enzymes involved in abiotic stress tolerance yielded 132 candidate genes. Sixteen wheat genotypes identified to be heat tolerant along with a susceptible variety were used to amplify 24 candidate genes. Five loci were amplified in wheat germplasm accessions and sequenced to identify nucleotide polymorphism. Details of the study will be presented with possible use in screening for heat tolerant wheat germplasm lines.

Keywords: Functional Markers Abiotic Stress Wheat

853 (P-173)

Genetic Diversity across Pathogen Recognizing Receptors: An Important Feature of Disease Resistance in Indian Bovines

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Pathogen invasion stimulates the host to mount an innate immune response primarily to keep the pathogens under check before the specific immunity through antibodies and immune cells fights the pathogens more precisely. One of the components of this innate immune system is the toll-like receptors (TLRs), which recognize conserved components among various classes of pathogens. India has a large biodiversity with respect to buffalo and indicine cattle, with better ability to withstand tropical climatic conditions and fight the pathogens as compared to taurine cattle. We have been able to characterize all the ten reported Toll-like receptors of cattle and buffalo in terms of genetic diversity, expression analysis and also impact of polymorphism on the structure and function of these important molecules. Total 191 polymorphic nucleotide loci have been identified across all the ten buffalo TLRs, out of which 6 were in the promoter, 15 in UTRs, 152 in exonic and 8 in intronic regions. Out of exonic region SNPs, almost 50% (74) were non-synonymous, which indicates most of the TLRs being under positive selection. Buffalo TLR1, TLR2, TLR4 and TL10 have been found to be highly polymorphic with 25 or more single nucleotide polymorphism (SNPs) in all of them, TLR5, TLR6 and TLR7 being moderately polymorphic showing around 10 SNPs and TLR3, TLR8 and TLR9 being least polymorphic with less than 8 SNPs. The polymorphism results also indicate bacterial ligand recognizing TLRs to be more polymorphic than the viral ligand recognizing TLRs, which reflects the diversity being affected by the

Keywords: Buffalo, Cattle, Toll-like receptors, Genetic diversity, Sequence analysis, Structure-function.

870 (P-174)

Effect of High Temperature on Physiological and Biochemical Behaviour of Thermo Sensitive Genotypes of Tomato (*Solanum Lycopersicum* L.)

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High temperature stress induces considerable changes in the biochemistry and physiology of plants. The aim of the present investigation was to evaluate the physiological response of some tomato genotypes to high temperature stress. Twenty one diverse tomato genotypes collected from different sources were field evaluated at the Experimental Farm, Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi during springsummer season for two consecutive years (March-June, 2013 & 2014). Analysis of variance revealed highly significant mean sum of square due to treatments for all the traits suggested thereby the substantial amount of genetic variability were existed in the material under study. Relative water content (RWC) and membrane stability index (MSI) under heat stress condition was recorded maximum in Pusa Sadabahar (83% and 86% respectively). Highest proline content was recorded in wild genotypes, like Spm followed by Spr1. Tolerant genotypes like Spr1 and SPM2 showed high value of chlorophyll b under heat stress condition as compared to sensitive genotypes. Chlorophyll b may be of prime importance, as it gives a better clue for its specific role in increasing tolerance to high temperature. So relative reduction in chlorophyll b may be utilized as an indicator of down regulation of photosynthetic system in general. The highest PCV and GCV

Keywords: Heat stress, Chlorophyll content, Proline, *Solanum lycopersicum*

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881 (P-175)

Recurrent Selection for Drought Tolerance and Modification of Plant Architecture in Bread Wheat

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Climate change and the resultant unusually warm and dry winters resulted in reduction of grain yield from 95million MT to less than 90million MT during past years. A modified recurrent selection program was devised, with two treatments (rainfed and restricted irrigation) and with two replications each, in an alpha lattice design. The recurrent selection was practiced on F5 lines developed from a drought resistant x drought susceptible cross (HI 1500 x HUW 510) rigorously phenotyped for Canopy Temperature (CT), chlorophyll content, Normalized Difference Vegetative Index (NDVI), Harvest Index (HI), grain yield and biomass. 11 F5 lines were selected as parents and were intermated amongst themselves in a rough diallel method; with original parents and popular varieties (HD 2987 and HD 3043) as checks. After three rounds of recurrent selection; the resultant 10 half sib families recorded 9-20% higher grain yield and increased tolerance to water stress. On an average 59% progenies were found to head earlier than the resistant parent and the checks which helped in faster mobilisation of stem reserves. 25.33% progenies recorded longer spike than resistant parent and a reduction in NDVI was noticed after anthessis. The mean biomass of the progeny was found to be lesser than the susceptible parent and check while for chlorophyll content resistant parent recorded higher values. As a result of recurrent selection, the plant architecture was modified as a high yielding and low tillering semi dwarf, with early heading and better grain filling along with increased resistance to water stress.

Keywords: Drought, Plant architecture, Phenotyping, Recurrent selection, Yield

1048 (P-176)

Impact Assessment of Drought Stress on Pollen Viability in Greengram [Vigna radiata (L.) R. Wilczek]

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An experiment was conducted to know the effect of drought stress on pollen viability. 25 Greengram genotypes were used for this study. Experiment was taken up during summer season of 2015. These genotypes were grown in two conditions with three replications in each. In the first condition, drought stress was imposed by withholding irrigation 25 days after sowing. During the entire cropping period there were no rains and hence drought was effectively imposed. In the second condition, genotypes were grown under well watered condition by following flood irrigation on weekly intervals. A distance of 15 metres was maintained between two sets of experiments to prevent accidental availability of water to drought imposed entries through seepage. Pollen was collected from both drought induced and well watered genotypes. The pollen viability was measured using 1% TTC (2,3,5-triphenyl tetrazolium chloride) solution. The factorial ANOVA revealed significant differences between mean values for pollen viability between drought induced (41.37%) and well watered (78.07%) genotypes. There was significant difference in the pollen viability within well watered and drought induced genotypes thus revealing genotypic differences. As anticipated, the pollen viability of genotypes differed significantly between well watered and drought induced groups (Fcal11.02 > Ftab1.62). The interaction effect between the groups was also significantly different. The SEM values for within group, between group and group interactions were 0.28, 1.02 and 1.44 respectively. Similarly CD values for within group, between group and group interactions were 0.80, 2.86 and 4.04 respectively. The study concludes that moisture stress significantly affects

Keywords: Pollen, Drought, Greengram

1145 (P-177)

Influence of Weather Parameters on Population Dynamics of Aphids in Cowpea

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Field experiment was conducted for two years (2013 to 2015) to study the effect of weather parameters on population dynamics of aphids in cowpea using correlation and multiple regression analyses. Aphids were present throughout the year and their population widely fluctuated with weather parameters. However peak aphid population (120-510/ Plant) was observed during 48th to 2nd standard weeks of the years. Correlation studies revealed that minimum temperature showed significant negative correlation (-0.822 and -0.461) whereas, remaining factors fail to show either positive or negative significant effect. The coefficient of determination (R2) between weather parameters and aphid population during 2013-14 and 2014-15 was 78.8 % and 41.4 % respectively suggesting importance of weather parameters in influencing the population dynamics of aphids. Path coefficient analysis was also revealed, the direct contribution of minimum temperature was substantially negative and highest (-1.112 and -1.066). Most of the weather parameters exerted their indirect contributions to the aphid population through sunshine hours. The direct effect of maximum relative humidity (0.436 and 0.111) and sunshine hours (0.006 and 0.288) on aphid population was low, though these parameters showed positive correlation with aphid population.

Keywords: Aphids, Cowpea, Correlation, Multiple regression, Weather parameters

1185 (P-178)

Impact of Climate Change on Crop Productivity in Long Term Experiments in India

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Changing climate is mainly influencing the overall agro-ecology and crop productivity as well. As field crops are quite sensitive to these parameters, here we study the impact of climate change on primary productivity of crop in long term fertilizer experiments going-on in India. For this study, we selected Jabalpur with soybean-wheat and Ludhiana having maize-wheat cropping system since 1972. The yield and climatic parameters like maximum and minimum temperature, rainfall, sunshine hours, and relative humidity were subjected to the regression analysis. Analysis of yield data over the years at Jabalpur indicated that there is decline in productivity of soybean and increase in wheat yield. Increase in temperature during kharif and rainfall distribution pattern are negatively correlated with soybean yield and positive relationship of wheat yield with temperature during rabi appears to be responsible. At Jabalpur increase in temperature during August and decline in temperature during December and January was noted. Balanced use of nutrient counteracted the adverse effect of climate change. However, at Ludhiana, there was a positive relationship of productivity with temperature and sunshine hours are responsible for increase in productivity of maize whereas decline in temperature and increase in sunshine hour during rabi are responsible for higher wheat yield. Increase in temperature might have favored more assimilation of CO_2 by maize being a C_4 plant. Thus, results from long term fertilizer experiments indicated that the changing climate has impact on primary productivity of crops which may eventually influence the soil health. The balanced use of nutrients to some extent could mitigate the adverse impact of climate change.

Keywords: Climate change, Long term, Crop productivity, India

1251 (P-179)

Resistance Performance of Rice Germplasm to Brown Planthopper, *Nilaparvata lugens*.

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Rice is not only a staple food crop worldwide, but also an excellent model organism. Rice crop teeming by more than hundred species of insects and about twenty of them are considered severe pests as they cause significant damage to rice crop. Among them brown planthopper (BPH), *Nilaparvata lugens .* is one of the most critical insect pests causing major yield loss in most of the rice cultivars of Asia. The six hundred promising core rice germplasm accessions were studied by adopting internationally accepted screening technique of IRRI with resistant (PTB-33) and susceptible check (TN-1) during *Kharif*-2015 in glasshouse at IGKV, Raipur (C.G). The results for BPH screening showed that six accessions IC No's 301732, 301734, 301736, 137414, 459148 and 454223X were showed highly resistant (HR) for BPH better to the resistant check Ptb 33, whereas eleven accessions showed resistance (R). Thirteen entries were found moderate resistance (MR) to the BPH. The genetic potential of accessions. IC 301732, 301734, 301736, 137414, 459148 and 454223X on account of excellent act for resistant to brown plant hopper. So these lines may be exploiting as breeding materiel in future rice breeding programme to boost up the grain yield.

Keywords: Brown planthopper, Rice germplasm, Resistance, Screening, Susceptible

1263 (P-180)

Mainstreaming Agrobiodiversity Conservation and use in Sri Lankan Agro-Ecosystems for Livelihoods and Adaptation to Climate Change

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Sri Lanka, which is a recognized mega-diversity hotspot, possesses unique agrobiodiversity. While this diversity remains under threat from the continuing adoption of inappropriate and ultimately unsustainable production practices, it also represents an essential element in the livelihood strategies of much of the population (70%) that still live in rural areas. It also constitutes an essential resource for rural communities and for the country, as Sri Lanka deals with the challenges of adapting to climate change with continuing rise in temperature, changes in rainfall quantities and patterns, and an increasing frequency of extreme events. An innovative project supported by the Global Environment Fund through UNEP is adopting an integrated approach to agrobiodiversity management and use that seeks to use agrobiodiversity to support improved livelihoods, adaptation to climate change and sustainable production. The project is implemented with farmers and communities in three internationally recognized agro-ecosystems " Kandyan home gardens, the village tank system of the dryland zone and the Owita system in the low country wet zone of the country. The activities undertaken have provided: (a) an assessment of the diversity of crops, animals, fish and useful wild species present in the ecosystems, and (b) an analysis of the ways in which agronomic practices could be altered to strengthen agro-ecological approaches to production. Using a participatory approach based on Community Based Management procedures, activities to introduce and maintain diversity that can improve adaptation and livelihoods are being undertaken. The results obtained and the challenges of developing an integrated approach to the management

Keywords: Agrobiodiversity, Climate Change, Genetic Resources, Resilience, Livelihoods

1327 (P-181)

Understanding Expression Characteristics and Sequence Variation of Na+/K+-Atpase Gene, an Important Candidate for Heat Shock Response in Riverine Buffaloes (*Bubalus Bubalis*)

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Na+/K+-ATPase maintains the transmembrane electrochemical potentials of Na+ and K+ ions and helps in active transport of nutrients. Genotypic variants of different Na+/K+-ATPase subunits might have different heat tolerance response in dairy animals. To date, expression kinetics and sequence variation of heat stress associated genes are not well understood in riverine buffaloes. In the present study, an effort was made to study the expression characteristics of all four isoforms viz., alpha1, alpha2, alpha3 and alpha4 (ATP1A1, ATP1A2, ATP1A3 and ATP1A4) of Na+/K+-ATPase gene across 12 different tissues of riverine buffaloes. For normalization of expression data across tissues; UXT, RPS23, RPL4, and RPS9 were identified as panel of stably expressed genes. The data showed ubiquitous and varied expression level of ATP1A1 and ATP1A2 isoforms across mammary gland, kidney, spleen, liver, heart, intestine, ovary, lung, muscle, brain, fat and testis. The ATP1A1 and ATP1A2 transcripts were predominant isoforms in kidney and muscle, respectively, while ATP1A3 and ATP1A4 isoforms were restricted to brain and testis, respectively. Our data indicated tissue specific expression of these isoforms. An attempt was made to assess the sequence variation across three exonic region (exon 19-21) of alpha isoform in 8 buffalo breeds (Murrah, Nili Ravi, Jaffarabadi, Mehsana, Marathwadi, Toda, Kalahandi and South Kanara). On comparing with cattle, a total of 18 variations were identified with varied frequencies. The identified variations could be evaluated in future for their role in heat tolerance trait in riverine buffaloes and cattle.

Keywords: Na+/K+-ATPase gene, Gene expression, Sequence analysis, Heat shock reposne, Revierine buffaloes

1377 (P-182)

Integrated Farming: An Opportunity to Conquer Climate Change

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Fish provides food, income, employment, and trade in fishery products contribute to poverty reduction and national economic growth in many developing nations. Fishery is, threatened by the effects of warming: changes in ocean currents, precipitation that affects lake levels, river flows, increasing storminess, extreme floods and droughts. Fish can provide opportunities to adapt to climate change by, integrating aquaculture and agriculture, which can help farmers to cope with drought while boosting profits and household nutrition. In the present scenario of climate change additional demands for maximizing food production has led to an approach of integrating fish farming with agriculture & fishery. The integration holds a considerable potential for augmenting production of animal protein, generation of employment opportunities in the rural areas and improvement of socio-economic condition of the farmer. Fish farming can be integrated with livestock, poultry, duck, cash crops, paddy fields, horticulture and floriculture. Integrated farming system has been experimented at Adilabad & Mahbubnagar, under an ICAR-NAIP & DST project. The main objective of the integrated recycling is to utilize the wastes and by-products from one component of the cycle to the other as a feed, fertilizer. Agriculture plays a significant role in fight against climate change: good practices can increase food security, and reduce emissions. Integrated farming can play a crucial to combat climate change. Rural populations are the future of food security and rural poverty reduction. Integration of fisheries with agriculture is the need of the present situation and a very effective way to overcome climate change.

Keywords: Integrated, Farming, Fish, Livelihood

1402 (P-183)

Evaluation and Selection of Rice (*Oryza Sativa L.*) Genotypes for Yield and Yield Contributing Characters under Aerobic Condition

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Rice cultivation in most of the rice growing countries like China and India is constrained by declining availability and increasing costs of water as well as lack of rainfall in rain-fed farming areas. The present investigation was a part of the efforts being done in various rice growing countries to develop varieties suited to aerobic conditions attempting to identify rice genotypes suited for aerobic conditions. The study was a part of CSISA (Cereal System Initiative of South Asia) –objective -3 sponsored by IRRI. The experiment was conducted at Norman E Borlaug Crop Research Centre at G.B.P.U. A. & T., Pantnagar, Uttarakhand. A total 24 genotypes were evaluated on the basis of 14 different morphological traits and significant results were drawn on the basis of statistical analysis. Based on the observations on various morphological characters, it was found that the genotypes namely US 359, NK 9080, Govind, Indam, PA 6129 and SVH026 were suitable for aerobic cultivation. Also these genotypes showed maximum mean value for several yield contributing characters suggesting their potential use as donors in further breeding programmes aimed at yield improvement. The identified genotypes holds promise for farmers in water-scarce irrigated or rain-fed environments where water availability at the farm level is too low, or where water is too expensive, to grow flooded lowland rice.

Keywords: Rice, Aerobic, Rainfed, Lowland

1426 (P-184)

Climate Resilience in Wheat Cultivars

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The abiotic stresses in one or other form occur in almost all the wheat growing areas in country. Among various abiotic stresses, high temperatures and soil moisture stress significantly influence wheat production. Individually each stress may cause 20 – 30% reduction in grain yield. The All India Coordinated Wheat and Barley Research Project is responsible for developing agro-climatic condition specific cultivars. However, with passage of time and change in climatic conditions, the adaptability and performance of these cultivars are also expected to change. In order to meet the future challenges, experiment comprising popular cultivars from four mega zones of wheat cultivation were evaluated for drought and heat stress individually as well as combined at four locations by staggered sowing under different irrigation conditions. In total 36 genotypes were evaluated under four conditions namely, timely irrigated (non-stress), timely rainfed (drought stress), late irrigated (heat stress) and late rainfed (heat and drought stress) at each location. The results revealed that some cultivars had narrow adaptation whereas others were widely adapted across locations as well as conditions. Correlation between grain yield and other traits was determined under all sowing conditions and locations. Under stress conditions, productive tillers and biomass had significant correlation with yield at all the locations.

Keywords: Climate resilience. Wheat, Drought, Heat

1437 (P-185)

Metabolic Diversity Analysis and Evaluation of Pseudomonas Spp. for Plant Growth Promotion

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Phosphate (P) is the major essential macro nutrient for biological growth and development. However, the concentrations of soluble P in soil are usually very low, and the largest proportions of P are present in unavailable form. Microorganisms play a central role in P solubilization. Bacteria in soil and in plant rhizosphere having high ability to solubilize inorganic phosphate compounds convert it in to available form which is beneficial for plant nutrition. Under this background, 37 Pseudomonas strains obtained from NAIMCC and NBAIM laboratories were phenotypically characterized and screened for different plant growth promotion activities. The metabolic profiling for the functional attributes of the Pseudomonas strains revealed huge level of diversity with similarity ranging from 26 to 100 %, among the strains the most diverse was P. mosseli D10. Out of 37 isolates, four strains (P. aresnicoxydans P1, P. koreensis P2, P. fluorescens NAIMCC-B-0687 and P. putida R13) showed high activities for different plant growth promoting traits. On the basis of P solubilization, Pseudomonas putida R13 and P. koreensis P2 were selected for pot trials in two crops (wheat and tomato) to evaluate their effect on plant growth. These two strains showed significant effect on improvement of biometrical attributes of Wheat and Tomato. Pseudomonas putidaR13 was found most effective on wheat crop while P. koreensis P2 showed significant enhancement of Tomato growth as compared to un-inoculated control.

Keywords: Pseudomonas, Diversity, P solubilization, Wheat, Tomato, Growth promotion

1473 (P-186)

Effects of Varying Environmental Conditions on Grain Yield and Its Components in Soybean [Glycine max (L.) Merrill] Genotypes

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Soybean is a short day plant exhibiting both photo and thermo sensitivity which influences the area of its adaptation. Changes in day length and temperature have a profound effect on yield potential of soybean genotypes. The present investigation was conducted to assess the effect of varying temperature and daylength on grain yield and its components under three different environmental conditions characterized by different temperature and photoperiod regimes. Seventeen diverse genotypes were grown under three different dates of sowing i.e. March 1, June 7 and August 5 at the Pulse Research area of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana. Observations were recorded for seven quantitative characters viz. days to flowering, days to maturity, plant height, number of pods per plant, 100-seed weight, grain yield per plant and harvest index. Pooled analysis of variance over the three environments revealed significant variance for genotype, sowing date and genotype × sowing date interaction for all the characters. Average highest number of pods/plant and grain yield were obtained from June sowing and maximum plant height, 100-seed weight, days to flowering and maturity belonged to March sowing. Relative ranking of different genotypes varied with sowing dates. From this study, it could be concluded that genetic variability is present in the genotypes and under crop diversification programme in northwest India, especially Punjab area where this study was carried out, presence of genotype × environment interaction could be exploited to get the maximum benefit.

Keywords: G × E interaction, Grain yield, Sowing dates, Soybean

1481 (P-187)

Drought-Tolerant Marama Bean Has Endophytes Promoting Its Growth

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Marama bean (*Tylosema esculentum*) is an indigenous non-nodulating legume to the dry agro-ecological parts of Southern Africa. It is a staple food for the Khoisan and Bantu people from these areas. It has high-protein content in its seeds albeit its natural habitat is nitrogen deficient. The aim of the study was to determine the presence of seed transmittable bacterial endophytes that may have growth promoting effects, which may be particularly important for the drought-prone conditions. Marama bean seeds were surface sterilized and gnotobiotically grown. From surface-sterilized shoots and roots, 123 distinct bacterial isolates were cultured, and identified by BOX-PCR fingerprinting and sequence analyses of the 16S rRNA and *nif*H genes. Phylogenetic analyses of 73 putative endophytes assigned them to bacterial species from 14 genera including Proteobacteria (*Rhizobium, Massilia, Kosakonia, Pseudorhodoferax, Caulobacter, Pantoea, Sphingomonas, Burkholderia, Methylobacterium*), Firmicutes (*Bacillus*), Actinobacteria (*Curtobacterium, Microbacterium*) and Bacteroidetes (*Mucilaginibacter, Chitinophaga*). Screening for plant growth-promoting activities revealed that the isolates showed production of IAA, ACC deaminase, siderophores, endoglucanase, protease, AHLs and capacities to solubilize phosphate and fix nitrogen. Marama bean seeds harbor endophytes that can be cultivated from seedlings. This community of bacteria has plant growth promoting characteristics with potential for use as biofertilisers.

Keywords: *Tylosema esculentum*, Marama bean, Drought-tolerant, Plant growth promoting endophytes

1484 (P-188)

The Seed Roadmap: An Online Guide for the Enhanced Use of Genetic Diversity in Crop Breeding

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Seeds of Discovery (SeeD) is a collaborative initiative seeking to unlock the genetic potential of wheat and maize biodiversity to address the production challenges of a climate-changed world. At the core of SeeD lies a dynamic capacity building strategy that promotes the access to and use of wheat and maize genetic resources by breeders and researchers through open-access data, software tools and workshops. To further strengthen the capacity building strategy, the 'SeeD Roadmap' is a novel initiative aiming to deliver self-learning online training modules to teach, promote and facilitate access to wheat and maize genetic diversity. The SeeD Roadmap consists of practical and theory modules, structured as a 'guided tour' through 'themed highways'. Practical modules will cover aspects of managing and analysing data in a step-wise manner and using 'real-life' scenarios, while theory modules will provide information on important principles and concepts to support practical modules. Learning material for the first module of a themed highway focusing on selecting a core set of accessions, 'Introduction to Genotypic Data', was developed. Funded by the Mexican Ministry of Agriculture (SAGARPA) as part of the MasAgro project, the Roadmap is currently in Spanish and available through the online open-source learning environment Moodle. Drawing on the initial concept and development phase of the SeeD Roadmap, I will (i) provide an outline of the SeeD Roadmap's structure and content, (ii) highlight and reflect on the challenges involved in establishing a self-learning online training platform and (iii) present future plans for the Roadmap.

Keywords: Capacity building, Crop genetic resources, Diversity, Online training

1518 (P-189)

Screening For Heat Tolerant Donors In Rice For Future Breeding Programme

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High temperature stress making rice production less efficient in many warming regions during rice cultivation, above 35oC during development stages significantly reduced the yield. To sustain the rice production, there is need for better donors with tolerance to high temperature stress. The identified heat tolerant donors ultimately used in breeding programme to generate rice varieties with tolerance to high temperature stress is utmost important in order to sustain future rice production. A total of 50 genotypes were received from IRRI were screened during the dry season of Rabi 2014 at ICAR-Indian Institute of Rice Research, ICRISAT campus with an altitude of at 17°29'40.39"N, 78°16'15.39"E. Sowing was done in order to ensure exposure of maximum genotypes to high temperature (>400 C) at the time of reproductive stage. The genotypes transplanting was done 25 days after seeding in two rows each row 3 m with a spacing 20x15cm. Recommended agronomic practices were done at optimum level. Observations on day to 50% flowering, plant height, productive tillers per plant, spikelet fertility were recorded. Existence of the genetic variability was observed among the genotypes. There was significant to drastic reduction for spikelet fertility recorded. In this present study the genotypes HHZ 8 SAL6 SAL 3 Y1, HHZ 5 DT 1 DT1, HHZ 8 SAL12 Y2 DT1had minimum impact of heat stress on seed setting, the same germplasm set under progress in screening for reconfirmation for their heat tolerance in temperature gradient tunnel (TGT) and these donors could be used in breeding programme.

Keywords: Germplasm screening, Heat tolerance, High temperature, Rice, Spikelet fertility

1541 (P-190)

Morpho-Physiological Characterization of Mexican Wheat Landraces for Traits of Economic Importance Under Punjab Conditions

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Landraces are the most important and rich source for genetic improvement of cultivars. The Mexican Creole wheats are the last traces of common wheat carried by the Spanish to Americas between 16t to 18thcentury. A wide collection of these old wheats collected from throughout Mexico is conserved at International centre for wheat and maize improvement (CIMMYT). This set was procured from CIMMYT and consisted of 1161 accessions. The set along with commercial checks was evaluated for morpho-physiological characters with an aim to explore the potential yield and yield components in Punjab conditions. The set was grown at Punjab Agricultural University, Ludhiana for two years viz.2014-15 and 2015-16 under timely sown irrigated conditions. The recommended package and practices were followed to raise the crop. The set was evaluated for yield and various yield components like tillers per meter, spikelets per spike, grains per spike ,thousand grain weight and grain yield. ~ 400 accessions had higher yield as compared to recommended commercial checks. Few accessions were identified to have long spikes (18), more number of spikelets per spike (27), more tillers per row (39) and higher thousand grain weight (10). The data was also recorded on stay green habit, chlorophyll content and canopy temperature depression. ~23 accessions could be identified to have better stay green habit, high chlorophyll content and ability to keep its canopy cooler. These traits may be used by breeders worldwide to develop climate resilient cultivars. Yield and yield related traits can be efficiently incorporated into elite wheat cultivars for wheat improvement.

Keywords: Wheat landraces, Yield

1548 (P-191)

Genotypic Variation And Mechanism For Early Heat Stress Tolerance In Wheat (*Triticum Aestivum* L.)

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The temperature has increased much as compared to previous years during the recommended time of sowing, which calls for a need to identify genotypes tolerant to early heat stress. Seed germination and seedling establishment are important characteristics for wheat which could provide advantages in terms of overall plant stand in genotypes tolerant to early stress tolerance over heat sensitive ones. Also, the role of alpha amylase too needs to be revisited in light of early heat stress tolerance. The study was conducted on 91 diverse wheat lines to analyse variation for early heat stress tolerance and relation of coleoptile length from ten days old seeds germinated in dark, rate of germination and alpha-amylase activity at three different temperatures 25°C, 30°C and 35°C. The genotypes with robust coleoptile growth, quick germination and high enzyme activity at higher temperature yielded better under timely and early sown conditions and the yield reduction was much less in these genotypes under stress environments. Genotypes BWL3460, BWL4412, BWL4435, BWL4431, BWL3458 and BWL3472 shows longer coleoptile length (4.6-5.4 cm), quick germination (4-5 seeds germinated per day) and high enzyme activity (0.15-0.27mg of Starch hydrolyzed min^{-1} g^{-1} FW) at 35°C. These selected genotypes were evaluated in field conditions under early heat stress and they had better yield (15-20 q/acre) as compared to commercial checks (13-20 q/acre) under stress conditions. Identified cultivars with tolerance to heat stress at germination could be exploited for increasing the crop duration translating into increase in productivity.

Keywords: Alpha amylase, Coleoptile length, Early heat stress, Wheat, Yield

1550 (P-192)

Integrated Farming: An Opportunity to Mitigate Climate Change

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Fish can provide opportunities to adapt to climate change by, integrating aquaculture and agriculture, which can help farmers to cope with drought while boosting profits and household nutrition. Integrated farming system has been experimented at Adilabad & Mahbubnagar, under an ICAR-NAIP & DST project with the main objective of utilizing the wastes and by-products from one component of the farming cycle to the other as a feed and fertilizer. Secondly, the farmers earn additional income from fishes, poultry besides using the pond water to irrigate the agricultural crops. Integrated farming holds a considerable potential for augmenting production of animal protein, generation of employment opportunities in the rural areas and improvement of socio-economic conditions of the farmers. Fish farming can be integrated with livestock, cash crops, paddy fields, horticulture and floriculture. The recommendation is that integration of fisheries with agriculture is the need of the hour and a very effective way to overcome climate change impact on livelihoods.

Keywords: Fish, Integrated farming, Livelihood

1581 (P-193)

Screening of Diverse Wheat Germplasm for Pre-Harvest Sprouting Tolerance

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Wheat contributes about 40 percent of the world's food basket and widely grown in a variety of climates globally. Among abiotic stresses, pre-harvest sprouting (PHS) is a major concern for wheat cultivation in eastern and far eastern parts of the country due to untimely rains around maturity. The PHS in wheat is characterized by premature germination of kernels in a mature spike prior to harvest (usually under wet and humid conditions) due to early breakage of seed dormancy usually the result of moist weather conditions that persist after physiological maturity. PHS tolerant cultivars and land races have been identified globally. For present study GI (Germination index) and SI (Susceptibility index) were used for the screening of 1100 diverse breeding lines including indigenous and exotic germplasm lines received from international nurseries/ trials, double haploid population, released varieties and some land races for PHS was carried out using rain simulation and germination test. Out of the total 1100 diverse breeding lines, a set of 179 lines were selected which showed tolerance to PHS under controlled conditions. GI of these lines varies from <0.25 (7 lines), 0.26 to 0.40 (10) and > 0.41 (162 lines). Confirmatory testing of this trait among the tolerant lines using molecular marker approach will serve as potential tool for screening against PHS tolerance in wheat.

Keywords: Sprouting tolerance, Wheat germplasm

1607 (P-194)

Genetic Stock Structure Investigations on Indian Mackerel, *Rastrelliger kanagurta* along Indian Coast

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Preserving intra-specific diversity and stock complexity is very important in marine fisheries management as stock complexity gives resilience to climate change and consequent habitat alterations in marine fishes. In view of this, a genetic stock structure investigation was carried out in Indian mackerel, *Rastrelliger kanagurta*, a commercially important marine pelagic fish in Indian waters with extensive distribution all over the coast of India using mitochondrial ATPase and control region sequences. The samples were collected from 10 locations along the Indian coast; Tuticorin, Nagapatnam, Paradeep, Mumbai, Kakinada, Calicut, Gujarat, Mangalore, Trivandrum and Portblair. ATPase and control region sequences were amplified in 271 and 241 individuals respectively. High haplotype diversity was associated with low nucleotide diversity in both sets of sequences. There were 155 haplotypes out of 271 individuals with a haplotype diversity value of 0.97 and nucleotide diversity value of 0.008 when ATPase sequences were analysed. The sequences of control region revealed 95 haplotypes out of 241 individuals with a haplotype diversity value of 0.90 and nucleotide diversity value of 0.004. Low but significant genetic differentiation was observed between mackerel populations from peninsular India and Portblair using both sets of sequences. The variations in oceanographic conditions between the two regions may be the reason for restricted mixing and consequent stock structure. Based on the above results we suggest devising management measures for mackerel populations of peninsular India and Andaman Sea separately so as to preserve intra-specific diversity and stock complexity.

Keywords: Genetic stock structure, Indian mackerel, Molecular markers, *Rastrelliger kanagurta*

1621 (P-195)

Population Genetic Structure of Indian Oil Sardine, *Sardinella longiceps* Assessed Using Microsatellite Markers

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Information on genetic stock structure is very important for conservation of marine fish genetic diversity as intra-specific diversity determines resilience of marine fish populations to climate change related habitat alterations and overfishing. Indian oil sardine, *Sardinella longiceps* is a commercially important marine pelagic fish in Indian waters and genetic stock structure investigations were carried out in it using microsatellite markers developed by cross amplification. The samples were collected from Gulf of Oman, Veraval, Mumbai, Mangalore, Calicut, Kollam, Trivandrum, Chennai and Vizag. Microsatellite genotyping was carried out on the ABI Prism genetic analyzer using 6FAM labelled primers. Alleles were identified using GENEMAPPER software and genetic stock structure analysis was carried out using standard software packages. We could detect distinct population units/ subpopulations with significant F_{ST} values. Bayesian clustering algorithm in STRUCTURE revealed the presence of six subpopulation (K=6). The distinct subpopulations are; Gulf of Oman (Mumbai &Veraval), Mangalore, (Calicut, Kollam and Trivandrum), Chennai and Vizag. A pattern of isolation by distance was evident in Mantel tests with significant correlation between geographic distance and genetic distance in addition to a low but significant correlation between genetic distance and environmental distance. Salinity was the most important factor when partial mantel tests were carried out after omitting the effects of geographical distance. The reasons for the low but significant genetic stock structure detected in Indian oil sardine may be attributed to natal homing, larval retention or environmental gradients causing restricted mixing between subpopulations. In view of these results, we suggest to devise management measures regionally so as to preserve intra specific biodiversity and stock complexity.

Keywords: Genetic stock structure, Indian oil sardine, Intra-specific diversity, Microsatellite markers

1687 (P-196)

Evaluation of CIMMYT's Advanced Wheat Pre Breeding Germplasm for Grain Yield and Yellow Rust Resistance in Punjab.

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There is an alarming concern regarding narrow genetic base of modern day commercial cultivars. Breeders usually prefer advance breeding elite lines for developing new cultivars rather exploring and exploiting the rich genetic diversity available in wild relatives of wheat or landraces. To address these issues, a number of initiatives have been undertaken at global level to pursue pre breeding in wheat. A total of 1000 advanced pre breeding linesdeveloped at CIMMYT, Mexico were evaluated for yield under yellow rust epidemic in Punjab Agriculture University and for yield potential under protected conditions at BISA, India. These advanced lines constituted the linked top cross population (LTP) panels which included a series of top cross populations in linked through common elite parents in their pedigree(so called LTPs). Crop was raised using recommended package and practices for the timely sown irrigated environment and no chemical spray was done for controlling the rust at PAU so as to assess yield losses due to stripe rust. Over 87 genotypes yielded better or at par with local commercial checks at BISA whereas 46 genotypes out of these best 87 succumbed to stripe rust at PAU and showed approximately 20-50% yield losses. Only 41 genotypes out of 1000 lines were found to be significantly higher yielding rust resistant lines as compared to the local commercial checks at both locations. High yielding and disease resistant lines were selected and grown at off season location in Himalayas (Keylong, HP) for multiplication of seed. These genotypes will be followed up in varietal pipeline in coming crop season.

Keywords: Pre-breeding, Wheat, Stripe rust, Yield

1711 (P-197)

Sequence Characterization of ARG2 and FOXR2 Genes in High Altitude Adapted Ladakh Cattle

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Hif-1± is one of the master regulators of the cellular response to hypoxia as it triggers wide transcription of genes involved in angiogenesis, vasodilatation and energy metabolism. Arginase 2 (Arg2) proteins affect Hif-1± stability and activity by regulating production of TNF-± and nitric oxide and also has key roles in numerous physiological processes while Forkhead box R2 (FOXR2) proteins are a family of transcription factors that play important roles in regulating the expression of genes involved in cell growth, proliferation, differentiation, and longevity. To understand the sequence differences in these candidate genes responsible for hypoxia and high altitude adaptation, sequence data was generated across 24 animals adapted to high altitude region (Ladakhi cattle, HF and Jersy) and 24 animals adapted to low altitude (Sahiwal, Rathi, Kankrej, Tharparkar & Nagori) region. In the 5and 3UTR of ARG2 3 SNPs were observed in transcription factor binding site USF/C-Ets-1, C/EBP;Oct-1 and HNF-1 respectively while in CDS, a total of 5 SNPs (A118G, G140T, T209A, G424T and T841C) were observed, and one of these was nonsynonymous (Asp242Tyr). The sequence characterization of forkhead box R2 (FOXR2) gene covering UTR and CDS revealed 2 SNPs in 5 UTR; 1 in 3UTR; 3 synonymous SNPs in CDS (Fig 4) across group of animals from low and high altitude regions. The observed variations could be evaluated for their specific role in high altitude adaptation and can serve as resource for identification of markers for high altitude resistance.

Keywords: ARG2, FoxR2, High altitude, Ladakhi cattle,

1754 (P-198)

Phenotyping of *Gossypium hirsutum* Germplasm for Waterlogging Tolerance

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Cotton (*Gossypium hirsutum* L.) is known to be poorly adapted to waterlogged conditions. Transient waterlogging occurs frequently in Vertisol of central India which have inherently low drainage rates. Field level phenotyping for waterlogging tolerance was taken for large cotton germplasm. The morpho-physiological changes induced due to waterloggging stress were quantified in standing crop subjected 20 d waterlogging of 45 d old plants and then permitted to recover. After termination of waterlogging treatment root growth showed a significant recovery in tolerant lines. Out of 3000 germplasm, selected two hundred twenty one cotton germplasm comprising susceptible and waterlogged tolerant were evaluated for leaf senescence traits and relative stem increment- along with yield. Measurements were taken on the youngest fully expanded leaf of 3 plants for both waterlogged tolerant and susceptible plants for leaf colour reaction at vegetative growth stage. The functional reaction in response to waterlogging stress on morphological adaptation results into four categories of plants viz; hypertrophied lenticels only, adventitious root only, hypertrophied lenticels and adventitious root growth and no morphological adaption. Theses selected germpasm lines were correlated with water logging tolerance and yield.

Keywords: Cotton, Germplasm, Waterlogging

1759 (P-199)

Effect of Establishment Methods, Nitrogen Levels and Azotobactor Seed Inoculation on Growth and Yield of Pearl Millet (*Pennisetum Glaucum* L.)

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A field experiment was conducted during the *kharif* season 2014 at the Crop Research farm Department of Agronomy, Allahabad School of Agriculture, SHIATS, Allahabad (U.P.) to evaluate the effect of establishment method, nitrogen levels and azotobactor seed inoculation on growth and yield ofpearl millet (*Pennisetum glaucum* L.) laid out in Randomized Block Design with eighteen treatments replicated thrice. The results revealed that transplanting on 5 August + application of nitrogen at 100 kg/ha + without azotobactor seed inoculation produced significantly higher length of ear (22.98cm).Although The highest grain yield (3.47 t ha^{-1}), net return (43220.70 Rs. ha^{-1}) and benefit cost ratio (2.32) was obtained with transplanting on 5 August + application of nitrogen at 100 kg/ha +with azotobactor seed inoculation.

Keywords: Azotobactor seed inoculation, Establishment method, Nitrogen Level and Pearl millet

1779 (P-200)

Collection, Documentation and Conservation of Local Maize Germplasm of Tribal Areas of Madhya Pradesh, India

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Maize was first domesticated in Mexico, from its wild species ancestor, teosinte, about 9000 years ago, but maize landraces are widely found across the continents. Maize has enormous genetic diversity, which is present in the form of landraces or populations. The maize landraces are typically selected by farmers for better adaptation to specific environment, nutritive value and resistance to biotic and abiotic stresses. Keeping this in mind an exploration was conducted for collection of maize local germplasm / landraces from three tribal districts viz., Dindori, Mandla and Chindwarra of Madhya Pradesh. This paper discusses the pattern of variability of collected germplasm and the observations on field evaluation. A total of 700 accessions were collected, evaluated and conserved for documentation. The samples were in the form of maize cobs with various color and size. The characterization was done in March 2012 at Research farm, BISA in Jabalpur. Results revealed good amount of variability in traits observed. The cob length varied from 09 to 46 cm, number of rows from 8 to 49 and number of columns from 8 to 25. Some lines among the material collected from district Chindwarra were found to be as good as improved maize hybrids yielding 248 gm/ plant showing excellent the terminal filling in hot summer. These germplasm lines were also screened for disease and insect pests. From this evaluation promising germplasm lines showing heat tolerance, tolerance to disease and insect pests were identified, which could be further used in maize breeding programs.

Keywords: Exploration, Evaluation, Landraces, Maize

1794 (P-201)

Who Will Kill Them First, Climate or Man?

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Managing marine fisheries resources in a changing climate requires clear understanding of the unique and combined effects of fishing and climate variability. As most of the fishery resources are currently under exploitation, distinguishing their effects can only be achieved by employing different statistical controls. The present study employs semi-partial correlation of Sea Surface Temperature (SST) and fishing effort (in hours) for specific species as independent variables with relative abundance of each species as response variable. Annual average of all the variables from 1985 to 2014 has been utilized for analysis. CPUE (in hours) was selected as a measure of relative abundance of each fish species. The study has revealed that mostly the demersal fish species are adversely impacted by both fishing and climate variability. Fishing was observed to have a higher negative influence on the abundance of these fishes whereas SST showed comparatively lesser negative impact. It has been also noted that though the singular influence of SST was less, the shared variance explained by both the predictors was high in most cases. This shows that that influence of fishing makes the population of these demersal fish species more sensitive to climate variability even though the actual impact of climate variability is lesser.

Keywords: Climate variability, Marine Biodiversity, Fisheries resource management

1799 (P-202)

Effect of *Meloidogyne Incognita and Fusarium Oxysporum* F. Sp. *Cucumerinum on* Cucumber Grown Under Protected Cultivation

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A disease complex involving *Meloidogyne incognita* and *Fusarium oxysporum* f. sp. *cucumerinum* was studied on cucumber in polyhouse under protected conditions. The experiment was conducted in pots to evaluate the effect of nematode and fungus individually as well as in various sequential combinations i.e simultaneous inoculation of nematode and fungus (SIS), nematode one week prior to fungus (1WBF) and nematode one week after fungus (1WAF). The results revealed that nematode inoculation caused significantly more reduction in plant growth parameter, viz., shoot length, root length, fresh shoot weight, fresh root weight, dry shoot weight and dry root weight of cucumber as comparison to fungus alone, however, combined inoculation of nematode and fungus was statistically significant with respect to reduction in plant growth parameter over their individual effect. Maximum and significantly more reduction in plant growth parameters viz., SL (125.5cm), RL (32.0cm), FSW (44.0g), FRW (24.3g), SDW (8.5g) and DRW (4.1g) was observed in the treatment where nematode was inoculated one week before fungus as compare to untreated check having SL (138.2), RL (47.5), FSW (58.5), FRW (37.5), SDW (21.5), and DRW (9.4). Nematode reproduction in terms of formation of galls and egg masses and final nematode population in soil was also significantly suppressed in the treatment where nematode was inoculated one week prior to fungus.

Keywords: *Meloidogyne incognita*, *Fusarium oxysporum* f. sp. *Cucumerinum*, Dry root weight.

1824 (P-203)

Resilience in Cotton (*Gossypium* spp.) through Development of Broad based Varieties

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Negative consequences of climate change on agricultural production are widely being recognized in recent years. Climate change has increased the concern of researchers and planners to meet the demand of ever increasing population for food, nutrition and clothing. It has generated a desire among the researchers to build resilience into agricultural systems. Development of broad based populations for development of varieties appears to be the most rational and cost-effective method that can improve resilience in crop species in a variety of ways. Broad based varieties developed involving number of genetically diverse genotypes/ germplasm accession would serve as buffer for adaptive management and environmental changes. Broad based populations/ varieties will be more resilient to adapt in fluctuating environment and have greater ability to suppress pest outbreaks. In cotton, narrow genetic diversity of the cultivated varieties and breeding material has adverse impact on improvement of yield, fibre quality and adaptation. To overcome this situation, we developed random mating populations in upland and *desi* cotton involving 20 genetically diverse germplasm lines and elite cultivars in each species. After several cycles of random mating, a resulting composite population was assessed for genetic diversity of various economic and fibre quality traits. The range of trait values has shown tremendous increase including resistance to pests and diseases. Several selections obtained from the population were evaluated for yield and fibre quality parameters. Development of population, breakage of linkages and the extent of diversity being generated shall be presented and discussed.

Keywords: Broad based populations, Breakage of linkages, Cotton, Genetic diversity, Random mating

Technical Session 4-A :

Science-led Innovation

Concurrent Session :

Trait Discovery and Enhanced Use of PGR

1123 (O-31)

Identification of Stable Heat Tolerant Wheat Germplasm Lines under Extreme Late Sown Condition

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Terminal heat stress has emerged as one of the major threats to food security. The popular commercial wheat varieties have inadequate level of tolerance to terminal heat stress hence, there is need to evaluate wheat germplasm lines to identify new sources of resistance. 496 selected germplasm lines were evaluated for various yield and phenology related traits including, chlorophyll fluorescence and cell membrane stability under extreme late sown condition during 2014-15 winter season at three different locations Karnal, Hisar and New Delhi. Sowing was done in augmented block design using 6 checks HI1571, UAS 320, HD 3118, WH 1105, HTW 11, HD 2967, repeated in each block. The daily average temperature ranged from 8.0^{0}C to 23.0^{0}C during pre-heading period and from 21.0^{0}C to 35.0^{0}C during post heading period. 47 germplasm lines were identified superior to best checks. These lines were further characterized in same three locations under timely and late sown conditions during 2015-16. Based on two years' trials, the accessions EC 445320, EC 445382, EC 445481, IC 252529, IC 252832, IC 290335, IC 539221with more than 40g TGW under very late sown conditions, high Fv/Fm values at all post anthesis stages and cell membrane stability (>45%); IC531176, IC 564121, IC 145815 for stay green habit and IC532037, IC531176, IC534434 for long peduncle were identified as promising heat tolerant lines. Germplasm lines were also characterized using linked molecular markers. These promising lines can be used as a source of resistance to develop heat tolerant wheat cultivars in future.

Keywords: Cell Membrane Stability, Germplasm Lines, Heat Tolerance

1694 (O-32)

Genetic Enhancement of Rice (*Oryza sativa* L.) through Inter-specific Crosses Involving *Oryza rufipogon* and their Potential in Improving Heterosis

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Genetic enhancement through utilization of wild species is an important step in diversifying the gene pool in crops. Even though, there are 22 diverse wild species in rice, their use has been limited to improvement of pureline varieties. In the present study, *Oryza rufipogon*, an A genome wild rice relative was crossed with Pusa 6A, the female parent of a popular aromatic superfine grain quality rice hybrid, Pusa RH 10. The F_1s were found to be completely fertile indicating the presence of fertility restorer in the *O. rufipogon*. From the F_2 population segregating for spikelet fertility, plants showing complete fertility were advanced through pedigree selection till F_6 to develop a set of 144 introgression lines (ILs). These ILs showed huge variation for various agro-morphological traits including plant habit, days to 50% flowering, plant height, panicle length, number of productive tillers and yield per plant, when characterized in augmented block design using PRR78 (the pollen parent of Pusa RH 10), Pusa 6B (the isogenic maintainer line of Pusa 6A) and two other improved genotypes namely, Pusa 1592 and Pusa Sugandh 5. Some of the ILs showed better panicle exsertion as compared to Pusa 6A, and higher yield per plant (22.1g) as compared to 16.3g in Pusa 6B. An IL was backcrossed with Pusa 6A to produce improved restorer lines with better quality. These improved restorers have produced heterotic hybrids with diverse CMS lines proving their potential in improving heterosis in rice.

Keywords: Genetic enhancement, Grain quality, Heterosis, Introgression lines, Rice

1941 (O-33)

Managing the Biodiversity of Neglected and Utilized Crops in China

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Crop biodiversity is essential for sustainable agricultural development. There are many kinds of neglected and underutilized crop species (NUS) in China, such as barley, buckwheat, millets, oat and sorghum. These crops are characterized by diversified species and types, rich genetic diversity, balanced nutritional components, and multiple uses. Considerable germplasm resources of these crops have been collected and conserved in the national genebank. Bioversity International has collaborated with Chinese partners to promote the NUS such as buckwheat and oat for adapting to climate change and sustaining livelihood in China. The phenotypic diversity of NUS were assessed and documented for most important agro-economic traits, including yield traits and nutrition components. Useful genepools and special collections were specified for meeting the needs of different users. Efforts have been made to evaluate genetic diversity and identify the useful accessions from existing collections of NUS with molecular tools. Multi-location trials have identified the most adaptable varieties of buckwheat and oat in Lingshan, Sichuan where the local people, particularly Yi Ethnic group is relied in buckwheat and oat for livelihoods. The accessibility of the adapted NUS diversity by local farmers is vital in sustaining the nutrition and food security and livelihoods in the marginal areas. The adaptation of NUS diversity to climate change will play a role in promoting the resilience of local agroecosystem in northwest and southwest of China

Key words: NUS, Phenotypic and genotypic diversity; Adaptation; Climate change

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1926 (P-204)

Evaluation of Genotypes for Enhancing Water use Efficiency and Productivity in Aerobic Rice (*Oryza sativa* L.)

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Irrigated rice production needs continuous flooding and high water inputs. Therefore alternate cultivation methods and new cultivars minimizing the use of water must be developed to sustain rice productions. During the crop season *kharif* 2014, the RIL population of the cross PR120 x UPLRi7 were planted in alpha lattice design with two replications under aerobic and anaerobic conditions in fields of School of Agricultural Biotechnology, PAU, Ludhiana. The plot size was 4 rows per entry. The whole set was also planted under anaerobic conditions to study genetic variation for morpho-physiological and quality parameters under both systems. Growth as well as yield attributes like plant height, number of productive tillers, days to flowering, number of panicles per plant, number of grains per panicle and yield per plot were recorded. At reproductive stages difference in anatomy of root structures was observed with wider air pockets in aerobic conditions than in anaerobic. 67 drought tolerant genotypes showed superior performances with respect to grain yield. Morpho-physiological traits viz., chlorophyll content of 35 SPAD units using SPAD-502Plus chlorophyll meter was highest in 84 genotypes in aerobic conditions. 9 genotypes flowered early (65-70) days in aerobic conditions and only 1 genotype in anaerobic conditions. Plant height (90-110 cm) of 24 genotypes was observed in aerobic condition. Maximum fertile spikes (49) were found in aerobic condition. Also mapped QTLs for adaptation to aerobic conditions. The genotypes performed well in aerobic conditions and thus can be tested for varietal development.

Keywords: Aerobic rice, Morpho-physiological traits, SPAD values, QTLs

28 (P-205)

Development of Core Set of Indian Collection of Cultivated Potatoes (*Solanum tuberosum* ssp. *tuberosum*)

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Globally, potato (*Solanum tuberosum* L.) is the most important non-cereal food crop which has proved its worth in providing food and nutritional security. In India, since its first introduction in early 17th century new need based germplasm are being regularly procured from different source countries and have been conserved in the potato gene bank. These imported germplasm are being evaluated for various biotic, abiotic stresses and quality traits and being used in different breeding programmes. The genetic base of potato varieties across world is narrow and therefore broadening the same can tackle many emerging issues and can help in identifying the best genotype among segregating progenies. At present the germplasm repository of Potato at CPRI, Shimla has a total collection of 1400 tuberosum accessions. Creation of core set is one approach of hastening and prioritization of the germplasm characterisation and ultimately its utilisation for different traits specific breeding activities. Considering above, a core set of 140 accessions of *Solanum tuberosum* was extracted from 1400 accessions based on 19 morphological descriptors *viz*., vegetative, tuber and sprout parameters. The validity of the core set by means and variances comparison and Shannon-Weaver diversity index and phenotypic correlations between different traits revealed that actual diversity of base collection have been conserved. The established core set forms the basis for wider exploitation of potato germplasm for effective utilisation in potato improvement programmes.

Keywords: Core Collection, Genetic Diversity, Germplasm, *Solanum tuberosum* ssp. *tuberosum*

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43 (P-206)

Colchiploidy and Sexual Seedlings for Pre-breeding Banana

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Agrobiodiversity forms the scientific basis for breeding of banana, the important tropical fruit crop. Genetic improvement of banana is hampered by polyploidy, sterility and parthenocarpy. Objective is pre-breeding of banana by induced polyploidy and sexual progenies. Banana suckers of Velchi (AB) were treated with colchicine to induce polyploidy. Nineteen putative tetraploid plants and seven untreated diploid plants are planted for characterisation. Putative polyploidy banana plants had fewer (3 to 24) roots than untreated plants (10 to 51). A rare banana plant with seedy fruits was located at garden of Ms. Rupali Padwalkar at Ponda of Goa state, India. About 252 sexual seedlings raised from the plant and after three months and were characterized using ten morphometric traits and an image. After transplanting 196 seedlings have survived. Height and collar girth of seedlings varied from 2 to 11.5 cm and 0.7 to 4.5 cm respectively. Leaf length /width ratio and weight of whole seedling ranged from 0.4 to 5.9 and 0.2 to 10 g plant^{-1} respectively. Phenotyping of salinity tolerance in banana was developed using a detached leaf tip assay with sodium chloride at 0 to 800 molar concentrations using varieties differing salt tolerance Sugandhi and Grand Naine. Change in in leaf (browning, drying, necrosis, rolling of tip, deposition of salt at edge) after few days of assay were found useful to discriminate the salinity tolerance. The population thus developed forms an important material using allele mining, phenotyping techniques for desirable traits of dwarf stature, tolerance to salinity and sigatoka disease.

Keywords: Abiotic stress, Colchiploidy, Half-sib, Konkan, *Musa*, Pomology

75 (P-207)

Utilization of Natural and Hybridization Derived Variability in Physic Nut (*Jatropha curcas* L.) for Domestication

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Natural variability of *Jatropha curcas* available in the centre of origin remains unexplored and underutilized. The innate potential of Jatropha could not be realized by R&D institutions in India due to limited genetic variability. Therefore, JNKVV resorted to prebreeding involving *J. curcas* and *J. integerrima* to generate variability and utilize to enhance and stabilize yield potential. These crosses generated tremendous variability including traits of economic importance viz. early flowering, reduced plant height, leaf size, shapes; flower size and desirably high female to male flower ratio. Exceptionally, a plant with pistillate flowers was observed and is being utilized for hybrid seed production. The derivatives of interspecific crosses following backcross resulted in identification of promising plants viz. A9-1, B9-14, E9-7, H1-5 and J34-6 with altered plant type, have been clonally propagated. The non-toxic plants have been identified among three provenances; NBJ-1, JA 9 and MNJ 007 as part of ICRAF project including non-toxic high yielding plants/lines in advance testing. Intensive screening resulted in isolation of elite types viz. early flowering, dwarf, small and non-pigmented leaves as spontaneous mutants in collected germplasm. The prebreeding and backcrosses utilizing key traits for domestication practically transformed plant architecture with low height (45-50 cm), small foliage with seed yield of 1.5 to 2 tons. The promising lines are now available at JNKVV for reintroducing Jatropha for plantation and its utilization to foster future breeding programme.

Keywords: Domestication, Non-toxic, Pistillate, Plant architecture, Prebreeding

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156 (P-208)

Sequence Polymorphism in Polyamine Biosynthetic Genes Associates with Abiotic Stress Tolerance Levels in Rice

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Rice (*Oryza sativa* L.) is one of the major crop cultivated under diverse agro-climatic zones across the globe at tropical and sub-tropical regions. Rice is one such crop where genetic diversity exists for each and every agronomic trait being studied especially, plant height, panicle length, number of tillers, grain size, and grain color. With its small genome size (389Mbp) and the first crop genome to be sequenced completely, rice is considered as a model organism for all “omic” approaches. Rice cultivars with drought and salinity tolerance might help a lot in avoiding yield losses due to water scarcity and poor soil quality that limits nutrient uptake. Polyamines are cationic compounds involved in normal physiology of the plants and its modulated expression pattern during stress are well known. Decarboxylases are known to play a regulatory role in polyamine biosynthesis during stress, especially ornithine decarboxylase (*Odc*), arginine decarboxylase (*Adc*) and S-adenosylmethionine decarboxylase (*AdoMetDC*). Key polyamine biosynthetic genes from rice genotypes exhibiting varied levels of stress tolerance was cloned and sequenced. Genetic variation at sequence level for key polyamine biosynthetic genes across rice genotypes with varied levels of stress tolerance was characterized. Our results revealed an association between the genetic polymorphism at sequence level and the stress tolerance in rice through polyamine biosynthesis besides their modulated expression pattern during stress – which is well known.

Keywords: Polyamines, Abiotic stress tolerance, Rice

173 (P-209)

Screening of Germplasm for the Source of Resistance to Root-knot Nematode (*Meloidogyne incognita*)

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The root-knot nematodes (RKN), *Meloidogyne* spp., are sedentary endoparasites of roots damaging a variety of agricultural crops, causing an estimated US $100 billion loss/year worldwide. They are one of the most widespread and are considered to be the most destructive nematode pest of various crops in tropical and subtropical regions including India. The economic damage to plants by their feeding and interactions with other soil microorganisms renders the plants further vulnerable to other biotic and abiotic stresses. Other than chemical methods, use of resistant cultivars is considered one of the most effective and environmentally-safe alternatives. Germplasm of various accessions (acc) of pulse and vegetable crops such as lentil (150 acc), pea (300 acc), okra (60 acc), brinjal (75 acc) and cucumber (40 acc) were evaluated for resistance to RKN (*Meloidogyne incognita*). Experiments were conducted in pots (10-cm-dia) filled with naturally *M. incognita* infected soil (500g/pot) collected from a sick plot, containing 3 juveniles per gram of soil (1500 J2/pot). After six weeks of sowing, plants were uprooted and host status was designated on the basis of number of root galls induced by *M. incognita*. Those accessions showing less than 10 root galls/root system were considered as promising/resistant. Based on two years screening data, 2 acc each of lentil (IC559673, IC559890), pea (IC208367, IC-219002) and okra (IC255758, IC306737), and one acc of brinjal (IC090869) and none of cucumber were found promising/ resistant against *M. incognita*. These promising accessions can further be used for RKN resistant breeding programme.

Keywords: Germplasm, Resistance, Root-knot nematode

177 (P-210)

Development of Inbred Lines of Maize with Multiple Disease Resistance

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Development of Inbred lines of Maize with multiple disease resistance Jyoti Kaul, DS Olakh, Khushbu Jain, Usha Nara, KS Hooda, Ramesh Kumar, Vinay Mahajan ICAR-Indian Institute of Maize Research, Pusa Campus, New Delhi-110012 Corresponding Author Email- dsolakh@gmail.com Abstract Deployment of nutritionally superior disease resistant varieties remains an economically viable and sustainable option of enhancing and stabilizing production as well as securing food and nutrition security of the masses. Maize, being one of the most nutritious food and feed crops of the world including India is constrained by a number of diseases like Turcicum leaf blight (TLB), Maydis leaf blight (MLB), Banded leaf and sheath blight (BLSB), Charcoal rot (CR) and Polysora rust (PR). Keeping this in view, a set of newly developed 25 QPM inbred lines along with two checks was screened during Kharif 2014 at different hot - spot locations at Delhi, Ludhiana and Karnal for MLB; Bajaura and Mandya for TLB; Karnal for BLSB; Ludhiana for CR and Mandya for PR, respectively. The disease severity was recorded on a rating scale of 1-5 (1 being resistant and 5 susceptible) for TLB, MLB, BLSB, PR and whereas, scale of 1-9 (1 being resistant and 9 susceptible) was used for CR. The same set of lines was grown under natural conditions at Delhi and evaluated for agro - morphological, Phenological, yield and yield -related traits. The Phenological data indicated that the lines took 45 to 62 days to Anthesis (50%) with a mean of 51.5 and 45 to 61 days

Keywords: Multiple disease resistance, Quality protein maize, Disease resistance

252 (P-211)

Screening of *G. hirsutum* Germplasm for Yield and Yield Contributing Characters

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Central Institute for Cotton Research, Regional Station, Sirsa-125055, Haryana The narrow genetic base developed due to extensive use of closely-related cultivars in breeding programme is observed the main cause for cotton vulnerability to biotic and abiotic factors. This problem can be overcome by involving genetically diverse genotypes to create unique gene combination necessary for new superior cultivars. Three thousand nine hundred fifty four geographically and phenotypically diverse lines from gene pool of *G. hirsutum* were evaluated under North Zone conditions, during 2011-2012 to 2015-16 at Central Institute for Cotton Research, Regional Station, Sirsa for yield and yield contributing traits. The information generated on genetic distance among germplasm lines for various traits could be useful for the utilization in cotton improvement pragramme. The wide variability among the accessions for all the parameters was observed. The yield /plant is an important parameter to increase the productivity of cotton and among the accessions evaluated, the superior accessions observed for this trait were IC 359586(192g) and IC358008(191.3g). The number of bolls in combination to boll weight are recognized as important traits for the breeder for developing high yielding genotypes. Under current study, the superior accessions for boll number were MSK-USSR-4 (70), H-1280(69) and CSH-3050(68) and for boll weight higher than 4 gm were IC-356615,IC-357027 and IC-358894. The monopodial plants are suitable for wider spacing and superior accessions for this trait were IC 357570, IC 357523 and IC 358512. The sympodia are the fruit bearing branches and the retention of bolls in sympodial plant is

Keywords: Cotton, Germplasm

268 (P-212)

CRP on Maize Agro-Biodiversity: A Platform for Cataloguing and Assessing Maize Diversity in India

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Maize, *Zea mays* L. is the major crop of the world which has largely benefited by utilizing diversity in germplasm collections. The maize germplasm ranges from inbred lines, genetic /breeding stocks to land races, OPVs and cultivars. Utilization of germplasm in India is primarily hindered by the lack of adequate information on traits of economic value/ importance. As a remedial measure, ICAR has come up with a long-term programme on characterization, evaluation and utilization of maize germplasm. This is a collaborative project under which different All India Coordinated Research Project (Maize) centres have been identified as partners in characterization / rejuvenation / multiplication of maize germplasm held in LTS at NBPGR, New Delhi. Accordingly, since 2014 Kharif, a total of 5000 accessions, have been characterized in phases at five centres, *viz.* IIMR New Delhi, Winter Nursery Centre, IIMR, Hyderabad, PAU Ludhiana, CSKHPKV Bajaura and MPUA&T Udaipur, respectively. The characterization was based on recording data on 30 common set of descriptors that included 12 quantitative and 18 qualitative traits of which 19 were recorded at standing crop and 11 were recorded at the post-harvest stage, respectively. Around 1000 germplasm accessions were rejuvenated and multiplied based on their biological status i.e inbred lines were selfed whereas populations and varieties were sib-mated with a purpose to maintain the identity as well as help conserve the allelic diversity. The data so generated is expected to provide potentially valuable information on traits of importance,improve curatorial efficiency and eventually encourage utilization in breeding programmes.

Keywords: Maize germplasm, Characterization, Rejuvenation, Genetic diversity

272 (P-213)

Morphological Diversity of Buckwheat (*Fagopyrum* Spp.) Landraces Collected from North-East Indian Himalayas

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Buckwheat (*Fagopyrum* spp.) is an important crop in the high altitude regions of North-east Indian Himalayas. The agro-climatic heterogeneity of this region offers a great deal of diversity in agro-morphology of buckwheat species. In the current study, a total of 97 accessions of *F. esculentum* and *F. tataricum* characterized for 16 morphological descriptors. Frequency distributions of *F. esculentum* (66) and *F. tataricum* (31) accessions showed significant variations for days to 50% flowering, days to 80% maturity, primary branches plant^{-1}, plant height and 100-seed weight. Wide range of variations observed for other traits. Clustering and principal coordinate analysis separated two buckwheat species into two distinct clusters. On the basis of UPGMA dendogram on morphological similarity values (simple matching coefficients), these buckwheat species formed two distinct clusters at 17% similarity level. Within the tartary buckwheat accessions, two sub-clusters can be discerned. Cluster A contains 14 accessions which were characterized by spreading plant architecture and triangular to ovate seeds. Rest 17 tartary buckwheat accessions of cluster B having highest average values for days to 80% maturity (88.8 days) and number of primary branches (12.6). Sixty six *F. esculentum* accessions clearly separated into three sub-clusters at approximately 30% morphological similarity. Cluster C grouped 50 common buckwheat accessions; Cluster D contained 15 accessions and single accessions, collected from Assam, formed cluster E. This study will facilitate in planning *in situ* management of buckwheat landraces in NE India and in selecting diverse parents in breeding programmes based on agro-morphological traits.

Keywords: Buckwheat, *Fagopyrum esculentum*, *Fagopyrum tataricum*, North-East India, Characterization, conservation.

320 (P-214)

Diversity in Bael, Jackfruit and Jamun Germplasm Evaluated and Maintained at Field Genebank of ICAR

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Indian gene centre holds rich diversity in major and minor fruit species occurring in temperate, subtropical and tropical climatic conditions. Though majority of them are not explored commercially but offer a significant source of livelihood support and nutritional security. Germplasm of several locally grown fruits species categorized as potential fruits needs to be identified for superior types to boost the socio-economic condition of rural communities.Considering their importance, germplasm of bael (Aegle marmelos), jamun (Syzygium cumini) and jackfruit (Artocarpus heterophyllus) was collected and established in the field gene bank at ICAR-NBPGR, Base Centre, Ranchi, Jharkhand.The rich diversity in above mentioned fruits (522 accessions) was assembled from 87 districts covering diverse edapho-climatic conditions in Jharkhand, Bihar and adjoining states. Out of these, 289 accessions were characterized and identified as promising types viz. IC376182 (fruit, pulp and stone weight), IC376183 (smallest stone)and IC331740 (maximum pulp percentage) in jamun; IC436490 (superior fruit, pulp weight and pulp percentage), IC348036 (early type with medium fruit size) in bael and IC591173 (heaviest and biggest fruit), IC591148 (longest flake), IC24362 (fruit length and diameter), IC24327 (maximum flake weight per fruit) in jackfruit.In the present communication, richness of diversity in bael, jackfruit and jamun, their local uses,promising types identified and germplasm conserved in field gene bank have been discussed.

Keywords: Diversity, Minor fruits, Germplasm, Field genebank

392 (P-215)

Effect of Acute Doses of Ionizing Radiation on Growth and Yield Characteristics of Foeniculum Vulgar

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Improvement programme in fennel is limited due to its low genetic variability, small flower size which hamper manual emasculation and pollination and self-incompatibility. The stakeholders requirement in fennel varieties is to develop short duration, short stature and high yielding varieties, which is not possible without creating variability. Therefore, to create genetic variability in fennel gamma rays was used develop variability in fennel. The seeds of fennel cv. Ajmer Fennel-1, was irradiated with gamma rays with the dose of 150, 175, 200, 225 and 250Gy. Among the different doses of gamma rays, the maximum germination was observed at 150Gy (76.67%), whereas the minimum seed germination was recorded at 250Gy (53.33%). The seed germination and seedlings survival was 70.00% and 50.67%, respectively at dose of 200Gy of gamma rays. The higher dose of gamma rays was lethal and seedlings were dying in latter growth stage after germination. After 30 days of seed sowing 150Gy of gamma rays gave maximum number of leaves (17.2), number of roots per plant (17.2), root length (32.4 cm), shoots length (9.3 cm) and fresh weight per plant (0.0601 g) followed by 175Gy, 200Gy, 225Gy and 250Gy. The control plants showed earlier (69.2 days) flowering compared to the all irradiated plants. In the same way, earlier maturity was recorded in control (184 days) followed by irradiated plants. Significant difference ($p<0.05$) was observed with regards to numbers of umbels per plant, number of umbellate per umbel, number of seeds per umbellate, number of seeds per umbel, 1000 seed weight (g) and seed yield per plant (g).

Keywords: Fennel, Gamma rays, Radiation, Growth

407 (P-216)

Phenotypic Characterization Sorghum Germplasm under CRP-Agro Biodiversity

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Germplasm characterization and documentation are the important activity in germplasm management. It eases data retrieval and short-listing accessions for genetic improvement. A set of 2459 sorghum germplasm accessions supplied by NBPGR, New Delhi under the CRP-Agrobiodiversity are characterized at IIMR, Hyderabad for 27 agro-morphological traits during rabi 2015-16. In the present study only 10 pre-harvest trait data was used to assess the variability and identify the distinct genotypes. From the qualitative data it was found that dark green midrib colour appeared in very low frequency (0.04%), only in one accession (EC 483674), followed by yellow midrib (1.0%). One accession (EC 484133) was found with 15 leaves and three accessions with 14. For clustering data on four quantitative traits days to 50% flowering, leaf length (cm), leaf width (cm) and plant height (cm) was used. There was wide range variation observed for leaf length (23.2 - 91.18 cm), leaf width (2.46 – 10.85 cm), days to flowering (44 - 97 days) and plant height (64 - 348 cm). The CV was highest for plant height 27.6%. Clustering was done using EM algorithm. Four clusters formed and the accession evenly distributed in the four clusters in the biplot. The attributes of clusters shows the difference in mean but with similar standard deviation. The trait relationship among the traits showed that the days to 50% flowering and plant height showed similar variation and are highly correlated.

Keywords: Cluster analysis, Sorghum, Variation

481 (P-217)

Characterization of the *Kharif* Sorghum Landraces for Yield and Some of the Seed Quality Parameters

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Landraces are the varieties nurtured and cultivated by the farmers through traditional method of selection by over the decades. These land races are store houses of genetic variability and ordinarily are adapted to local soil types, climatic conditions etc. They are sources of many valuable genes, including those for adaptation. So there is need to conserve and study the characteristics of land races and their further utilization in the breeding programme. In the present study the material consisted of 99 landraces of kharif sorghum received from Directorate of Sorghum Research (DSR), Hyderabad during kharif 2011. Good variability was observed for all the characters under study. The days to 50% flowering ranged from 54.33 (ERN-25) to 95.33 (ERN-29) days. Plant height ranged from 110 (ERN-26) to 434 (GGUB-34) cm. Seed hardness ranged from 4.03 kg/ cm^2 (EB-6) to 10.13 (GGUB-57) kg/cm^2 . Threshed grain mold rating ranged from 3.06 (GGUB-57) to 11.36 % (GGUB-21). Specific gravity of seed varied from 0.98 g/ml (EA-10) to1.08 g/ml (GGUB-57). Germination percentage of seed ranged from 71.50 (GGUB-21) to 86.00 (E-106). Electrical conductivity ranged from 0.79 dsm^{-1} (GGUB-21) to 1.46 dsm^{-1} (GUB-29). 1000 seed weight ranged from 14.75 g (GGUB-34) to 40.08 g (E-163) g. Fodder yield per plant varied from 35.00 (GGUB-68) g to 435.00 g (E-246). Grain yield per plant ranged from 5.13 g (E-202) to 44.83 g (ERS-15). There is need to exploit these promising land races in further breeding programme.

Key words: Germination percentage, Landraces, Seed hardness, Specific gravity

506 (P-218)

New Vistas for Utilizing *Saccharum* Complex through Distant Hybridization for Diversification of Sugarcane Agriculture as well as Industry

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Sugar industries diversifying with bio-energy production need sugarcane varieties having specific composition of sugar, fibre and biomass yield termed as 'Type-II' cane unlike traditional varieties which are assigned as 'Type -I' cane. Further, in case of 'Type-III' and 'Type-IV' canes, moderate to severe concession is made for sucrose content to the advantage of fibre content. Inter-specific crosses between *Saccharum officinarum* and *S. spontaneum* were attempted at ICAR-SBI, Coimbatore out of which 21 selected clones were evaluated for sugar content, fibre content and total biomass yield at ICAR-IISR, Lucknow. Observations revealed that IkshuISH-21 and IkshuISH-22 were grouped under 'Type-III' as these possessed low sugar along with high fibre content and high biomass. IkshuISH-2 was 'Type-II' cane with moderate sugar, high fibre content and high biomass yield. IkhsuISH-17 had shown high sugar and moderate fibre content and may be regarded as 'Type-I' cane. However, none of the clones under study had shown exceptionally high fibre content to designate as 'Type-IV' cane. These 'Type-II' and 'Type-III' clones may be utilized as future energy cane for the production of first and second generation bio-ethanol as well as for cogeneration. These clones can also be utilized as parents for developing sugarcane varieties needed for the bio-energy production by advanced sugar industry complexes.

Keywords: Sugarcane, *Saccharum,* Bio-energy, Distant hybridization

533 (P-219)

Analysis of Phenotypic Diversity for Oil Content and Yield in Maize (*Zea Mays* L.)

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Corn oil is pale yellow, tasteless and odorless oil procured from the corn kernel. Corn oil is gaining acceptance among other conventional oils on account of its health benefits. Information about the oil percentage and morphological variation in germplasm is an important prerequisite for efficient improvement towards high oil corn. To assess the potential of maize as source of oil, a total of 108 inbreds were evaluated in randomized complete block design with two replications at one location for ten morphological traits and oil content for two years. Oil was estimated in self-pollinated grains by Soxhlet method varied from 2.4% (EC646076) to 7.3% (Temperate XTropical(HO)QPM-B-B-B-60BB). Six inbreds (TemperateXTropical(HO)QPM-B-B-B-60BB, TemperateXTropical(HO) QPM-B-B-B-100BB, DMHOC4, HKI-Tall-8-1-1, TemperateXTropical(HO)QPM-B-B-B-57-BB and HKI Talar) with more than 6.00 percent oil were high oil corn lines. Multivariate analyses including principal component analysis (PCA) and cluster analysis (Ward's minimum square) were performed to assess the patterns of morphological variation. The PCA extracted three components, which explained 70.91% of the total variation for eleven quantitative traits. The cluster analysis grouped 108 inbreds into three clusters, and the number of inbreds in each cluster was 10, 64 and 34 respectively. High oil inbred (TemperateXTropical(HO)QPM-B-B-B-60BB) with maximum inter cluster distance from other inbreds was genetically most divergent. Divergent high oil inbreds with suitable morphological traits can be valuable in improvement of oil in maize.

Keywords: Maize oil, Principal component analysis, Clustering

536 (P-220)

Assessment of Genetic Variability of Wheat Landraces from North-western Himalaya and their Differential Resistivity to *Sitophilus oryzae* L.

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Wheat is being traditionally grown in North-western parts of Himalayas where several landraces are still under cultivation in niche micro-climatic agroecologies under subsistence farming. These landraces are differentially adapted to specific niche environments and can be a potential source of useful genetic diversity for crop improvement programmes. The study was, therefore, undertaken to assess the genetic diversity and screening against *Sitophilus oryzae* L., an important storage pest. Twenty one SSR primer pairs were used to assess the diversity of 96 prominent landrace populations. A total of 51 alleles (eighteen rare) were recorded with mean number of 2.428 alleles per locus. AMOVA revealed maximum variation among individuals within populations (83.1%) followed by within individuals (15.12%) and rest (1.78%) among populations. Screening of landraces (varying in their seed parameters) against *S. oryzae* under no-choice artificial infestation conditions revealed significant variability. The landraces were categorized on the basis of insect growth index and loss in grain weight. Four landraces *viz*., IC393109, IC392578, IC444217 and IC589276 were found resistant based on both parameters, of which, three were from Kumaon division and one from Garhwal division. Landraces from the Kumaon division also recorded highest molecular diversity indices *viz*; observed number of allele, effective number of alleles and Shannon's diversity index. The study, therefore, revealed that the wheat genetic diversity in Kumaon region maintained under traditional subsistence farming need to be conserved which could be a potential genetic resource for various crop improvement programs including weevil resistance in wheat.

Keywords: Genetic diversity, Landraces, North-Western Himalaya, *Sitophilus oryzae*

543 (P-221)

Biodiversity of Farmers Varieties of Rice (*Oryza Sativa* L.) in Chhattisgarh State

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Rice (*Oryza sativa* L.) is a major cereal crop which supplies food for about 50% of the widespread population. It is initiate the point of food harbor and is comprehensively linked with conventional ethnicity and customs. Chhattisgarh is traditionally known as the Rice Bowl of India. More than 23,000 rice varieties have been recorded in the region. These are a result of centuries of rice farming by indigenous communities through selection and adaption to a variety of soil, water and micro-ecosystems conditions including predators. Bastar region of Chhattisgarh is known as biodiversity hot spot in India. Land races / Farmers varieties is still popular in most of the tribal areas of Chhattisgarh due to some unique properties viz. high nutritious value, medicinal value, aroma and other features. In the present investigation 327 farmers varieties were tested on 62 DUS characters. This experiment was conducted during kharif 2016. Research works were conducted at Research cum instructional form college of Agriculture, IGKV, Raipur (C.G.). About 1500 farmers varieties were collected from different parts of Chhattisgarh for their characterization and evaluation. 7 farmers varieties viz Amari Dhan, Bandi Luchai, Godadani Dhan, Ghoda Chavar, Kala Umri, Kurlu Dhan Dharohar and Munda Ghotiya have been identified that varieties have high yield with better nutritional value as compared to modern high yielding varieties and these varieties will plays a key role to overcome malnutrition problem in tribal areas of Chhattisgarh.

Keywords: DUS, Farmers varieties, Quality Characters, Rice

549 (P-222)

Assessment of Genetic Diversity in Linseed (*Linum usitatissimum* L.) Germplasm of Himachal Pradesh and Jammu and Kashmir Region

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Linseed is an important oilseed crop grown since ancient times for fibre and seed oil. It is the potent source of omega -3 fatty acids, the desirable cholesterol for healthy living. For a successful breeding programme, the identification of potential donors for seed yield and oil yield combined with desirable traits is a prerequisite. Hence, an attempt has been made to study the diversity in linseed germplasm from the state of Himachal Pradesh and Jammu Kashmir. Fifty one accessions of linseed germplasm belonging to Himachal Pradesh (39) and Jammu Kashmir (12) along with three checks were used in the experiment and grown in RBD during the *rabi seasons* of 2013-14 and 2014-2015 at Akola, India. Seven qualitative and six quantitative traits were recorded. The seed oil content was determined by NMR method. The morpho-agronomic traits indicated significant diversity among the genotypes of Himachal Pradesh and Jammu and Kashmir *i.e.* in early plant vigour, flower color, shape, size, seed size, seed luster and seed coat color and in quantitative traits days to 50 % flowering (59.0-87.5), capsules per plant (27.5-49.6), plant height (45.6-63.4 cm), days to maturity (108 -129), 100 seed weight (0.27-0.74g), yield per plant (0.65-2.88g) and oil content (36.11-45.31 %).High coefficient of variation was observed in yield per plant (33.4 %) followed by 100 seed weight (28.0 %). Two accessions from Himachal Pradesh i.e. IC-96649 identified as promising for high seed weight (0.74g) and yield per plant (2.88g) and IC 96637 for high oil content. (45.31 %) respectively and could be utilised in crop improvement programme in the country.

Keywords: Agro-morphology, Linseed, Germplasm, Oil content

612 (P-223)

Assessment of Genetic Divergence across Different Genotypes of Tall Fescue Grass (*Festuca arundinacea*) in North Western Himalayas

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Tall Fescue grass (*Festuca arundinacea*) is a perennial, high yielding, fodder crop widely grown throughout the cold and temperate regions of the world. It is preferred over other winter season grasses for its better stock piling property and to produces leafy green herbage throughout the summer. Considering its potential forage value and limited genetic information at morphological level, present study was aimed to assess the genetic diversity among 36 genotypes of tall fescue grass using morphological traits. On the basis of mean performance two genotypes namely, Hima-3 and EC-178181 were found superior for green forage yield/ plant, dry matter yield/ plant, plant height, leaf stem ratio and crude protein yield/ plant among all the genotypes. "Selection-85" was superior for tillers/ plant and leaves/ plant whereas "Selection-48" was found superior for stem thickness and leaf length among all the genotypes. Cluster analysis based on D^2 statistics differentiated 36 tall fescue genotypes into 13 clusters indicating significant genetic diversity among the genotypes. Based on the pooled analysis, Hima-3 and EC-178181 were found to be diverse and superior for most of the characters. So these could be used in future breeding programmes for genetic improvement in Tall fescue. The classification of these 36 genotypes may be of wider application as it will avoid genetic redundancy of genotypes in hybridization programme.

Keywords: Genetic diversity, Morphological traits, Tall fescue

609 (P-224)

Genetic Diversity of Traditional Loose Flower Crops under Coastal Humid Ecosystem of Goa

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Demand and popularity for traditional flowers like Crossandra and Jasmines has come down in Goa due to cut flower advent and Western culture impact. Hence an attempt was made to collect and conserve Goa's precious local germplasm resources at ICAR-CCARI. Systematic surveys were conducted for collection of different *Jasminum* and *Crossandra species*. Materials used for the study consisted of crossandra accessions viz.,C-1(Big dark orange),C-2(Ratan-aboli),C-3(light-orange),C-4(bright-yellow) and C-5(dark-orange) and fourteen *Jasminum* accessions belonging to *J.sambac, J.auriculatum, J.grandiflorum and J.multiflorum*. Significant variation was noticed among accessions for various morphological and floral-quality traits. Plant height,leaf length and width,no.of branches/plant,length and diameter of flower,flower stalk length, no.of flowers/month and weight of individual flower in crossandra varied from 25.87cm to 67.49cm, 9.43cm to 11.10cm, 3.03cm to 4.19cm, and 3.00 to 6.24,3.13cm to 4.67cm, 2.14cm to 4.29cm, 1.91cm to 2.43cm, 90.23 to 153 and 0.02g to 0.11g respectively. Plant height,bud and flower fresh weight,bud diameter and length,bud stalk length,corolla tube length,flower diameter,no.of petals/flower,length and width of petals and flower stalk length in jasmine accessions ranged from 66cm(J-7) to 143cm(J-5),0.052g(J-5) to 0.563g(J-1),0.05g(J-5) to 1.37g(J-10),1.14cm(J-8) to 0.264cm(J-5),2.54cm(J-6) to 0.85cm(J-5) and 2.30cm(J-14) to 1.08cm(J-8), 2.70cm (J-14) to 0.864cm(J-10), 6.68cm(J-6) to 1.96cm(J-5), 43(J-10) to 5.0(J-1), 0.96(J-5) to 3.50(J-6),0.32cm(J-5) to 1.74cm(J-4) and 2.80cm(J-14) to 1.10cm(J-10) respectively. Local accessions thus exhibited an incredible diversity with potential floricultural traits. Study documented various morphological and floral characteristics of different flower genotypes to represent the existing broad diversity.Data generated would be helpful in future crop improvement programmes to cater to the needs of floriculture industry.

Keywords: Broad diversity, Local accessions, Traditional flowers

1905 (P-225)

Molecular Mapping of a Novel Genetic Loci, *Bph31(t)*, Conferring Resistance to Brown Planthopper (*Nilaparvata lugens* Stål) in Wild Species, *Oryza nivara*

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The brown planthopper (*Nilaparvata lugens* (Stål), BPH) is one of the most destructive pests of rice causing 60% of yield loss worldwide in its severity. The natural host plant resistance is the most economic way to manage BPH. Wild species are valuable source for resistance to BPH. In the present study, we screened approximately 2000 accessions of wild species germplasm of rice for two year, 2012 and 2013, against BPH. Out of which 32 accessions showed consistent resistant response to BPH for both the year. A wild species accession, *Oryza nivara* acc. IRGC104646 was selected for mapping of the genetic loci conferring BPH resistance. Genetics of resistance loci was performed in 462 F_2 and 193 $F_{2:3}$ populations revealed presence of single dominant gene. A 50K SNP chip (OsSNPnks) was used for genotyping of 96 individuals of F_2 population. . The novel resistance gene, tentatively designated as *Bph31(t)* was mapped between two SNP markers, AX-95952039 and AX-95921548 at 28.8 LOD score value on long arm of chromosome four. The phenotypic variance explained by this gene was 68.3%. The physical distance of this locus was 91 Kb containing eleven candidate genes, out of which one belongs to Leucine- Rich Repeat (LRR) family protein. In addition to that, two SSR markers, RM16994 and RM17007, were co- segregated with the BPH resistance gene. These two tightly linked markers can be efficiently used in marker- assisted breeding program for incorporation of this gene into elite rice cultivars.

Keywords: Brown Planthopper, Linkage Map, *O. nivara*, SNP Markers, Wild Species

627 (P-226)

Characterization of Ashwagandha (Withania sommnifera (L.) Dunal) Germplasm Accessions Conserved at Indian National Gene Bank

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Ashwagandha (Withania somnifera (L.) Dunal) is an important widely used medicinal plant in various traditional systems of medicines. Ayurvedic texts have described it as possessing stimulant, aphrodisiac, diuretic, anti-inflammatory and also mildly sedative and hypnotic properties. To facilitate the utilization of conserved germplasm at National Gene bank, NBPGR, a total of 122 germplasm accessions were characterized and evaluated for 22 agro-morphological characters under Consortium Research Platform on Agro-biodiversity Project during the year 2015-16. Significant diversity was observed for leaf length (3.7-8.2 cm), leaf width (1.9-4.3 cm), main root length (10.0-33.5 cm), main root diameter (5.2-40.0 mm), number of secondary roots per plant (0.7-6.0), fresh root weight per plant (1.8-222.3 g), days to flower initiation (76-128), plant height (29.0-89.0 cm), days to fruit (berry) formation (22-39), number of berries per plant (219.2-543.9), number of seeds per berry (28.0-48.0), berries diameter (4.9-6.7 mm) and days to seed harvest (178.0- 223.0). The promising accessions for high root yield (IC0510841) and more berries (IC0553945) were identified.

Keywords: Medicinal plants, Ashwagandha, National Genebank, Charectarization

629 (P-227)

Genetic Variability for Agro-Morphological Characters in Kalmegh (*Andrographis Paniculata* (Burm.F.) Wall. Ex Nees) Germplasm Accessions Conserved at Indian National Gene Bank

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Kalmegh (Andrographis paniculata (Burm.f.) Wall. ex Nees) or King of Bitters is an important medicinal crop of India grown mainly for its anti-inflammatory, antihyperglycemic, hepatoprotective, and antibacterial properties. To facilitate the utilization of conserved germplasm at National Gene bank, NBPGR, a total of 66 germplasm accessions were characterized and evaluated for 20 agro-morphological characters under Consortium Research Platform on Agro-biodiversity Project during the year 2015-16. A wide range of variability was observed for branching pattern (branched or profusely branched), number of primary branches (5-14), leaf shape (ovate to lanceolate to oblanceolate), leaf surface texture (glaberous or hairy), leaf colour (pale green to dark green), inflorescence type (lax panicle or compact panicle) and capsule shape (linear to lanceolate), leaf lamina length (4.2-10.2 cm), leaf lamina width (1.2-3.4 cm), plant height (45-87 cm) and number of seeds per capsule (6-13). Promising accessions were identified for various yield and quality traits.

Keywords: Medicinal plants, Kalmegh, Gene bank, Genetic variability

636 (P-228)

Profiling of Essential Oils in French Marigold (*Tagetes Patula*) Genotypes

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Marigold is one of the most important ornamental crop grown worldwide. It belongs to family Asteraceae. There are about 33 reported species in genus Tagetes. Among them, Tagetes patula commonly known as French marigold is one of the important species grown for loose flower production in India. Besides, it is also reported to be rich in essential oil compounds. The essential oils are being utilized in perfumery industry worldwide. The present investigations were carried out at Division of Floriculture and Landscaping, IARI, New Delhi to screen Tagetes patula genotypes (11No.) for essential oils. The different components of oil derived from fresh leaves and flowers at full bloom stage of the crop were estimated by hydro distillation and examined by gas chromatography (GC) and GC-mass spectrometry (GC-MS) and mean values were calculated on fresh weight basis. The forty nine compounds of essential oil were identified. On an average, leaves were found richer in total oil content as compared to flowers. However, both leaves and flowers were found very similar with regard to composition of essential oil for all the compounds identified. Oil content extracted from leaves ranged from 0.06 to 0.15% v/w, whereas, in flowers oil content ranged from 0.02 to 0.09% v/w. The major components of essential oil identified were terpinolene, piperitenone, (z)-Î²-ocimene, piperitone, limonene and Î²-caryophyllene .

Keywords: Tagetes patula, Essential oils, Hydro distillation, Gas chromatography (GC), GC-mass spectrometry (GC-MS)

682 (P-229)

Development of Wheat Genetic Stocks Imparting Resistance to Ug99 Pathotypes

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Rusts are devastating diseases of wheat around the world. Stem rust has been considered one of the great threats to wheat production in Central Zone (including Rajasthan) and Peninsular Zone of India. Stem rust of wheat had became a disease of past, till a new race was observed in Uganda in 1998 (Ug99), designated as TTKSK. It has the ability to overcome the resistance imparted by majority of the resistance genes including Sr31 which used to protect 40% of wheat from stem rust worldwide. Indian wheat researchers lead by Regional Station, ICAR-IIWBR have already initiated activities in association with CIMMYT and BGRI to identify and develop suitable resistant cultivars/genetic stocks for rapid deployment in its different wheat zones.Three advance stocks were characterized for stem rust resistance and yield components. In these three resistant stocks viz. FLW31, FLW32 and FLW33, varieties of Central Zone (CZ) and Peninsular Zone (PZ) were used to introgress Sr43, Sr26 and Sr32 genes, respectively. These genetic stocks have been developed through backcrossing and pedigree selections to remove winter wheat behaviour of donor parent and the resistance genes have been confirmed through molecular markers. These resistance genes were selected for transfer as they provide complete resistance against all the virulent pathotype of black found in Indian subcontinent and Sr31 virulences (Ug99). Besides this, FLW31 and FLW33 also provide complete resistance against all the brown rust pathotypes in India as they carry Lr24/Sr24. Seed of these genetic stocks has been multiplied in the 2015-16 for registration with NBPGR

Keywords: Pre-breeding, Wheat, rust resistance, Ug99, Puccinia

690 (P-230)

Evaluation of USDA Core Set of Safflower (*Carthamus tinctorius* L.) Germplasm for Identification of Trait Specific Accessions

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Genetic resources form the basic components for enhancing important traits in crop improvement. For optimal utilization of germplasm, suitable characterisation and evaluation for target traits is essential. Augmentation of diverse trait specific germplasm into the Indian safflower breeding programme was undertaken through import of safflower core set developed at USDA-ARS, WRPIS, Pullman, USA during 2012 through NBPGR, New Delhi, India. The core set comprising 207 germplasm accessions from 51 countries was assigned the national identity EC 739346 to EC 739552. The accessions were raised in *rabi* 2012-13 at IIOR, Hyderabad for seed multiplication; prior to flower initiation, the plants were covered with white nylon nets to prevent the entry of bees/pollinators and facilitate self pollination. Observations for nine agro morphological descriptors were recorded and accessions with unique morphological traits were identified through scoring. Of these, a set of 22 accessions were evaluated along with national check (A-1) during 2013-14. Two accessions (EC 739535 and EC 739537) recorded seed yield on par to the check and seven accessions with more number of capitula (>30) were identified. EC 739547, 739531 and 739541 (40-42%) were confirmed as high oil sources out of the seven accessions evaluated. Non spiny accessions with orange-red corolla (8) were selected for suitability for petal harvest and their fatty acid profiling was done. Variability was recorded for lauric, myristic, palmitic, stearic, oleic, linoleic, linolenic and arachidic acid. Unique accessions possessing no rosette period (EC 739358) and more bract number (EC 739435) were identified. Donors for important traits like seed yield, oil content, petal colour and quality were identified for utilization in breeding programmes.

Keywords: Safflower, Trait specific accessions, USDA core evaluation

692 (P-231)

Evaluation of Sesame (*Sesamum indicum* L.) Genotypes for Identification of Trait Specific Accessions for Biochemical Constituents

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Sesame is the oldest oilseed crop grown in India. Archaeological records indicate that it has been known and used in India for more than 5000 years. India ranks first in world with 17.06 lakh ha area and 6.8 lakh tonnes production. It has major area in the states of Rajasthan, Uttar Pradesh, Madhya Pradesh and Gujarat. The oil is used for cooking, and has medicinal value. The seeds are rich in protein and are used in confectionary. The crop is traditionally important in India as sesame seeds are used in many rituals. To identify germplasm sources for improvement of biochemical constituents, evaluation of forty genotypes including released varieties, land races, breeding lines and genetic stock/germplasm was undertaken during 2014-15. Gas Chromatograph was used to identify and quantify the fatty acids. Nuclear Magnetic Resonance spectroscopy was used to estimate oil content and protein content was estimated by the Lowry method. Wide variability was recorded for oil content, fatty acid profile and protein content among genotypes. Oil content ranged from 32.6-58.2%. IC-204090 (land race from Andhra Pradesh) and RJS-123 (breeding line) recorded higher values of oil content (>56%). The seed is rich in protein and it varied from 17.2 (EC-303419) to 22.48 (NIC-7935). Oleic and linoleic acids were the main fatty acids of sesame and constituted 41.89 and 43.34% of total fatty acids, respectively. Identified trait specific genotypes can further be utilized in breeding programmes.

Keywords: Fatty acid, Germplasm, Oil, Sesame

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707 (P-232)

Rice Germplasm Accessions Resistant to Rice Planthoppers *Nilaparvata Lugens* and *Sogatella Furcifera*

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Rice planthoppers, brown planthopper (BPH) *Nilaparvata lugens* and whitebacked planthopper (WBPH) *Sogatella furcifera* are the most important sucking insect pests. They suck the sap from the phloem resulting in wilting and drying up of the plant, a condition called hopper burn in the field and cause 100% yield loss, also transmit important viral diseases like grassy stunt and ragged stunt. Throughout the world, planthopper problem is increasing in recent years due to the changing climatic conditions. Host plant resistance is the most important means of managing the planthoppers. Identification of resistant entries/donors is the prerequisite for this. 4372 germplasm accessions were evaluated for their reaction to planthoppers. The accessions were mass screened in the IIRR greenhouse by following standard seedbox screening technique (SSST) and scored by following Standard Evaluation System (2002) on 0-9 scale. Mechanisms/components of resistance in the identified accessions were studied which include days to wilting, nymphal survival, nymphal duration, sex ratio, orientation of insects and feeding by way of honeydew excretion and probing marks. Out of the 4372 germplasm accessions, 2 were highly resistant, 62 were resistant and 137 were moderately resistant to BPH; 39 accessions were resistant and 247 accessions were moderately resistant to WBPH. In the resistant accessions days to wilting was more, feeding was low, probing marks were more, nymphal survival was not affected and % egg hatching was low. The above identified germplasm accessions can be used as new donors in the breeding programme to develop planthopper resistant varieties.

Keywords: Host plant resistance, *Nilaparvata lugens,* Rice planthoppers, *Sogatella furcifera,*

750 (P-233)

Non Destructive Quality Evaluation of Brinjal Germplasm using NIRS Prediction Model

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Despite the importance of production and trade of food and vegetables, there is relatively scant information available on the rapid and non- destructive measurement of quality parameters. Near Infrared Reflectance Spectroscopy (NIRS) is a multi-trait quantitative estimation technique with ready-to-use calibrations. Therefore, an experiment was conducted to simultaneously measure various quality parameters of fresh eggplant using NIRS. For the first time, NIRS 6500 model is used to develop the calibration model for eggplant fruits using fruit disc matching the size of cuvette. Transverse sections of fresh fruit samples were scanned (400nm -2500nm) and thereafter immediately processed for estimation of moisture, ash, protein, phenol, total soluble sugar, iron, copper, zinc and magnesium as per AOAC approved methods. To develop prediction model WINISI II chemometric software was used for 2, 3 & 4th derivative treatment of spectra, PCA and modified partial least squares (MPLS) regression analysis. The prediction and lab analysis values were within the ranges which, for each parameter are as protein (0.88-2.02%), sugar (0.88-3.85), phenol (0.008-0.214), ash (0.397-1.005), moisture (88.56-93.97%), iron (2.29-14.607), Mg (93.67-158.5), Cu (0.050-3.706) and Zinc (0.786-4.112). Calibration equation demonstrated close relationship between NIRS and laboratory data as evident from significant positive correlation of more than 0.9 for each parameter viz. protein (r2=0.9636), sugar (r2=9656), phenols (r2=0.9859), ash (r2=0.928), moisture (r2=0.9865), iron (r2=0.9373), magnesium (r2=0.844), copper (r2=0.9675) and zinc (r2=0.9832). Based on low SECV (Standard Errors of Cross Validation) and high r2 (coefficient of determination in calibration) it is confirmed that prediction model is giving prediction in close.

Keywords: Brinjal, NIRS, Quality

755 (P-234)

Potential Growth and Yield in the Selected Brazilian Wild *Hevea* Germplasm in India

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The para rubber tree (*Hevea brasiliensis*) is native to the Amazon rainforests of Brazil, is a strategic industrial crop domesticated in the Southeast Asian countries. Twenty-two potential wild *Hevea* accessions along with three modern clones *viz*. RRII 105, RRIM 600 and RRII 208 were evaluated in the seventh to eleventh years of growth in the traditional rubber growing region of Kerala, India. Highly significant clonal differences were observed for yield and growth traits, except bole height. AC 2629 had the highest yield of 29.37 g/t/t followed by AC 716 (24.87 g/t/t) and AC 4149 (23.59 g/t/t) respectively. AC 2629 also had the highest girth, girth increment per year over 4 years and bole volume. The girth in the seventh year ranged from 26.85 cm (RO287) to 47.75 cm (RO 2629); girth increment from 3.59 (RO3804) to 6.36 cm (RO 2629); branching height from 2.19 m (RO 3804) to 3.07 m (MT2233); wood quantity from 0.03 m^3 (RO 3804) to 0.10 m^3 (RO 2629). PCV was higher than the GCV for all the characters and the highest PCV was recorded for mean yield over 2 years. Heritability and genetic advance are also high for mean yield. Girth was significantly correlated with girth increment and wood quantity. RO2629, MT2233, AC4149 and AC626 ranked top with the maximum number of desirable traits. Having a completely different genetic background from the traditional Wickham clones, these accessions will serve to broaden the genetic base of present-day cultivated *Hevea* by introgression into the elite cultivars.

Keywords: Correlations, Genetic variability, *Hevea brasiliensis*, Rank, Wild germplasm.

764 (P-235)

Embryo Rescue of *Solanum lycopersicum* × *S.* N*eorickii* Tomato Cross for Early Blight Resistance

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The tomato wild genotype EC-786252 (*Solanum neorickkii*) shows strong resistance to early blight caused by *Alternaria solani*. To study genetics of the resistance and to transfer the resistance to cultivated tomato crosses were made between the resistance genotype and highly susceptible genotype, Hawaii 3998. The crosses yielded no viable seeds. In the next season, pollen from EC-786252 was used to pollinate the susceptible cultivar and proembryos were collected from developing fruits of 39-49 days after pollination. Rescue of immature embryos was done on MS-medium. Pro-embryos from fruits of 42 - 44 days after pollination gave good response and ten plants were regenerated. Hybridity of the regenerated plants was confirmed with co dominant cleaved amplified polymorphic sequences (CAPS) marker. Currently, two stocks of clonal copies of all ten regenerated plants are being maintained in vitro. In the next season, the plants can be selfed and back crossed to obtain segregating generations for the study of genetics of the early blight resistance.

Keywords: *In vitro*, Resistance, Early blight, Inter specific hybrids, Co dominant marker

784 (P-236)

Assessment of Diversity and Morphophysiological Characterization of Traditional Aromatic Rice of Assam, India

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Rice (*Oryza sativa* L.) is the staple food of more than three billion people in the world. The climatic and physiographic features of Assam, India is favorable for rice cultivation and the crop is grown in a wide range of agro-ecological situations. Scented or aromatic rice, a unique class of rice grown as winter rice in Assam is very popular and highly valued due to its quality, palatability and popularly known as *'Joha'* rice. The *Joha* (non-basmati aromatic rice) rice cultivars are known for its unique aroma, superfine kernel, good cooking qualities and excellent palatability. The agricultural productivity of *Joha* is the lowest with the demand for the production and the gap is increasing over time. Thus extensive exploration and collection of *Joha* rice were undertaken during 2015-2016 thoroughly in Assam. A total of 22 traditional *Joha* germplasm were collected with detailed passport information and submitted to NBPGR. A number of quantitative morphological characters such as grain length, width and length/width ratio analysis were carried which showed very significant results. The length and width of seeds were ranges from 0.51 cm (*kunkuni joha*) - 0.88 cm (*keteki joha*) and 0.15 cm (*kunkuni joha*) - 0.27 cm (*kola kunkuni joha*) respectively. In all the experiments, *Basmati 370* was used as control. Germination index (GI) ranges from 5.2 (*kunkuni joha*) - 66.32 (*keteki joha*). Shoot and root length of 15 days old plants were found to be 13.34 cm (*nepali joha*) - 24.65 cm (*joha bora*). Shoot fresh weight ranges from 0.035 g (*kala jeera*) - 0.11 g (*joha bora*), whereas *basmati* showed 0.18 g. Shoot dry weight was found as 0.006 g in *kala jeera* and 0.01g *kola kunkuni joha* followed by in *basmati,* it was 0.03g. Root fresh weight revealed 0.01 - 0.05g in *gobinda tulsi joha* and the control showed 0.6 g. Root dry weight was measured as 0.001 g in *guti joha* and *nepali joha*, 0.17g in *kunkuni joha* and *basmati* showed 0.006 g only. Chlorophyll 'A' content was found as 79 - 215mg/ml in *kola kunkuni joha* and *joha bora,* whereas in *basmati* it was 206mg/ml. Again, Chlorophyll 'B' was found as 78 – 176 mg/ml in *kola kunkuni joha* and *gufur phisajwsa*, hat was significantly greater than *basmati.* In terms of aroma content, 4 germplasms showed high aroma as compared with *basmati.* Moisture content of rice flour were 5% in *kala jeera* -10% in *boga kunkuni joha* and maximum number of sample have 7-8% moisture content. From the above morphophysiological observation, it can be concluded that *Keteki joha* was found as more superior as compared with the *basmati 370.*

Keywords: Non-basmatic aromatic rice, Joha rice, Traditional rice in Assam, Morphophysiological properties

811 (P-237)

Conservation and Utilization of Gourd Vegetable Crop Diversity for Varietal Development under High Temperature and Abiotic Stresses of Hot Arid Agro-climate

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The landraces and local types / cultivars are source of genes for adaptability, stresses and quality, and therefore evaluation under a set of climatic variability is the pre-requisite for potentially utilization of genetic resources in the country. Realizing the importance of gourd vegetables in the hot arid region of north-western parts of India, the systematic germplasm collection was started at Bikaner since 1994 under mission mode of NRCAH, NATP on plant bio-diversity and institute programme of CIAH. During the last two decades, several crop specific and multi-crop explorations / trips were made for survey and collection of vegetable germplasm from parts of arid, semi-arid and tribal areas of Rajasthan and Gujarat, and also augmentation for varieties and lines was done from national net-work including NBPGR. The gourd cucurbits such as bottle gourd, ridge gourd, sponge gourd, bitter gourd, ivy gourd and spine gourd are adapted to arid areas near to the Arawalli hills and semi-arid including tribal areas exhibiting scope of crop improvement through trait specific varietal development for vegetable diversification in the Indian Thar Desert. The compilation of research work on gourd cucurbits from 1995–2010 at CIAH revealed that a total 175 accessions were collected at Bikaner and out of them 60 were deposited in NGB, NBPGR for conservation. On evaluation under extremes of arid environment, the crop germplasm exhibited wide range of variability for agro-morphological, flowering, fruit yield and quality contributing characters, besides resistance or tolerance to abiotic and biotic factors.

Keywords: Gourd vegetable, Conservation and utilization, Hot arid agro-climate

817 (P-238)

Identification of Sources of Resistance to Eggplant Fruit and Shoot Borer

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Eggplant is recognized as a popular vegetable in India and other parts of world. Among various insect pests that attack, eggplant fruit and shoot borer (EFSB), *Leucinodes orbonalis* is most destructive causing 90% yield losses. Around 25 to 80 sprays are undertaken for control of this pest. To protect environment from adverse effects of pesticides, use of host plant resistance is environmentally safe technique. Field experiments were carried out during rainy seasons of 2012 and 2013 at Experimental Farm, Pusa Campus, New Delhi in ABD. A total of 181 accessions of eggplant core set with 5 checks were screened for resistance to EFSB. Out of 181 accessions, 43 accessions were found promising based on the per cent infestation on number and weight basis. These promising accessions were screened during rainy season of 2014 in RBD with 3 replications. Out of 43 accessions, 22 accessions were found resistant to EFSB. These accessions were again evaluated during rainy season of 2015 with three replications at two locations *viz*., Experimental Farm, Pusa Campus, New Delhi and Issapur Experimental Farm. Results indicated the infestation level ranged from 9.58 to 55% on number basis and 5.87 to 68.44% on weight basis. Out of 22 accessions, 4 accessions such as EC305048, EC384970, IC111415 and IC111439, were found resistant as the infestation level was less than 10% both on number and weight basis compared to check Pusa Bindu (55%). These accessions could be used in breeding programme for developing resistant cultivars to eggplant fruit and shoot borer.

Keywords: Eggplant, Screening, Fruit and shoot borer, Resistance

820 (P-239)

Assesment of Germplasm Accessions for Qualitative and Quantitative Traits in Rice (*Oryza Sativa* L.)

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The major objective of characterization is to establish the distinctiveness among the germplasm for their qualitative and quantitative traits prescribed by DUS guidelines. The 3136 accessions including six checks were studied in present investigation. The qualitative distinctiveness present among the accession, viz. Leaf sheath colour (purple line - IC 252133, light purple - IC 252244 and purple - IC 252259), ligule shape (acute - IC 376568, and split - IC 300838), stigma colour (yellow - IC 252125, and purple - IC 252067), seed coat colour (light brown - IC 300314, brown - IC 299482 and red kernel colour -. IC 252246) and hull colour (golden - IC 299798, purple - IC 252116, purple furrow on straw - IC 299474 brown (towny) - IC 252302 and black - IC 377401) etc. Among the quantitative traits viz. grain yield per plant (g.), panicle length (cm.), and hundred seed weight (g.) etc. on the basis of their mean performance of grain yield/plant. The accessions viz. IC 252201, IC 252225, IC 252050, IC 252280, IC 252226, IC 377050, IC 252206, IC 252207, IC 252048 and IC 252179 were identified and superior from all checks in grain yield and its important traits and these accessions can be utilized for crop improvement programme.

Keywords: Germplasm, Qualitative traits, Quantitative traits and Variability

835 (P-240)

Phenological Diversity in Exotic Vegetable Fababean Germplasm

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Fababean (*Vicia faba*) an important legume is considered as a cheap source of protein and consumed as pulse and vegetables. Information on diversity available in vegetable fababean germplasm is lacking and consequently affecting the sustainable use. Sixty one accessions of exotic vegetable fababean alongwith check cv. Pusa Sumeet were studied for assessing the genetic diversity pattern during winter season for four years (2011-13, 2014-16) at NBPGR, New Delhi using 26 phenological characters (18 qualitative and 8 quantitative). The pooled analysis revealed significant differences among the accessions for all the eight phenological quantitative characters *viz* plant height, number of branches, days to 50% flowering, pod length and width, 5 fruit weight, number of fruits/ plant and fruit weight/plant. Wide range of variability for all the quantitative characters was observed. Higher co-efficient of variation (>20%) was observed in number of fruits per plant and fruit weight per plant. The Shannon diversity index showed higher diversity (≥0.40) for three qualitative and all the eight quantitative characters. The Ward's Minimum Variance Dendrogram showed 4 clusters consisting of 25, 31, 5 and 1 accession. The principal component analysis explained 84% cumulative variation by four informative principal components. PC1 and PC2 together explained ~57% variation with greater weightage on pod length, pod width, 5 fruit weight, number of fruits/plant and days to 50% flowering, respectively. The PCA biplot showed that majority of the accessions were tightly grouped and two out of four groups were distinct. The accessions from different groups will be more useful in crop improvement.

Keywords: Diversity, faba bean, vegetable

836 (P-241)

Cytomorphological and Molecular Characterization of Interspecific Hybrids between *Helianthus annuus* and *Helianthus argophyllus* T. & G.

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Successful interspecific hybrids were obtained through sexual hybridization between cultivated *Helianthus annuus* (ARM-243B; 2n=34) and a wild *Helianthus* species [*H. argophyllus;* 2n=34*;* PI-468649], using the later as pollen parent for transferring desirable traits like downy mildew resistance, oil content and hopper resistant from wild species into cultivated background. Morphological, cytological and simple sequence repeats (SSR) based molecular analyses were carried out to confirm the hybrid nature of F_1 plants. The hybrids exhibited morphological features intermediate to both the parents for few attributes and more related to wild *Helianthus* species like, leaf and stem hairiness, flower colour, stem size, branching, disc floret pigmentation, plant height, seed size and seed shape, etc. A reduction (89.9%) in pollen fertility was recorded in F_1 plants as compared to both the parents. Meiotic analysis revealed a mixture of univalents, bivalents, trivalents and quadrivalents in all the pollen mother cells (PMCs) analysed. In addition to bivalents and univalents, a trivalent was also observed in few PMCs, indicating segmental homology between chromosomes. Higher level of chromosome configurations like quadrivalents was also observed in 42 out of 50 PMCs. Frequently observed chromosome configurations in diakinensis were 15 II + 1 IV and 13 II + 2 IV. The results suggested that the species *H. argophyllus* and *H. annuus* differ by 1-2 translocations and 1-2 inversions. Hybridity of interspecific hybrids was confirmed through sunflower specific molecular markers. Primers ORS-05, ORS-896 and ORS-908 were found to reveal highly polymorphic bands in the parents and were used for confirmation of hybridity of the F_1s. The informative SSR markers screened in the study will be useful marker resources for tracking the flow of *H. argophyllus* genetic material among the progenies that may be produced by future backcrosses to *H. annuus*. Results show that the classical method of crossing is applicable in sunflower breeding programs for obtaining interspecies hybrids.

Keywords: Interspecific hybridization, Meiotic study, Phenotype, Pollen viability, SSR marker, Sunflower

859 (P-242)

Genetic Diversity Analysis of Indian Soybean Cultivars using SSR Markers

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Soybean [*Glycine max* (L.) Merrill] is an economically important leguminous crop for oil, feed, and soy food products. In India, soybean has become a leading oilseed crop and more than 100 soybean cultivars have been developed and released in India for commercial cultivation. The degree of genetic variability available for selection can play an important role in overcoming yield barriers. Therefore, the current study was carried out to study the genetic diversity of Indian soybean cultivars using SSR markers. A total of 45 SSR markers were screened on 90 soybean cultivars and total 232 alleles were generated with an average of 5 alleles/locus. The number of alleles ranged from 2 to 10 and polymorphic information content (PIC) of the SSR markers ranged from a minimum of 0.10 to a maximum of 0.83 with an average of 0.61. Cluster analysis based on SSR genotypic data grouped the 90 soybean cultivars into six major clusters and most of the genotypes showed grouping based on their pedigree. Cluster I had 8 genotypes and Cluster II contained 30 genotypes. Cluster III was the largest group and contained 41 genotypes. Cluster IV had 6 genotypes, and cluster V and cluster VI carried two genotypes each. Soybean cultivars Gujarat Soya-2, Hardee, Improved Pelican, LSb-1, and MACS-13 were found quite distinct from other soybean cultivars. The study showed that Indian soybean cultivars had good genetic diversity and result would be useful in the selection of genetically diverse parents in soybean breeding program.

Keywords: Soybean, SSR, Genetic diversity

885 (P-243)

Morphological and Biochemical Characterization of Potato (*Solanum Tuberosum* L.) Germplasm in *Terai* Region of Uttarakhand

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Potato (*Solanum tuberosum* L.) is one of the most important non-grain food crops of the world but productivity in India is quite low that stands at ~ 22 metric tons per hectare as compared to the European countries that ranges between 30-40 tons per hectare. Potato production in *Terai* region of Uttarakhand is lower than other potato growing belts, because of the low yield. This fluctuation is may be due to narrow genetic base of the germplasm used for development of cultivars. Therefore, considering the above facts potato germplasm was evaluated at G.B.P.U.A&T, Uttarakhand. The experiment material consisted of 28 genotypes and 4 checks grown in Augmented Block Design. The results revealed Block effects were highly significant for plant height, number of leaf per plant, tuber size, number of tuber per plant, tuber weight per plant, dry matter, ascorbic acid, TSS and tuber yield. Correlation studies indicated that tuber yield was highly significant and positive correlation with average weight of tuber (0.966), tuber weight per plant (0.650), leaf length (0.484). These may be key criteria for selecting high tuber yield lines. Path coefficient analysis revealed that average weight of tuber showed positive direct effect (0.854) towards tuber yield followed by tuber weight per plant (0.463), number of tuber per plant (0.348) however, protein (-0.577) showed negative effect. Genotypes 97-P-27 (464.52 q/ha), TPSK-05-06-007 (454.97 q/ha), J/96-48 (454.04 q/ha) were promising for yield and can be utilized to develop varieties or may utilize in hybridization for crop improvement.

Keywords: Correlations, Path coefficient analysis, Potato, Tuber yield.

925 (P-244)

Screening of Advanced Lines of Long Slender and Medium Slender Rice Against Major Diseases of Rice Under Natural Conditions and their Yield Performance

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In Chhattisgarh, rice occupies average of 3.6 million ha. with the productivity of the state ranging between 1.2 to 1.6 t/ha depending upon the rainfall. The prominent advanced long slender and medium slender lines were screened under natural conditions against major diseases of rice. Sixty eight long slender and medium slender advanced rice genotypes along with eleven checks namely Indira Sugandhit Dhan 1, Pusa basmati-1, IR 64, Chandrahasini, Indira Sona, Badsha Bhog, Chinnor, Mahisugandha, Dubraj, Shamjeera and Vishnu bhog were evaluated in field condition for yield and major diseases of rice prominent at Chhattisgarh during kharif 2014. Entries AS 996-HR 1, R 1656-1936-1-1-800-1, R 1656-2821-1-3245-1 and R 1629-234-6-1883-1 had exhibited moderately resistant reaction (score -5) against BLB whereas rest of the varieties showed susceptible to highly susceptible reactions for the disease. Under natural conditions, None of the genotype showed highly resistant reaction against sheath rot. Whereas, genotypes R 1656-1936-1-1-800-1, PR 26703-3B-PT25, R 1679-1860-1-783-1 and RSR 2011-12-1 were found for resistant reactions (score -3) for sheath rot disease. Three genotypes namely, R 1656-3173-1-415-1, R 1545-184-3-22-1 and RRF 75 were showed highly resistant reaction for sheath blight. Hybrid check Indira Sona (6385 kg/ha.) was highest yielder followed by IR 84887-B-15 (5847 kg/ha.), R 1700-308-3-170-1 (5653 kg/ha.), IR 83376 B-B 110-3 (5484 kg/ha.) and R 1917-951-1-541-1 (5483 kg/ha.). all top five yielder entries were susceptible againt BLB, Sheath rot and Sheath blight diseases except entries R 1700-308-3-170-1 and R 1917-951-1-541-1, which was resistant against sheath blight.

Keywords: Screening, Rice and Major diseases

939 (P-245)

Genetic Enhancement for Rust Resistance by Pyramiding *Lr19* and *Yr15* in Wheat (*Triticum aestivum* L.) Variety HS240

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HS240, a popular wheat variety in Northern hills zone of India, became susceptible to leaf and stripe rusts during the preceding years. The study was aimed to enhance genetic resistance to leaf and stripe rusts in wheat variety HS240 by pyramiding rust resistance genes from donor stocks *viz*., FLW20 with *Lr19* and FLW13 with *Yr15*. Validation of SCAR marker SCS265$_{512}$ for *Lr19* and Xbarc8 for *Yr15* was done in advanced bulks of a double cross HS240*2/FLW20//HS240*2/FLW13. The SCAR marker SCS265$_{512}$ showed the presence of *Lr19* in all the advanced bulks. Similarly, microsatellite marker Xbarc8 gave typical band (221bp) in Avst-*Yr15*, FLW13 and same base-pair band was seen in all the advanced bulks of double cross confirming the presence of *Yr15* gene. The genetic stock FLW20 and advanced bulks were recorded resistant to most virulent leaf rust pathotype 77-5 whereas, HS240 was susceptible. Similarly, the genetic stocks, FLW13 and Avst-*Yr15* and advanced bulks were recorded resistant against virulent pathotypes of stripe rust. The data revealed consistency between seedling resistance test and molecular marker assisted validation for *Lr19* and *Yr15* in advanced bulks. Fixed gene populations carrying *Lr19* and *Yr15* are being evaluated under preliminary yield trial for grain yield and its associated traits. The rust resistance genes fixed in good agronomic background of wheat and their use in rust resistance breeding programme would prove an effective strategy to develop potential leaf and stripe rust resistant genotypes.

Keywords: *Lr19,* Rust resistance*,* Wheat, *Yr15*

960 (P-246)

Development of Superior Hybrids through Conventional and Non Conventional Breeding Approaches in Apple (*Malus Domestica* Borkh)

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Central Institute of Temperate Horticulture, Srinagar is having the largest field gene bank of temperate fruit crops in India representing about 253 indigenous and exotic cultivars of apple. Apple cultivars commercially grown in India have good color and taste but less shelf life and aroma. Also most of the commercially grown cultivars are susceptible to scab. Apple cultivars used for pollination like Golden Delicious have less acceptability in market due to poor fruit quality. Breeding programme for development of superior varieties in apple was initiated in 2009 at Central Institute of Temperate Horticulture with the main aim of transferring the traits like disease resistance, regular bearing, higher shelf life, earliness, fruit quality, pollinizer ability etc into commercially acceptable apple cultivars. Trait speific varieties in apple (Firdous, Mayan, Mollies Delicious, Red Spur, Starkrimson, Golden Delicious, Granny Smith etc) were used as source for trait transfer to the elite cultivars like Winter Commercial, Top Red, Gold Spur, Well Spur, Oregon Spur, Cooper IV, Red Delicious etc. A total of 250 crosses were made out of which 220 crosses showed fruit set. Eighty hybrids have been established in the field successfully from which fifty hybrids were top worked on M-9 clonal root stock to obtain early fruiting for further evaluation. Superior hybrids have been identified for different traits which are being multiplied on large scale for further evaluation and commercialization. Molecular markers specific to traits like scab resistance, S-allele typing etc have been used for screening of hybrids.

Keywords: Apple, Ambri, Hybridization, Shelf life, Aroma

976 (P-247)

Wheat Pre Breeding Germplasm Evaluation for Resistance to Yellow Rust and Leaf Blight Pathogen

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Genbanks are the repository of useful gene(s) and allele(s) conferring stress tolerance, yield and quality. The thrust of useful or trait based genetic diversity is increasingly important for the global wheat community as the yield potential is approaching a plateau. Infusion of trait based diversity from GeneBanks through a pre breeding approach will provide impetus to wheat varietal improvement in India. Experiments were conducted at ICAR-Indian Agricultural Research Institute, New Delhi, India to evaluate one thousand and twenty eight advanced wheat pre breeding germplasm set derived from International Maize and Wheat Improvement Center (CIMMYT)'s GeneBank lines. These accessions were evaluated for yellow rust and leaf blight diseases to identify new sources of resistance. Preliminary results provided encouraging information. Sources for resistance to the above said diseases were identified and since lines were in adapted background, their mobilization to breeding pipelines should be a fast track process. Another round of evaluation of the newly identified sources will be performed in coming wheat growing season. Genotypes showing resistance consistently will be used in developing next generation wheat variety for the disease prone wheat environments. Further a genome-wide association will be carried out using genotyping-by-sequencing data of these germplasm sets (GBS being carried out at CIMMYT, Mexico). Trait donors have been identified and identification of allele donors is underway. The trait and allele donors will help wheat breeders significantly in enhancing yields under disease prone environments.

Keywords: Pre breeding, Wheat, Germplasm, Yellow rust, Leaf blight, Resistance

978 (P-248)

Identification of Superior Linseed (*Linum usitatissimum L.*) Genotypes Based on their Mean Performance and Disease Reaction for Future Success

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Linseed (*Linum usitatissimum L.*) is among the most important oilseed crop because it's numerous uses. It contains about 36 to 48% oil which is high in unsaturated fatty acids, especially linolenic acid (ALA), omega -3-fatty acid (Khan et al. 2010). Variability of the genotypes is paramount importance for selection in any breeding program. This study is carried out about, mean performance of 34 genotypes of Linseed (*Linum usitatissimum L.*) including three checks (Nagarkot, Him Alsi-2 and Binwa) were evaluated in Randomized Block Design during *rabi* 2012-13 at the Experimental farm of linseed, Department of Crop Improvement CSKHPKV, Palampur. Data on sixteen various morphometric traits were recorded. Reactions to wilt disease were also recorded under natural epiphytotic conditions. Perusal of results revealed that, out of 34 genotypes used for study genotypes (KL-220) were found to be superior for most of the traits including days to maturity, Primary branches per plant, secondary branches per plant and capsules per plant. On the basis of disease reaction, 28 genotypes were found to be highly resistance/resistant to wilt, which needs further evaluation under artificial conditions for their use as source of resistance in the future breeding programmes. Hence, the genotype can further be utilized for future breeding programmes and it was found that among all the genotypes studied, genotype KL-220 was to be superior for most of the traits as well as resistant to wilt *(Fusarium oxysporum f.sp. lini)* disease

Keywords: *Linum usitatissimum L.* , Mean performance, Wilt

981 (P-249)

Identification of Potato Germplasm with Combined Resistance to Late Blight, PVY and PCN through Molecular Markers

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Potato is the most versatile food crop which can grow under temperate, tropical as well as subtropical climatic conditions. The food production efficiency of potato is 2.8 and 1.9 times higher than rice and wheat, respectively. Potato crop is subjected to a wide range of pathogens, among which viruses (PVY, PLRV, and PVX), fungi (Phytopthora infestans) and Potato Cyst Nemtodes (Globodera spp.) have devastating effects on potato yields. The recent breeding strategy across the globe involves introgression of major resistance genes or major QTL's using molecular markers along with superior agronomic traits. Pyramiding multiple genes in single genotypic background can increase the number of resistance factors to breakdown, the greater the number of virulence mutations required in the pathogen genome and the less likely their incidence in the host plant. Keeping this in view, the study was initiated to characterize a set of 150 exotic germplasm collection for imparting monogenic resistance to late blight (R1, R2, R3a & R3b), PVY (RYadg, and RYsto) and Potato Cyst Nematodes (H1 HC_QTL) using PCR based molecular markers. Out of 150 genotypes, R1 was present in 16 genotypes, 49 genotypes possessed R3a and R3b genes, 13 genotypes possessed R2 gene conferring resistance to late blight. While 18 genotypes possessed HI and HC_QTL genes providing resistance to PCN. Four genotypes possessed RYadg and RY sto genes against PVY. Six genotypes were identified with multiple resistance genes. The promising genotypes thus identified can be exploited as elite parental lines for breeding multiple disease resistant potato.

Keywords: Genotypes, R-genes, Molecular markers

985 (P-250)

Utilization of Genetic Resources of Important Indigenous Medicinal Plants of India

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Most of the plant species used in the Indian system of medicine are indigenous in nature and collected from the wild. Kalmegh (Andrographis paniculata (Burm. F) Nees) is one of the important medicinal herb commonly known as "King of Bitters" has antipyretic and hepato protective properties and used in the Indian system of medicine. The plant is widely distributed in Himalyan Foot hills, Indo-gangetic plains and sub humid tropics of peninsular India. Indian Giloe (Tinospora cordifolia (Willd.) Miers.) is a deciduous, climber shrub found in waste lands, gardens and deciduous forests throughout India. Besides, immune modulator properties, it is used in treatment of jaundice, fever and liver malfunctions. Forty two accessions of Andrographis paniculata and 25 accessions of Tinospora cordifolia augmented from different sources were characterized and evaluated for agro-morphological, molecular and quality parameters and value rich accessions were identified. In Andrographis paniculata, the variability was observed at agro-morphological and molecular level and two value rich accessions, namely, IC 342135 (3.14%) and IC471913 (2.94%) were identified for andrographolide content. In Tinospora cordifolia, two value rich accessions, namely, IC 281972 and IC 281963 were identified for bitter content. Considering SSR's wide application, transcriptome of Tinospora and Andrographis was done and TcMDB (Tinospora cordifolia Microsatellite Database) and ApMDB (Andrographis paniculata Microsatellite Database) have been developed. Also using microsatellite enrich genomic library, 90 genomic SSR sequences for Tinospora cordifolia submitted with NCBI (Accession: KT384079- KT384168; August, 2015). The SSR markers developed is an important genomic resource for utilization in crop improvement.

Keywords: Accession, Medicinal plants, SSR, Utilization

990 (P-251)

Post Flowering Stalk Rot Resistance Germplasm from North-Eastern Region of India for Sustainable Maize Production

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Diversity of maize is majestic in the North-Eastern Himalayan region, specifically in Sikkim, where maize based cropping system is predominant, but the yield is very low. Germplasm of purple and yellow maize from this area were collected and evaluated continuously up to S5-S6 generations against post flowering stalk of maize. Response of total phenolic compound (TPC), total flavonoid acids (TFA), and total soluble sugar (TSS) in maize plant in different stages against fungi Fusarium verticilloides and Macrophomina phaseolina, causal agent of Post flowering stalk rot was investigated. Germplasm exhibited significant variation viz., TPC ranged from 65.1 to 189.27; TFC from 8.93 to 69.60 and TSS from 9.71to 66.02 mg/100g dry weight. Overall, highest amount of TPC-189.27; TSS-82.71 and TFA-46.29 mg/100g dry weight was estimated in genotypes viz., Mixture purple-; Mixture purple-2; Mixture purple-4 obtained from North East and PFSR (Y)-C1-B-Ã„-1-1-1 lines derived from pools at maturity (cob formation) when inoculated with M. phaseolina and F. verticilloides respectively. It is evident from the data that there is more than 4 fold increase in total phenol content in diseased (inoculated) plants in genotypes obtained from North East as compared to healthy plants. Varied response of these genotypes for phenolic compounds was observed as a defence mechanism when challenged with stalk rot pathogens. However in susceptible check minimum increase of these compounds as compared to other genotypes was observed. This increase in diseased plant shows elicitation of biochemical defence by host tissue.

Keywords: Maize, Post flowering stalk rot, Macrophomina phaseolina, Fusarium verticilloides

1015 (P-252)

Screening and Identification of Maize Inbreds Resistant to Stem Borers

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In India, maize is the third most important crop and accounts for nine percent of total food grain production. It is attacked by more than 140 pests and stem borers are of prime important as they cause yield loss of 24-75 per cent. The recent reports indicated that climate change has led to increasingly displacement of other stem borer species in maize with Chilo partellus but the control of this pest through insecticides and biological control agents is very difficult. Hence, host plant resistance forms an important part of integrated pest management without environmental issues and compatibility with other pest management approaches. The availability of donor sources for resistance to this pest are very rare and there is a need to identify genotypes resistant to stem borer. Thus, the present study was conducted with forty maize inbreds collected from different genetic back grounds against stem borers resistance during rabi 2015-16 at Agricultural College, Bapatla in natural conditions without plant protection measures in a randomized block design with two replications. Significant difference was found for stem borer resistance in terms of leaf injury rating, percentage of infested plants and percentage of dead hearts. The genotypes, BM-53, BM-131, BM-127, BM-260-2, BM-198 and K-14 (1812), recorded highly of resistant reaction and DHK-14 (7216), DHK-14 (7171), DHK-14 (7025), HKI-163, DHK-14 (7175) and DHK-14 (7018) showed high levels of leaf injury rating, infested plants and dead hearts. The present study identified resistant genotypes for exploitation in maize breeding programmes as donors for stem borer resistance.

Keywords: Maize, Screening, Stem borers

1046 (P-253)

Combining Ability Studies for Yield and Water Use Efficiency Related Traits in Groundnut (*Arachis hypogaea* L.)

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In the present context of climate change, it is very difficult to expect higher crop yield. Development of climate change resilient varieties especially high water use efficient genotypes which can tolerate drought situation is much needed. In order to develop high yielding and high water use efficient genotypes, information on the combining ability of diverse parents and gene action is required. Hence, eight high water use efficient lines were hybridized with four high yielding testers in Line × Tester fashion to produce 32 F_1's. The variances due to SCA were found to be higher than GCA variances for all the eleven characters studied indicating the predominance of non-additive gene action in the inheritance of these characters. Three lines GKVK 16, GKVK 8B and GKVK 5 and the tester KCG 2 were appears to be good general combiners to produce high water use efficient and high yielding genotypes as these have shown significant gca effects in the desirable direction for SPAD Chlorophyll Meter Reading (SCMR), Specific Leaf Area (SLA), pod and kernel yield. However, lines GKVK 16, GKVK 5 and GKVK 8B were best combiners for most of the characters studied and among testers KCG 2 was the best combiner. The crosses *viz*., GKVK 16 × ICGV 91114, GKVK 6 × KCG 2, GKVK 8B × GPBD4 and GKVK 16 × KCG 2 were recognized as best cross combinations for most of the traits studied and these crosses were further forwarded to generate high yielding and high water use efficient genotypes.

Keywords: Combining ability, SCMR, SLA

1052 (P-254)

In Vitro Mutagenesis in Finger Millet (*Eleusine coracana L.*) for Blast (*Pyricularia grisea*) Tolerance

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For creating Agrobiodiversity, the present investigation was carried out for raising blast (*Pyricularia grisea*) tolerant plants of finger millet VAR. GN4 (*Eleusine coracana L.*) employing in vitro mutagenesis.The concentration of 10% CF was optimized with callus regeneration (49.50%) for determination of 50% survival plants. For in vitro induced mutagenesis, lethal dose (LD50) of 0.2% EMS for 0.5 h was determined for regeneration of calli (50.20%). The three tolerant lines were obtained from calli treated with 0.2% EMS for 0.5h duration and under pressure with 10% CF in regeneration MS medium supplemented with 1.0 mg/l BAP and 1.0 mg/l kinetin. Among these tolerant mutant plants, mutant plant (V1) was observed resistant (R), while two mutant plants (V2 and V3) were reported moderately resistant (MR) against blast disease. Molecular (RAPD and ISSR) analysis of the regenerated tolerant mutant plantlets (V1, V2 and V3) exhibited different banding pattern in plant, which confirms the presence of variations at genetic level.Overall, mutant plant (V1) observed resistant, while two mutant plants (V2 and V3) reported moderately resistant (MR) against blast disease of finger millet var. GN-4 were showed variation at biochemical and molecular level. However, alteration at genetic level was observed less in V1 mutant plant.

Keywords: Blast, Mutagenesis, Callus, Regeneration, Resistant

1069 (P-255)

Study of Correlation Coefficient between Physico-Chemical Properties of Wood From Different Provenances of *Tectona Grandis* L.

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The study was conducted on thirty selected provenances at National Teak Germplasm Bank, Lohara, Chandrapur (Maharashtra). The wood samples were collected from these selected provenances of teak and analyzed for different wood properties in the departmental laboratory of Forest Products, College of Forestry, Akola (M.S.). Observation were recorded for eleven growth and quality parameters, viz., height, diameter, grain angle, bark percentage, specific gravity, fibre length, cold and hot water soluble extractives and alcohol-benzene extractives and lignin percentage of wood and holocellulose percentage of wood. Among the correlation coefficient for all the character with 55 combination of simple correlation, five combinations had found positively significant and two were negatively but significantly correlated in teak were assessed and found that relationship between specific gravity and height (0.383), holocellulose content and height (0.392) and alcohol-benzene soluble extractives and cold water soluble extractives (0.366) were positive. Negative correlation coefficient was observed between cold water soluble extractives and diameter (0.461) and lignin content and alcohol-benzene soluble extractives (0.381). These associations among the parameters could help in establishing indirect approach for selection in teak.

Keywords: Correlation, Teak, Timber quality, Tree improvement

1085 (P-256)

Evaluation and Characterization of Genetic Diversity in *Bixa orellana* L.

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Interest on revival and use of natural edible dyes has been increasing day by day due to safe and non-toxic nature. *Bixa orellana* (Annatto) yields seed specific red pigment is called bixin (ie.*apocarotenoid*) and it is exploited around the world. The study objective is to identify superior genotype of *Bixa orellana* with high bixin content. The major annatto growing areas were surveyed and selected 34 genotypes from diverged locations of three states of India *viz*., Tamil Nadu, Kerala and Karnataka. The identified Candidate Plus Trees (CPTs) have shown significantly spectacular genetic variation and diversity and each CPTs were assessed for important fruit and seed traits. On basis of overall fruit and seed traits, the following five CPTs viz., KLBi 3, TNBi 4, KLBi 5, TNBi 12 and KABi 8 were found superior in terms high bixin content and recommended as potential genotypes/ parent's sources for developing high yield clones. PCV and GCV analysis also indicating index of genetic variation. Heritability (broad sense) and genetic advance were observed higher in 100 seed weight (99.70 %, 32.98%), seed dye content (93.82%, 29.05%) and bixin content (90.58 %, 34.32 %) respectively. Hence, this study envisaged that fruit weight, number of seeds /fruit and seed bixin content could be used as selection criteria for early selection plus trees. The plus trees of KLBi 3, TNBi 4 and KABi 8 could be utilize for developing high yielding clones for commercial cultivation, intended as parents for hybridization and genetic improvement programme of the species.

Keywords: Bixin, Edible dye, Fruit shape, Genetic Diversity, Improvement.

1092 (P-257)

Seed Color as an Index for Assessing Rapeseed Meal Quality

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Cultivated varieties of oilseed Brassica belonging to seven different taxa were scored from 1 to 5 based on seed coat color and compared with other quality parameters. Oil content and crude fiber content was estimated by FT-NIR. Total phenol and flavonoid content was estimated by spectrophotometric method. Varieties belonging to the yellow sarson group scored the lowest while the *Brassica napus* group scored highest because of their darker seed coat color. The average crude fiber content was highest in *B. juncea* (10.89 %) while lowest fiber content was in the yellow sarson group (7.47 %). There was a significant positive correlation between the seed coat color and fiber content (r= 0.61) that shows its crucial role in imparting seed coat color. Also, the seed color did not have any significant correlation with total phenols (r= -0.06) and total flavonoids (r= -0.16) even though the flavonoid compounds, proanthocyanidins are considered primarily responsible for pigmentation of seed coat. Seed coat color can thus be used as a morphological marker or index for easier identification and grading of low fiber lines of oilseed Brassica.

Keywords: Oilseed Brassica, Seed coat color, Crude fiber, Flavonoids, Phenols

1097 (P-258)

Screening of Bottle gourd Germplasm against Downy Mildew (*Pseudoperonospora cubensis)* through Artificial Inoculation

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In cucurbits, bottle gourd [(*Lagenaria siceraria* (Monila) Standl.)] is a popular vegetable widely cultivated in summer/*kharif* season across all over India, However, its cultivation is threatened by several disease particularly by Downy Mildew *(Pseudoperonospora cubensis* (Berk. & Curtis., Rostovzev). Seeing the worsen situation, it is essential to develop a consistent and reliable method to screen bottle gourd genotypes for identifying resistance source to this melody. Screening were conducted in 51 germplasm with 3 plants per germplasm as per assay and repeated two times. The plants were inoculated with a suspension of *P. cubensis (*10^4 *sporangia ml*$^{-1}$*)* at the two cotyledon stage. The adaxial and abaxial surfaces of the cotyledons were sprayed with the inoculum suspensions until incipient run-off. Later, inoculated plants were placed in the dark at 20^0 C and high humidity for 21 hours. Subsequently, they were transferred to the greenhouse under ambient conditions of $24\text{-}28^0$ C and 80-90% relative humidity. After 7 days, the disease reactions on the host plants were recorded. A set of the host plants without fungal inoculation were used as a control. Plants were rated on a scale of 0–5 in which 0 stands for immune and 5 stands for highly susceptible. Among all accession screened, No single line found immune, only one was found resistant (VRBG-12). Besides, 3 others (VRBG-26, VRBG-47, and VRBG-17) showed moderately resistant and four others were moderately susceptible to the fungus. The remaining 43 lines were range from susceptible to highly susceptible for the fungus. The most resistant and most susceptible cultigens were retested, to verify their reaction. The identification of resistant line and highly tolerant or moderately resistant bottle gourd lines in this study points at the ICAR-IIVR germplasm collections of potential materials that could be included in further disease resistant breeding programmes.

Keywords: Artificial screening, Bottle gourd, Downy mildew

1121 (P-259)

Genetic Cataloguing of Bittergourd (*Momordica Charantia* L.)

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Bittergourd (*Momordica charantia* L.) belonging to the family Cucurbitaceae, a popular vegetable in India, is having considerable nutritional, economic and medicinal importance. Being a monoecious and highly cross-pollinated crop, diverse visual variation is observed in fruit and vegetative characters. Thirty three genotypes of bittergourd collected from different agroclimatic regions of the country upon cataloguing pointed out wide biodiversity in morphological and qualitative characters e.g. vine length, 103.75 - 620.00 cm; internodal length, 1.25 to 5.58 cm; fruit length, 4.91 - 38.83 cm; fruit girth, 6.96 - 25.53 cm; fruit number, 8.75 - 34.25; average fruit weight, 4.26 - 578.75 g; β-carotene, 52.58 - 138.96 µg/100 g; Vitamin C, 62.54 - 124.29 mg/100 g; iron content, 2.38 - 6.88 mg/100 g; chlorophyll a, 0.00110 - 0.54365 mg/g; chlorophyll b, 0.00045 - 0.03075 mg/g; total chlorophyll 0.003 - 0.12 mg/g and bitterness value, 1227.50 - 10400 units/g. Leaf size varied from small to large with ovate, pedate or reniform shape. *Variability was more* pronounced for flower and fruit characters. Flower and fruit size ranged from small to very large. Fruit form showed wide variation. Skin texture was either smooth, rough or with spines. Majority of genotypes had green skin coloured fruits. Seed quantity per fruit ranged from very few to many with small to very large seed size. The rich variability among bittergourd genotypes have many value-added characters and will bring fruits in its improvement. If they are considered while breeding, no doubt bittergourd will be a promising vegetable.

Keywords: Biodiversity, Bittergourd, Cataloguing

1155 (P-260)

Evaluation and Characterization of Agro Morphological Diversity in Local Rice (*Oryza sativa* L.) Collections from Different Altitudes of Uttarakhand Hills

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Rice(*Oryza sativa* L.) is a major food crop of Uttarakhand hills, grown under rainfed upland and irrigated ecosystem in different altitudes (250-2500m asl). A huge diversity of this crop exists in this region and 201 hill rice collections from low (≤950 msl), mid (951-1500 msl) and high (≥1501 msl) hills of Uttarakhand were evaluated and characterized for 12 quantitative traits with 5 checks during *Kharif* 2015. Data analysis exhibited a considerable range of variability for phenological traits *viz.,* days to 50% flowering(71-106days), days to maturity(102-130days) as well as for other important traits *viz*., stem length(29-99cm), panicle length(12-26cm), kernel length(4.61-7.41mm), kernel width(1.58-3.13mm), LB ratio(1.13-3.87mm), plant height(48-121cm), grains/plant(24-178), flag leaf length(16-29.5cm), flag leaf width(1-1.9cm) and grain yield/plant(0.04-7.07g). As per principal component analysis, first four principal components expressed 70.61% of total variation in which PCI, PCII, PCIII and PCIV accounted for 27.48, 17.90, 16.37 and 8.85% of total variation, respectively. Highly significant positive correlation was observed between PCI with panicle length(0.46), number of grains/plant (0.46), LB ratio(0.36), grain yield/plant(0.29), flag leaf width(0.18), kernel length(0.17); PC II with plant height(0.47), stem length(0.43), Kernel length (0.37), flag leaf length (0.29), grain yield/plant (0.28), number of grains per plant (0.26), panicle length(0.21), days to maturity(0.17); PC III with kernel width(0.57), days to maturity(0.53), days to 50% flowering (0.31), flag leaf width(0.27) and PC IV with flag leaf length(0.66), days to 50% flowering(0.55) and kernel length(0.18). The plotting of first and second PCA scores confirmed the existence of variability which might have arisen due to altitudinal differences.

Keywords: Altitude, Diversity, Rice (*Oryza sativa* L.)

1190 (P-261)

Genetic Variation in Oil Palm (*Elaeis guineensis* Jacq.) Germplasm for Leaf Nutrients Concentration

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Selection of oil palm accessions of germplasm capable of maintaining required leaf nutrients concentration with high oil yield is the need of the hour. Leaf samples from 14 Cameroon, 11 Guinea Bissau, 7 Zambian and 6 Tanzanian accessions were collected from the field gene bank of ICAR- Indian Institute of Oil Palm Research, Pedavegi, Andhra Pradesh., India and analyzed for N, P, K, Ca, Mg, S and B concentration (by following standard procedures) to assess genetic variation among them. Differential response with respect to leaf nutrients concentration was recorded among and within the germplasm accessions. Among the four sources, Tanzanian and Guinea Bissau were having the highest (1.00 %) and the lowest (0.84 %) K concentration, respectively. Similarly, Tanzanian accessions were having the highest Mg (0.65 %) and B (68.55 mg kg^{-1}) concentration; whereas Zambian accession had the lowest Mg (0.54 %) and B (52.9 mg kg^{-1}) concentration. Highest variation in N, P, K, Ca, Mg, S and B concentration was recorded among CA-3, CA-5, CA-5, CA-4, CA-9, CA-12 and CA-5 accessions of Cameroon, respectively and among GB-22/311, GB-23/312, GB-10/306, GB-23/312, GB-10/306, GB-5/301 and GB-5/301 accessions of Guinea Bissau germplasm, respectively. Likewise, ZS-2, ZS-5, ZS-8, ZS-1, ZS-1, ZS-5 and ZS-1 accessions of Zambian and TS-10, TS-10, TS-4, TS-4, TS-11, TS-4 and TS-11 accessions of Tanzanian germplasm were having highest variation in N, P, K, Ca, Mg, S and B concentration respectively. These findings could play a vital role in identification and development of nutrient efficient oil palm varieties.

Keywords: Leaf nutrients concentration, NUE, Oil palm germplasm

1192 (P-262)

Evaluation of Oil Palm (*Elaeis guineensis* Jacq.) dura Germplasm for Drought Tolerance using Biochemical Markers

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Water is considered as one of the most critical inputs for realizing higher yields of oil palm, as water deficits not only leads to reduced growth but also affects plant physiology. In this context, a study consisted of two dura crosses namely 44 CD (ZS-1) X 435 CD (CA-12) and 60 CD X 62 CD (ZS-8 inter se cross) with two irrigation levels (IW/CPE) of 1.0 and 0.5 was taken up to identify dura germplasm with better drought tolerance. One hundred palms were evaluated during the study. Biochemical parameters like epicuticular wax content (EW), protein content, superoxide dismutase (SOD) activity, proline content, total sugars, lipid peroxidation (LP), chlorophyll a content, chlorophyll b content, total chlorophyll content and carotenoids (Car) content were studied. Significant variations in different biochemical parameters were observed in the palms belonging to the two crosses with two irrigation levels. Palms possessing higher SOD activity are efficient scavengers of H2O2, indicating an efficient oxidation system under water stress. Higher amounts of total sugars were observed in palms irrigated with 50 percent compared to that of palms irrigated at IW/CPE = 1.0. Under water stress, increased levels of sucrose and/or reducing sugars have most often been observed, which contributed towards the maintenance of turgor. Tolerant palms possessed higher carotenoids contents indicating its higher level of photo protection. Rankings are given to palms based on their tolerance to water stress and are given as follows “ Palms are ranked higher (tolerant to water stress), which possessed greater amounts of epicuticular wax, protein, SOD, proline, sugars, lipid peroxidation, chlorophyll a, chlorophyll b, total chlorophyll and carotenoids. The three best palms belonging to dura cross 44CD (ZS-1) x 435CD (CA-12) tolerant to water stress were palm nos. 23, 38 and 15. Palm nos. 76, 84 and 91 are the best palms of dura cross 60 CD x 62 CD (ZS-8 inter se cross) tolerant to water stress. The selected drought tolerant dura palms could be effectively utilized as mother palms in the Oil Palm Improvement Programmes.

Keywords: Drought tolerance, Dura, Oil palm germplasm

1197 (P-263)

Genotyping-by-Sequencing Characterization of Bread Wheat for Mapping of Yellow Rust Resistance Qtls

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Wheat (*Triticum aestivum* L.) is the most widely grown staple food crop and is important for global food security. One fifth of the total calories consumed by the world population comes from wheat. Yellow Rust, caused by Puccinia striiformis, is one of the most devastating diseases in worlds staple food crop, wheat, causing significant lost to the grain yield globally. Genetic modification of varieties is a prefer alternative among different management options. Genomics assisted approaches offer promise of fast track breeding in wheat. A synthetic by elite population (RIL population; synthetic parent: Botno/ Ae. Squarrosa (666) and elite parent: Kachu) was evaluated for yellow rust disease in two different environments in Mexico, CIMMYT experimental fields El-BatÃ¡n and Toluca. This population was subjected to Genotyping by sequencing (GBS) for an in-depth genetic characterization. A major effect rust resistance QTL explaining up to 45% phenotypic variance was found to be contributed from Kachu. Further analysis revealed this QTL to be contributed from a segment of Triticum ventricosum on chromosome 2NS translocated at short arm of bread wheat chromosome 2AS in Kachu. QTL position was confirmed using T. ventricosum specific primer VENTRIUP-LN2. Identified genomic regions are being introgressed in to the popular but susceptible wheat varieties through marker assisted breeding for enhancing yellow rust resistance and thereby grain yield.

Keywords: Genotyping by sequencing, QTL, *Triticum aestivum*, *Puccinia striiformis*

1208 (P-264)

Genetic Diversity in Popular Land Races Over Cultivars of *Capsicum* spp. Grown in North Eastern Region of India Based on Morphological and Molecular Analysis

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In this study106 germplasm of chilli including cultivars (hot and sweet pepper) and popular land races like King-chilli, Cherry chilli, Dalle chilli and Bird Eye chilli were collected from different states of north eastern hill regions of India and characterized using yield contributing traits and microsatellite markers. Wide range of variations observed for all yield contributing traits. A total of 205 alleles were generated with an average of 4.36 alleles per locus using 47 microsatellite markers. The number of alleles ranged from two (in HPMSE 7) to 8 (in HPMSE 72 and CAMS 91). Based on the value of Shannon's Information index CAMS 91 (1.96) was identified as the most informative marker in this study. Out of 205 alleles only 10 alleles were common in all different *Capsicum* spp. under study. Nine alleles were found specific to Dalle chilli (*Capsicum chinense*) and five to Bird eye chilli (*C. frutescens*). Two alleles were also found specific to King chilli (*Capsicum chinense*) and 21 alleles were specific to chilli (*C. annum*). The results of cluster analysis revealed that the King chilli is closer to Bird eye chilli than the Dalle chilli. The popular land races were found more diverse over commercial cultivars of both chilli and capsicum. High level of genetic diversity assessed in this study at both morphological and molecular level emphasized the importance of this region for conserving *Capsicum* spp. germplasm. The pattern of genetic diversity identified in this region may used to develop in-situ conservation strategies for Capsicum spp.

Keywords: Bird Eye chilli, Cherry chilli, Dalle chilli, King-chilli, Microsatellite

1223 (P-265)

Evaluation of Landraces of Odisha for Leaf Blast Resistance in Uniform Blast Nursery

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Rice blast, caused by the fungus Magnaporthe oryzae is a major problem in most rice growing regions of the world. Use of host resistance is the most effective and economic way to control plant diseases, therefore, the identification of donors and utilization of disease-resistant genes and the development of broad-spectrum resistant varieties are considered to be the most effective strategies to control rice blast. The present study aims to screen landraces (150) from Odisha state for their resistant to leaf blast. These varieties were evaluated for their reaction to leaf blast in the Uniform Blast Nursery (UBN) at National Rice Research Institute; Cuttack using standard method during Kharif 2015. A 50-cm-long row of each entry was planted in nursery bed with a row spacing of 10 cm. A row of susceptible check (Co-39) was planted after every five entries and also on the borders to facilitate uniform spread of the disease. Data on the blast reaction of the entries were recorded three times using a scale of 0“9 scale (SES, 1996) at 10-day intervals starting 30 days after sowing. Out of 150 landraces, only 10% (15) were found to be resistant, showed (0-3) rating to leaf blast, 36.6% were moderately resistant, 38.6% were moderately susceptible while 14.6% were found to be highly susceptible. These resistant landraces can be promising donors for breeding local rice varieties in the Eastern India particularly in Odisha.

Keywords: Rice blast, Landraces, Odishas

1250 (P-266)

Tapping the Vast Diversity Existing in Indian Tobacco

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India is known for its diverse tobacco types having distinct morphological traits and utilities. Most of the tobacco types belong to *Nicotiana tabacum* and few to *N. rustica*. Various types differ in plant height, stem colour, leaf shape, size, spangling, droopiness, colour and petiole, flower size & colour, chemical characteristics etc. Tobacco types are classified as light cast and medium/dark cast, Flue-cured Virginia (FCV) and non-FCV (air/sun-cured, smoke-cured, fire-cured and pit-cured) based on leaf colour and curing, respectively. Cigarette (FCV, burley and oriental) and non-cigarette (cigar-filler, cigar-wrapper, binder, cheroot, *bidi*, *zarda,* chewing, snuff, hookah etc.) types are named based on their ultimate use. Cigarette types are exotic and export oriented, and non-cigarette are indigenous and locally used. In India, different tobacco types are cultivated in well-defined zones with discrete agronomical practices for specific use. For preserving the diversity of tobacco types, ICAR-CTRI maintains around 3000 accessions including 60 wild *Nicotiana* species. Wide variation found in these accessions for morphological traits, molecular diversity, resistant/tolerant to biotic and abiotic stresses, harmful constituents and valuable phyto-chemicals. This diversity was utilized by ICAR-CTRI and AINPT in releasing high yielding and/or stress tolerant 30 FCV, 16 *bidi*, 22 chewing, 9 *hookah* & chewing, one oriental, 2 motihari, 9 cheroot, 2 cigarwrapper and 2 burley tobacco varieties. The diversity existed in this versatile model plant in India can further be utilized for exploiting tobacco for various non-conventional uses viz., oil, production of industrially important phyto-chemicals, molecular farming, basic research in biology and comprehensive studies on climate change.

Keywords: Diversity, Germplasm, *Nicotiana*, Tobacco

1252 (P-267)

Screening of Rice Germplasm for a Resistance against Major Insects and Diseases

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Rice is an important cereal and a source of calories for one-third of the world population. Many diseases and insects attack the rice plant. Among the insect pests, planthoppers cause significant yield losses. One thousand two hundred rice genotypes were screened against Brown planthopper (glass house), Bacterial leaf blight and sheath blight at the Instructional form , IGKV, Raipur (C.G.) under ICAR Network project‘ Consortium Research Plateform on Agrobiodiversity on Germplasm Characterization and Evolution’ during 2014.The five accessions IC98886, IC98976, IC104797, IC104849, IC462159 were categorized as Highly resistant (HR) to BPH. Whereas 91 accessions shows resistance (R) and 193 lines as moderate resistance to the BPH. The rice germplasm screened for bacterial leaf blight and sheath blight under inoculated conditions, One accession IC 579030 showed resistance (R) whereas 14 accessions was found moderate resistant (MR) to the BLB. The two accessions IC466399, IC579050, showed highly resistant to the sheath blight, while 78 accession recorded as resistant (R) to sheath blight. The genetic potential of accessions IC98886, IC98976, IC104797, IC104849, and IC462159, excellent performance for resistant to BPH and IC 579030, for BLB and IC466399, IC579050 to sheath blight, respectively may be used in future resistant rice breeding programme.

Keywords: Brown planthopper, BLB and Sheath blight, Rice germplasm, Resistance, Screening

1271 (P-268)

Evolution of Diverse Genes (Pusa Dwarf Genes) for Short Height in *Triticum Turgidum* Var. *Dicoccum* through Nuclear Technique, their Inheritance, GA Insensitivity, DNA Markers and High Grain Yields

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Local selection from Rishi Valley of Andhra Pradesh, christened as NP 200 (Triticum dicoccum) was released for cultivation during 1958-59, which is being used as the national check in the special trials of dicoccum , by the All India Wheat Co-ordinated Improvement Project ever since, it was released. Though the variety is tall, it has special quality traits among dicoccum varieties. However, the variety being tall lodges and causes considerable yield loss. In order to develop dwarf dicoccum without altering its quality traits, the variety NP 200 was given to 10, 20, 30 and 40 Kr doses of gama ray at BARC, Mumbai during 2002-03 winter. Desirable dwarf mutants, viz.,HW 1095,HW 1096, HW1097and 1098 were picked from treatment 20 Kr at M2 stage, during Monsoon 2003. These plants conferring resistance to yellow rust and powdery mildew under natural epiphytotic conditons at Wellington posses high tillers and dark green foliage. The mean plant height of the mutant (HW1095)was 71cm as compared to NP 200 (110cm.) The non-sergeants semi-dwarf line having luxuriant growth, high tillers and resistance to yellow rust and powdery mildew was constituted at M4 stage. HW 1095 was crossed with NP 200 and the F1 showed the dominant character for tallness and dark green foliage as that of the mutant. The other traits remained same as compared to NP 200. The F2 segregation revealed that the short stature in dicoccum is controlled by two independent complementary genes, which are designated as Pusa Genes of Dicoccum Rht-Pd A Rht-Pd B.

Keywords: Mutation, Complementary genes, Semi dwarf, Dicoccum, GA insensitiveness

1283 (P-269)

Cryopreservation of Cassava Pollen for Long-Term Conservation of Nuclear Genetic Diversity

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The objective of storing cassava pollen is to preserve material for future use, providing optimal conditions to maintain their germination, vigour and genetic integrity. Non-synchronous flowering, monoecious and protogynous nature, poor and irregular flower production makes difficult to breed between the clones of cassava. Crossing desirable genotypes involves multiple and staggered plantings in order to synchronize flowering. This can be avoided when cryopreserved viable pollen is available for hybridization. Cryopreserved pollen is usually subjected to less stringent quarantine restrictions. The international transfer of germplasm in the form of cryopreserved pollen is not generally restricted. Hence, the study on cryopreservation of cassava pollen was undertaken. Anther of cassava variety Vallayini Hraswa was dried in desiccator for 24 hours before storage in liquid nitrogen. Pollen viability was tested by *in vitro* germination in solution media and aceto-carmine staining techniques. The results showed after 30 days of storage in liquid nitrogen, the pollen staining and pollen germination was higher in dried pollen than fresh. The pollen stained 29.37% while pollen germination 23.81% was obtained in the laboratory assessment. Hand pollination in the field was done using cryopreserved pollen and normal fruit set was observed. This finding will be the base information in helping the breeders to plan hybridization programme in cassava.

Keywords: Cassava, Cryopreservation, Pollen Conservation

1310 (P-270)

Isolation and Characterization of New SSR Markers for *Bougainvillea* using NGS Technologies

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Bougainvilleas are one of the most important garden plants, particularly in the tropical and sub tropical parts of the world. Indian Agricultural Research Institute (IARI), New Delhi is the International Crop Registration Authority for bougainvillea has a collection of hundred diversified cultivars. Many bougainvillea cultivars which show only minor differences in leaf shape, variation in flower colour are difficult to identify accurately based on morphology. A scientific study to understand rich collection made from different sources was indeed essential to effective identification of species and cultivars. To address the forgoing concerns we designed 175 SSR markers using Roche 454 and Illumina pair end sequencing technologies to study the genetic diversity among larger set of bougainvillea cultivars. 83 markers produced clear amplification and 33 markers were found to be highly polymorphic. Di and tri-nucleotide repeat motifs were found to be most common ones which accounted for higher polymorphism. All the markers detected 165 alleles of average of 5 alleles per locus with the amplicon size range of 90-320bp. Genetic diversity and PIC values ranged from 0.13-0.91 and 0.134-0.958 with a mean value of 0.71 and 0.678, respectively. The newly identified SSRs will facilitate genetic diversity studies, fingerprinting and population structure pattern of bougainvillea. This would also helpful to know the origin of unknown group of cultivars at certain level apart from their further improvement. The investigation further demonstrated the ability of SSR markers in detecting molecular polymorphism to characterize and group the bougainvillea cultivars.

Keywords: Bougainvillea, SSR markers, Polymorphism

1326 (P-271)

Discovery of Haploid Black Pepper (*Piper nigrum* L. ‘PAJ’)

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Piper nigrum L. is the source plant of Black pepper- the ‘King of Spices’. Crossing between a wild genotype of the crop ‘PMM’ (♀) and a high yielding cultivar ‘Karimunda’ (♂) has been carried out, aimed at transferring the quality traits - high piperine and oil content of fruits - of the former to the latter. Among the progeny, a haploid genotype has been identified, and this is the first report of haploid Black pepper. The discovery of haploidy in Black pepper is significant since it opens up a new vista of genetic improvement in Black pepper – heterosis breeding – and it is also useful for genome analysis of the crop. Ten young spikes of each of the parent plants were selected and bagged. The selected spikes of ‘Karimunda’ were washed with drops of distilled water and collected the wash. The wash –a water suspension of pollen grains of the cultivar – has been applied on the selected flowering spikes of the female ‘PMM’ plant. Nine seeds were produced and five of them germinated and produced seedlings, of which four were normal and one was odd in its morphology. Mitotic studies were carried out in the plants raised from all the five seedlings. The studies revealed that chromosome constitution of the plants belonging to the odd seedling is 2n=26, whereas that of the other seedlings 2n=52, which corresponds with the normal somatic chromosome constitution of Black pepper. Repeated mitotic studies on the plants obtained from the odd seedling have confirmed their haploid genome constitution. This first haploid genotype of Black pepper has been named ‘PAJ’.

Keywords: Black pepper, Haploid, *Piper nigrum*

1411 (P-272)

Assessment of Pollen quantity, Viability and In Vitro Pollen Germination of Litchi Cultivars

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Litchi (Litchi chinensis Sonn.) a member of Sapindaceae family, is one of the important commercial fruits of the subtropical region. Its short flowering period couple with narrow genetic base serves as the major constraints in litchi genetic improvement. Litchi has three different types of flowers and the quantity and quality of pollen produce by each flower is different. Pollens are known to directly influence reproductive success and genetic structure of the plant population. In this study, we compare the pollen quantity per anther, viability and in vitro pollen germination of M1 and M2 flowers of five litchi cultivars viz., Shahi, China, Bedana, kasba and bombai. Pollen quantity was evaluated by blood count method. Highest pollen quantity was observed in Shahi followed by China, Kasba, Bomabai and Bedana. Acetocarmine, 2,3,5-triphenyl tetrazolium chloride (TTC), 2,5-diphenyl monotetrazolium bromide (MTT) and aniline blue-lectophenol staining methods were conducted for pollen viability. Acetocarmine solution (1%) showed best results for pollen viability test. Different concentrations of sucrose, boric acid (H3BO3) and agar were used in germination medium in which 15 % sucrose + 100 ppm Boric acid + 1.0% agar showed promising results. Pollen from M1 and M2 flower was incubated at different temperature and duration. Highest germination rate was observed at 25oC for 12 hours but maximum pollen tube growth was at 25oC for 24 hours. Pollen from M2 flower had significantly higher pollen quantity, viability and germination rate compared to pollen from M1 flower.

Keywords: Litchi, Pollen, Viability, Germination rate

1429 (P-273)

Climate Resilience in Wheat Cultivars

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The abiotic stresses in one or other form occur in almost all the wheat growing areas in country. Among various abiotic stresses, high temperatures and soil moisture stress significantly influence wheat production. Individually each stress may cause 20 “ 30% reduction in grain yield. Increasing temperature trends of the order of 0.60Â°C during last 112 years and increase in heavy and decrease in low and medium rainfall events over India have been observed. Mean minimum and maximum temperature and diurnal temperature range have increasing trends for the period 1951-2010 during the months of November to March in most of the wheat growing states. The All India Coordinated Wheat and barley Research Project is responsible for developing agro-climatic condition specific cultivars. However, with passage of time and change in climatic conditions, the adaptability and performance of these cultivars are also expected to change. In order to meet the future challenges, experiment comprising popular cultivars from four mega zones of wheat cultivation were evaluated for drought and heat stress individually as well as combined at four locations by staggered sowing under different irrigation conditions. In total 36 genotypes were evaluated under four conditions namely, timely irrigated (non-stress), timely rainfed (drought stress), late irrigated (heat stress) and late rainfed (heat and drought stress) at each location. The results revealed that some cultivars had narrow adaptation whereas others were widely adapted across locations as well as conditions. The performance of genotypes and climatic conditions will be presented in the paper to explain their adaptability.

Keywords: Adaptability, Climate change, Heat stress, Drought stress

1430 (P-274)

Genetic Diversity Analysis of Greater Yam (*Dioscorea Alata* L.) Landraces of Kerala

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Yams belonging to Dioscoreaceae family are important climate resilient food security crops and widely cultivated in India, one of its center of origin, and Africa. In India, one of the major cultivated yam species is greater yam (*Dioscorea alata* L.) and is a polyploid, with several ploidy levels, revealing a predominance of tetra ploidy and provides a good source of dietary carbohydrates in tropical and subtropical regions. This research work attempts molecular, morphological and biochemical characterization of landraces for greater understanding of the distribution and extent of genetic variation existing within the D. alata germplasm collected from Kerala. The morphological variation among accessions was also determined using 33 IPGRI descriptors which included 7 quantitative traits. Weight/ tuber ranged from 0.120 Kg (Da 53) to 6.950 Kg (Da 340). The tuber flesh colour of the accessions varied from yellowish white to purple colour. The biochemical study on protein, dry matter was done to determine the nutritional quality of the selected accessions. Among the accessions Da 69 recorded highest dry matter content (48.24 %) and Sree Neelima recorded highest protein content (5.233 %). The genetic diversity of 40 accessions representing different districts of Kerala was analyzed on the molecular basis using 9 simple sequence repeat (SSR) and 15 inter simple sequence repeats (ISSR). All the SSR primers and ISSR primers studied showed high polymorphism. The results of the present study serves to facilitate the development of better varieties by plant breeding and marker assisted breeding programs.

Keywords: *Dioscorea*, Genetic diversity, Yams, Molecular markers

1435 (P-275)

Assessment of Rice Biodiversity for Diverse Agro Morphological Traits

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The agro-morphological characterization is fundamental in order to provide information for plant breeding programs. The aim of the present study was to characterize 6000 accessions of rice germplasm (*Oryza sativa* L.), based on qualitative and quantitative agro-morphological descriptors. The experiment was conducted at Research and Instructional farm of IGKV, Raipur, under Network project 'CRP on Agrobiodiversity' project during year 2015.A total of 5839 rice germplasm accessions were evaluated for characterization for 19 qualitative and 11quantitative traits. The qualitative traits ***viz.***, stigma color, Basal leaf sheath color, Apiculus color, Seed coat color, Kernel colour etc. Unique quality characters viz., purple colour stigma found in accession i.e. IC 202409, IC 207803 etc. Apiculus red colour: apex colour showed in i.e. IC135223, IC 389873 etc. The accession no's IC 123121, IC123467 showed red seed coat colour and black hull colour was found in accession IC 80043, IC 386997. The quantitative traits ***viz*** 50% flowering most of the accessions comes in medium to late group with range of 63-144 days whereas IC 311862 (63 days), IC 319524(69 days) comes under very early group .The maximum panicle length was recorded in IC323564 (36.80) followed by IC 124700 (35.60) while the maximum tillers were recorded in IC 299557(23.50) and IC 378624 (23.00) however the highest grain weight were recorded in IC 386974 (4.88 gm) followed by IC 125696(4.87 g) and IC 206617 (4.86 g). The maximum value for L/B ratio was recorded in IC 125043 (4.95) followed by IC 124277 (4.86). The genetic potential of the IC 125696,IC 323564 IC379019, IC 299557 and IC 378624 accessions for the desired traits can be utilized in future rice breeding programs to get promising results.

Keywords: Rice, germplasm, Agro-morphological traits .

1470 (P-276)

Scouting New Sources of Rust Resistance and Various Traits Contributing to Yield in Wheat (*Triticum aestivum*) Germplasm

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Germplasm evaluation for agro-morphological traits contributing towards yield and disease resistance provides valuable information to plant breeders for developing their breeding materials. Evaluation of 1485 accessions of wheat germplasm obtained from the NBPGR was done for yield contributing traits and rusts during 2015-16. The range for spike length was 6.2cm – 20.8cm, number of spikelet/spike was 13 – 29 and number of grain per spike was 22-106. Based on the flowering time, the germplasm was divided into different categories as early flowering (75-90 days), medium flowering (91-100 days) and late flowering (101-115 days). The yield for the accessions ranged from 17-185g/m and 1000 grain weight ranged from 7.9-67.2g. Out of the total 1485 accessions, 65 accessions had outstanding yield and 1000 grain weight as compared to the local checks. Another most serious constraint to yield enhancement in wheat, is rust susceptibility and available sources of resistance run the risk of over exploitation and a narrowing of resistance base. There is an immediate need to identify and exploit novel resistance sources. The germplasm set was screened for stripe rust as well as leaf rust resistance under artificial epidemic conditions and 406 and 101 lines were found to be resistant to stripe and leaf rust respectively. 28 lines were resistant to both rusts and can be used as novel sources of resistance. Few lines were identified to have desirable grain weight, yield etc along with resistance to either of the rusts and these lines hold a promise for wheat improvement through breeding.

Keywords: Rust resistance, Wheat, Yield

1472 (P-277)

Genetic and Environmental Variation in stay-green Sorghum [*Sorghum bicolor*. (L) Moench] Grain Amino acid Profile and Relations to Physiological processes

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Genetic and environmental effects on sorghum grains amino acid (AA) profile and linkage to plant functions were studied in sorghum stay-green QTL introgression lines (originated from senescent lines R-16 & S35). Crop was raised under well-watered (WW) and water stressed (WS) conditions in the field. Matured grains were dried, ground (Cemotech grinder) and scanned for near infra-red reflectance spectra signature (NIRS). AA contents predicted using world aqua feed amino acid calibration model.Total protein content ranged from 7.7-10.5% (w/w; WW) and 7.1-9.8% (w/w; WS) and S35 (~9.32%) lines attained higher protein content compared to R16 lines (7.68%). WS reduced total protein content.WS affected grain size in S35 lines and therefore most of the AA contents variability in S35 was explained by grain size (except Glycine, Cysteine and Methionine) while same relation was not significant in R-16 lines. Some amino acid contents in the grain related to the plant functions underlied by stay-green mechanisms; e.g. tryptophan, a physiological precursor of auxins (essential amino acid; (range: 0.01-2.14%)); was negatively correlated with plant tillering propensity. We found strong positive correlation of proline and histidine with stem/stover ratio (i.e. proxy for photosynthetic efficiency), indicating that photosynthetic processes may influence the grain amino acid composition. Altogether, we showed significant stay-green QTL and environmental effects on sorghum AA content and suggested that some plant functions can explain AA content in the grain. Literature is poor on knowledge of these processes and their interactions with environment despite such understanding is essential to support the crop improvement programs.

Keywords: Amino acids, NIRS, Sorghum, Stay-green QTL, Tillering

1478 (P-278)

Exploration and Collection of Drought Tolerant Rice Landraces from the Southern Districts of Tamil Nadu, India.

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Traditional landraces are valuable genetic resources possessing huge genetic variability to complement and broaden the genetic base for crop breeding. They serve as potential source of genes for novel traits and play an important role in ensuring food security. However, the adoption of modern high yielding varieties and adverse climatic changes had led to the reduction in genetic base and increasing genetic vulnerability. So there is an urgent need to explore, collect and evaluate the untapped germplasm to develop elite breeding materials for future needs. In the present study a total of 49 drought tolerant traditional rice landraces native to southern districts of Tamil Nadu (Sivagangai, Ramanad and Pudukottai) were collected by students and staffs of the Department of Plant Genetic Resources, TNAU in collaboration with scientists from NBPGR, New Delhi. Characterization studies on seed traits revealed the existence of sufficient variability among 49 rice land races which varied from 16.0 to31.1g (1000 seed weight), 0.53 -1.03mm (grain length), 0.18-0.40mm (grain breadth) and different seed coat colours were observed as Yellow, Brown, Speckled Brown, Black and Red. The geographical coordinates of distribution were recorded with a Garmin hand held GPS instrument mapped using DIVA-GIS software. From the exploration, it was concluded that traditional land races are under threat due to increased pressure in environmental changes, so there is a need for conserving maximum diversity in the gene banks and on-farm for the sustainable utilization.

Keywords: Exploration, Climatic change, Landraces, Conservation, Sustainable utilization

1487 (P-279)

Radiation Induced Translocations Between Bread Wheat and Rye Genome as a New Means of Creating Useful Diversity

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The narrow genetic base of wheat as a crop is to an extent mitigated by its potential to accommodate alien genetic transfers, further facilitated by availability of well developed genetic tools. The practical utilization of this natural as well as man made opportunity to enhance diversity however, falls short of meeting challenges posed by emerging biotic and abiotic threats to wheat. One of the approach is using radiation to induce translocations between wheat and Rye with a mandate to obtain some segments of R genome. But, the optimum stage, dose of gamma radiation and the best tissue to radiate for a targeted result is not well defined. An experiment was carried outusing different tissues (female tissue and pollen) for radiation, different sources of radiation (gamma rays and X rays) and different stages (ovary before fertilization, pollen just before fertilization and zygote within 24 hours of fertilization). The seed was formed maximum in pollen just before fertilization, moderate in ovary before fertilization, zygote and minimum in ovary and pollen just before fertilization. Seed germination was maximum in pollen just before fertilization (Xrays) while minimum in Gamma rays, moderate inovary before fertilization, zygote andin ovary and pollen just before fertilization.The immature spike samples were taken for cytological studies to confirm any translocations and is in progress. The translocations between *Triticumaestivum*genome (ABD) and rye genome (R) would be of immense use to be used as sources of resistance to biotic and abiotic stresses in wheat breeding programs.

Keywords: Radiations, Rye, Translocations, Wheat

1506 (P-280)

Resynthesis of *Brassica Juncea*: Exploiting Diversity Contained in Progenitor Diploid Species for *B. Juncea* Improvement

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Indian mustard *Brassica juncea* (AABB, 2n=36) is second most important oil seed crop next only to groundnut. It is an amphidiploid that evolved in nature by the intercrossing between *B. rapa* (AA, 2n=20) and *B. nigra* (BB, 2n=20). Occurrence of wide genetic diversity in the germplasm of a crop guarantees its further improvement and development for desired traits. Since *B. juncea* evolved naturally from a few chance crosses between its progenitors species, the genetic diversity among *Brassica juncea* accessions is limited whereas a vast untapped diversity is present among the progenitor species. By resynthesis of *B. juncea* we can exploit this diversity for development of desired economic traits in the crop. In present study twelve diverse *B. rapa* and six *B. nigra* accessions were used for resynthesis. Embryo rescue technique was resorted to obtain hybrids. Out of the total 305 embryos rescued, only 85 plantlets belonging to 15 cross combinations were obtained which were transferred to pots for further evaluation. Of these, only 14 plants from seven crosses were found to be true hybrid (amphihaploids) as confirmed by SSR markers. Colchicine (0.2 %) treatment of apical buds of these plants and bud pollination has yielded a few seeds. Finally, we got ten resynthesized *B. juncea* lines derived from three crosses. Progeny from these lines initially had ≈ 50% fertility which significantly increased to ≥ 85% in subsequent generations. These synthetic *B. juncea* lines carry many desirable agronomic features can be used in mustard breeding program.

Keywords: Amphidiploids, *Brassica juncea* resynthesis, Diversity.

1553 (P-281)

Evaluation of DNA Barcode Loci for Cataloguing *Nicotiana* Accessions

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DNA bar coding is a new system of species identification and discovery using a short section of DNA from a standardized region of the genome and can be effectively used in large-scale biodiversity surveys. Since there is no single locus of barcode as in animal systems, a multilocus DNA barcoding system was suggested by (CBOL Plant Working Group, 2009) in which slowly evolving loci delineate individuals into families, genera, or groups within genera and the more rapidly evolving loci differentiate species within those higher groups. ICAR-CTRI being the part of the National Active Germplasm Site is maintaining around 200 accessions of *Nicotiana* species. In order to identify the suitable barcode regions for Identification and differentiation of *Nicotiana* accessions at molecular level four different bar coding loci with a combination of slow and rapid evolving loci namely rbcL, matK, trnH-psbA and ycf1 were selected and screened selectively in 40 *Nicotiana* accessions. All the amplicons except trnH-psbA are found to be mostly monomorphic in length among the accessions analyzed. Further among the four loci, one rapid and one slow evolving loci i.e., trnH-psbA and ycf1 were primarily sequenced for studying the variation of the loci in selected accessions. The results indicates that rapid evolving loci trnH–psbA is found to be polymorphic with respect to amplicon length and sequence and ycf1 has sequence variation between the species. This indicates that the barcode loci, trnH-psbA and ycf1 can be used to catalogue the *Nicotiana* accessions.

Keywords: Diversity, DNA barcode, Tobacco

1559 (P-282)

Morphological Diversity of Maize Landraces of Jammu and Kashmir

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Landraces constitute a very important component of agro-biodiversity harbouring rare alleles for various important traits. A total of 66 maize landraces which were collected from different parts of Jammu and Kashmir were planted at Srinagar and evaluated for 30 DUS traits. Observations were recorded and dissimilarity matrix was worked out using Euclidean distance. Clustering was performed using this dissimilarity matrix by UPGMA method. Four major clusters were identified grouping most of the landraces. Cluster analysis showed that the landraces collected from same geographical locations grouped into different clusters. Two out of the 66 landraces namely Kulgam-2 and pulwama-8 constituted very distinct group indicating their evolution and maintenance in isolation. Principle component analysis was conducted using observation of 9 morphological traits which showed that first three principle component represented 24.79, 17.79 and 14.03% of the total variance. Biplot analysis of first two principle components also arranged landraces collected from same region into different groups. It can be concluded that landraces of Jammu and Kashmir studied under present investigation harbour genetic variation for several traits such as grain colour, tassel size, tassel shape etc. and more conclusive grouping of these landraces requires further information regarding molecular marker pattern to decipher their evolutionary pattern.

Keywords: Landraces, Diversity, Maize

1564 (P-283)

Screening for Heat Tolerant Donors in Rice for Future Breeding Programme

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High temperature stress making rice production less efficient in many warming regions during rice cultivation, above 35°C during development stages significantly reduced the yield. To sustain the rice production, there is need for better donors with tolerance to high temperature stress. The identified heat tolerant donors ultimately used in breeding programme to generate rice varieties with tolerance to high temperature stress is utmost important in order to sustain future rice production. A total of 50 genotypes were received from IRRI were screened during the dry season of Rabi 2014 at ICAR-Indian Institute of Rice Research, ICRISAT campus with an altitude of at 17°29'40.39"N, 78°16'15.39"E. Sowing was done in order to ensure exposure of maximum genotypes to high temperature (>40°C) at the time of reproductive stage. The genotypes transplanting was done 25 days after seeding in two rows each row 3 m with a spacing 20x15cm. Recommended agronomic practices were done at optimum level. Observations on day to 50% flowering, plant height, productive tillers per plant, spikelet fertility were recorded. Existence of the genetic variability was observed among the genotypes. There was significant to drastic reduction for spikelet fertility recorded. In this present study the genotypes HHZ 8 SAL6 SAL 3 Y1, HHZ 5 DT 1 DT1, HHZ 8 SAL12 Y2 DT1had minimum impact of heat stress on seed setting, the same germplasm set under progress in screening for reconfirmation for the heat tolerance in temperature gradient tunnel (TGT) and these donors could be used in breeding programme.

Keywords: Rice, Heat tolerance, TGT

1572 (P-284)

Evaluation of Jackfruit Germplasm Accessions and Genetic Diversity Analysis

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Jackfruit (*Artocarpus heterophyllus* Lam.) is a fruit crop believed to be originated in Western Ghats of Indian Sub-continent. It is heterozygous, cross-pollinated and mostly seed propagated, resulted in wide range of variation with respect to yield and fruit quality. Collection, characterisation and evaluation is still the most sought after method for releasing of new jackfruit varieties, owing to this vast amount of variability. Being a National Active Germplasm Site (NAGS) for jackfruit, ICAR-Indian Institute of Horticultural Research, Bengaluru has collected 69 germplasm accessions from states where in Western Ghats lays. In this study, the conserved accessions in the field gene bank were evaluated for superior fruit quality traits. Variability observed for fruit shape, average fruit weight (3 kg to 13.9 kg), length, rind thickness, skin and pulp colour, number of flakes per fruit (40 to 220), bulb weight, length and width, rachis length, total soluble solids (17.7 to 34.2 °B), seed weight, length, width, shape and colour. Two superior accessions, one red flaked and another less gum type, were identified and found suitable for commercial cultivation. Further, these 69 genotypes were grouped into five clusters based on the genetic diversity analysis. The dendrogram obtained using phenotypic characters separated the accessions into five major clusters based on Euclidean distance. The Euclidean tree demonstrated a genetic distance between the clusters I (G-70 and G-78) and cluster V (G-34, G-75, G-38 and G-51) were genetically apart based on the fruit traits studied.

Keywords: *Artocarpus*, Genetic diversity, Jackfruit germplasm

1576 (P-285)

Seed Viability in Soybean: Donor Identified and RILs Developed

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Loss of seed viability in ambient storage is a serious problem of cultivated soybean in tropical and sub-tropical regions of the world. Upon ambient storage, the seeds lose 30-40% viability in a year; however it may go far below depending upon the genotype and condition of storage. Poor viability of the seed increases seed rate at sowing resulting in higher cost of production. Attempt was made to identify genotype having higher seed viability in soybean. Seeds of 29 accessions of *G soja* were stored in ambient condition during 2007. The seeds of all the genotype were dull black color with average 100-seed weight 1.30g. During 2014, the seeds were subjected to germination test in 3 replications. In parallel, seeds of 10 genotypes of *G max* and 30 inter-specific (*G soja* x *G max)* recombinant inbred lines (RILs) were stored in similar condition and samples were tested for germination. Seeds of the *G soja* genotypes had hard seed coat while seeds of the *G max* genotypes and most of the RILs had soft seed coat. Variation for seed viability was observed among the cultivated and wild type soybean genotypes. Out of the 29 wild type accessions, only 18 germinated with 10-50% germination (average 25%). No cultivated genotypes remained viable beyond 3 years of ambient storage. However, seeds of the RILs had 30-90% germination after 3 years of ambient storage. In this study, genotypes and RILs with soft seed coat and higher seed viability were developed.

Keywords: RIL, Seed viability, Soybean

1543 (P-286)

Genetic Diversity of Hyacinth bean Collections in Bangladesh

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Bangladesh posses a wide diversity in hyacinth bean (*Lablab purpureus*). The objective was to identify divergent parents for varietal improvement of hyacinth bean. The experiment was conducted with 150 accessions from Bangladesh and 16 other countries of Asia, Africa and Europe for characterization and genetic diversity study. Alpha Lattice Design with two check varieties and three replications were used in the experiment. High Shannon-Weaver Diversity Index (H'≥0.75) was observed in colour of hypocotyl, epicotyl, stem, leaf vein, flower as well as the shape and size of seed. The accessions were exhibited 4.92 to 16.74 cm edible pod length, 1.35 to 4.36 cm pod width, 2.10 to 17.07 g pod weight and 84 to 537 pods/plant The genotypic coefficient of variations was ranged from 3.59 to 40.08 % from leaf ratio (L:W) and rachis length, respectively among the 19 quantitative characters. Accessions were grouped into ten clusters using D^2 values. Number of accessions in each cluster was ranged from 8 to 25. Accessions collected from the same districts of Bangladesh or abroad were distributed into different clusters. No clear relationship was found among the accessions from different geographical region. Crosses between accessions belonging to maximum divergent clusters of CPI 106548 (India), ILRI 14437 (Zimbabwe) and TOT 7905 (Uzbekistan) from cluster IX with accessions of BD 122 (Bangladesh) and BD 8785 (Bangladesh) from cluster I, and BD 8770 (Bangladesh) from cluster VI could be done for obtaining better variability to the subsequent generation. By strategically using this diversity, breeder can develop high yielding varieties in hyacinth bean.

Keywords: *Lablab purpureus,* CHaracterization, Cluster analysis, Bangladesh.

1585 (P-287)

Utilization of Natural Variation of B-Carotene Hydroxylase (*Crtrb1*) Gene for Development of B-Carotene Rich QPM Genotype

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Vitamin A is an essential micronutrient for the normal growth and development; deficiency of which causes high mortality and morbidity especially among children and pregnant women. Though traditional yellow maize possesses abundant variation for kernel carotenoids but are low in β-carotene (<2 μg/g). β-carotene hydroxylase (*crtRB1*) is a key mutant gene associated with β-carotene concentration in the maize kernels. Here HKI1128Q, an elite inbred already improved for lysine and tryptophan, and parents of three popular hybrids was used as recurrent parent (RP) to introgress *crtRB1* for enrichment of kernel β-carotene. HP704-22, inbred from CIMMYT-HarvestPlus having favorable allele (543 bp) for *crtRB1* was used as donor; and the F_1s were backcrossed to RP after hybridity testing. Foreground selection identified progenies homozygous for *opaque2* and heterozygous for *crtRB1* in BC_1F_1 generation. The selected plants were backcrossed to RP to generate BC_2F_1 generation. Progenies heterozygous for *crtRB1* were further selfed to generate BC_2F_2. Progenies homozygous for both *opaque2* and *crtRB1* in BC_2F_2 were selected for advancement and quality testing. Background selection using polymorphic 97 SSRs coupled with phenotypic selection for RP characteristics was also carried out to identify plants similar to recurrent parent. 76%, 89% and 92% recovery of RP genome was achieved in BC_1F_1, BC_2F_1 and BC_2F_2 populations, respectively. Homozygous BC_2F_3 genotype recorded ~17.0 μg/g of kernel β-carotene compared to ~1.5 μg/g in HKI1128Q. This improved genotype with *crtRB1* and *o2* alleles assumes great significance in the breeding programme besides serving as valuable genetic resource.

Keywords: Maize, Provitamin A, *Opaque2*

1593 (P-288)

Genetic Enhancement of Indian Mustard (*Brassica Juncea* L. Czern & Coss) and Ethiopian Mustard (*B. Carinata* A Braun) through Interspecific Hybridization

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Interspecific hybridization between two oilseed crops; *B. juncea* and *B. carinata* was followed to improve both species simultaneously by transferring desirable traits. 36 lines could be derived in F_6 generation of which 30 were of *B. juncea* and six were of *B. carinata*. These lines alongwith both parents were evaluated for agronomic traits and disease reaction. Derived *B. juncea* lines were compared with *B. juncea* parent and similarly, derived *B. carinata* lines were compared with *B. carinata* parent to estimate the extent of improvement. Results of present study depicted significant improvement in derived *B. juncea* lines for long reproductive phase, seed yield, plant height, main raceme length and resistance to white rust. Derived *B. juncea* lines were, however, of long maturity duration. It was quite interesting to note improvement for short plant height and for length of main raceme in derived *B. juncea* lines looking contrasting phenotype of *B. carinata* parent. In *B. carinata* lines, significant improvements were for short maturity duration, short plant height and enhanced length of main raceme. It was obvious from these findings that interspecific hybridization between these two species was effective in improving both species through introgression of desirable traits of one to other species.

Keywords: Ethiopian mustard, Indian mustard, Interspecific hybridization

1601 (P-289)

Development of Diverse Maize Genetic Resource Possessing *Crtrb1*, *Opaque2* and *Shrunken2* Alleles Through Marker-Assisted Selection

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Maize is one of the most important cereal crops in the world with diverse end uses. Among the specialty corn types, sweet corn has gained great acceptability with the rapid urbanization. At milky stage, total sugar content ranges about 18-25% in sweet corn compared to 5-7% in normal corn. Of the various mutants in starch biosynthesis pathway that alter the types and amount of polysaccharides produced in the kernel, *shrunken2* (*sh2*) has been extensively used for sweet corn cultivar development. While favourable allele of *crtRB1* enhances provitamin A by nearly 10-fold, the recessive *opaque2* (*o2*) causes two-fold higher accumulation of lysine and tryptophan in maize endosperm. The present study was aimed to introgress *sh2* allele in MAS-derived introgression lines of HKI161, HKI163, HKI193-1 and HKI193-2, possessing high provitamin A, lysine and tryptophan. These genotypes were used as female parent and crossed to *sh2*-based sweet corn genotype. F_1s were backcrossed to the recurrent parents after hybridity testing. Foreground selection was successfully carried out in BC_1F_1 generation and the progenies homozygous for *opaque2* and *crtRB1*; and heterozygous for *sh2* were selected. Background selection using >85 polymorphic SSRs and phenotypic selection for plant and ear characteristics led to the selection of progenies resembling the respective recurrent parent. Genotypes with *o2+crtRB1+sh2* to be selected from further generation(s) would serve as rich genetic resource, and assumes great significance in the sweet corn breeding programme.

Keywords: Provitamin A, QPM, Sweet corn

1602 (P-290)

Genetic Analysis and Transfer of Stripe Rust Resistance Genes from European Winter Wheat Lines

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Present study aimed to identify stripe rust resistance donors in a set of 376 European winter wheat varieties procured from National Institute of Agricultural Botany, UK. Backcross derivatives from 148 crosses were generated with the objective of primarily developing a long duration high yielding plant type. Gene pyramided rust resistant spring wheat lines adapted to North-Western India were used as recipients in most of the backcrosses while about 30 populations involved parents which have now become susceptible to stripe rust e.g., PBW621 and HD2967. Sufficiently large backcross populations comprising BC_1F_1 (2013-14), single plant derived BC_1F_2 (2014-15) and single plant derived BC_1F_3 (2015-16) were subjected to selection and screening for stripe rust resistance. Creation of artificial epiphytotic using prevalent virulent stripe rust races *Pst*pt 78S84, *Pst*pt 46S119 and *Pst*pt ASL (Anandpur Sahib Local) and single plant observation allowed demarcation of clear genetic segregation in 5 out of 30 resistant x susceptible cross derivatives. Three European winter wheats *viz*., Aciento (France), Acienda (France) and Pulsar (France) were seen to carry one gene governing stripe rust resistance. Two European cultivars PR-22-R-28(France) and Brilliant (Germany) were inferred to carry two individually effective major genes for stripe rust resistance. We are working towards molecularly tagging these putatively new seven stripe rust resistance genes for their further use in wheat breeding.

Keywords: Resitance, Stripe rust, Winter wheat

1605 (P-291)

Characterization of Exotic- and Indigenous Maize Genotypes for Phytic Acid and *lpa* Genes

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Phytic acid is an anti-nutritional factor that reduces the bioavailability of minerals *viz*. Fe and Zn. Thus identification of genotypes with low phytic acid assumes significance for alleviating micronutrient malnutrition. A set of 84 diverse maize inbreds was evaluated for grain-phytic acid (PA) and -inorganic phosphorus (Pi). PA and Pi ranged from 12.24-16.09 mg/g and 0.07-0.61 mg/g respectively. None of the genotypes were found to contain low PA. However, two of the genotypes screened exhibited medium PA (12.97 and 12.41 mg/g) and high Pi (0.55 and 0.61 mg/g), respectively. Most of the genotypes had either medium- or high-PA with low or medium Pi. Two *lpa* mutants, *lpa1-1* and *lpa2-1* in two genetic backgrounds namely A632 and A619, possessed low PA. *lpa1-1* is a missense mutation in *ZmMRP4* and *lpa2-1* has a genomic sequence rearrangement in *Zmlpk* gene. The low PA inbreds showed slower germination and less early seedling vigour compared to normal inbreds. *umc2230*, a linked SSR to *lpa2* generated polymorphism among the contrasting lines. *ZmF1302/ZmGSPR1580* primer could also differentiate the selected normal and *lpa* lines. The inbreds with low PA would serve as potential donor in the breeding programme, and the marker information can be effectively utilized in the marker-aided selection for low PA in maize.

Keywords: Bioavailability, Maize, Phytic acid

1608 (P-292)

Genetic Diversity and Variability in Greengram [*Vigna radiata* (L.) Wilczek] Germplasm Under Rice Fallow Condition

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Fourty one genotypes of greengram including thirty-eight local landraces collected from diverse agro-climatic regions of Odisha and three promising varieties were studied to assess the magnitude of genetic variability and diversity based on yield contributing characters. The experiment was carried out during 2013-14 at ICAR-NBPGR Base Centre, Cuttack in RBD with three replications. The plot size comprised three rows, 3.0 m long, with inter- and intra- row spacing 0.3 and 0.1 m respectively. Observations were recorded on ten quantitative traits namely Days to flowering, Plant height, Branches/plant, Clusters/plant, Pods/cluster, Seeds/pod, Pod length, 100 seed weight, Yield/plant, Yield/ha from five competitive plants randomly selected from each genotype in each replication. The data collected for each quantitative trait was subjected to analysis of variance (ANOVA), including estimation of phenotypic, genotypic, environmental variances and Mahalanobis D2-statistics. Observation of significant differences for all the traits indicated enough scope for greengram improvement programme. Heritability in broad sense (h2) was high for all the traits, highest being recorded for yield/ha (0.884). High genetic advance coupled with high heritability was observed in yield/ha, Clusters/plant, Branches/plant suggesting the role of additive gene effect and possibilities of high genetic gain from phenotypic selection. The difference between PCV and GCV was minimum (0.94) for days to flowering suggesting that the trait was least affected against high degree of difference in yield/plant (13.83) indicating high value of environmental influence. Genetic divergence among the genotypes revealed thirteen clusters. Yield/ha (21.4%) contributed maximum towards divergence followed by plant height (15.2%) and pods/plant (14.7%).

Keywords: Greengram, Heritability, Genetic divergence

1610 (P-293)

Creation of Genetic Variability through Wide Hybridization in Soybean

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Soybean [*Glycine max* (L.) Merr.] is an important source of edible oil, nutritious food and feed worldwide. It is the numero uno oilseeds crop in India. However, productivity of Indian soybean (~1.2t/ha) is far below the global average (~2.5t/ha). In this study, an accession of wild type (G soja) soybean (DC2008-1) was crossed with a cultivated soybean variety (DS9712) to create genetic variability and introgressing gene(s). The cross breds were advanced through single pod descent approach to isolate 308 recombinant inbred lines (RILs) in F7 generation. For studying genomic variation, 329 SSR markers spanning uniformly over the 20 chromosomes (@16 markers/ chromosome) were selected. Enormous phenotypic variability was observed between the G soja and G max genotypes for plant type, flower color, seed size, seedcoat color, etc. Similarly, large variations were observed among the RILS for agro-morphological traits. Out of the 329 SSR markers tested 210 were polymorphic (63.83% polymorphism). Distribution of the polymorphism was not uniform across the genome; some chromosome exhibited higher polymorphism than others. Highest level of polymorphism (80%) was observed on chromosome No. 9 and the least (46.15%) was on chromosome No. 13. Molecular genotyping of the RIL population exhibited expected 1:1 segregation ratio for the SSR locus tested. The study thus indicated creation of genetic variability through distant hybridization and introgression of important traits from G. soja in to the G. max genotype (DS9712). Polymorphic markers identified in this study will be useful in mapping and marker-assisted introgression of gene/ QTL for important traits in soybean.

Keywords: Genetic Variability, Wide Hybridization, Soybean

1611 (P-294)

Microsatellite Markers from Rice Drought Responsive Ests and their Transferability to Marvel Grass (*Dichanthium Annulatum*)

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Marvel grass (*Dichanthium annulatum* L. (Stapf)) is an important perennial range grass widely distributed in tropical and subtropical zones of India. It is a constituent of two major grass covers and one of the most commercialized fodder grasses, due to its adaptability to intense grazing and tolerance to drought and fire. Co-evolution and large-scale synteny among grass genomes facilitate further investigation in other perennial grass species with more complex, polyploid genomes. Among grass species, rice is a good model because of its diploid genetics, and available genetic and genomics resources. To develop transferable genetic markers for estimation of genetic diversity in the available germplasm, drought responsive ESTs of rice were data mined for SSR markers. Mono nucleotide motifs were the most abundant (67%), followed by tri- (19%) and di- nucleotide repeats (11%). The most abundant tri nucleotide repeat motif was CCG/CGG (39.64%). Majority of the SSR containing ESTs were annotated to proteins having distinct biological process such as stress response, biosynthetic processes, protein modification, catabolic process and signal transduction. Upon initial screening of the 80 SSR markers in two genotypes of marvel grass, 50 rice SSR primer pairs were found to be transferable (62.5 %). A total of 528 amplified alleles from 16 polymorphic SSR markers were used for the genetic diversity analysis of 25 genotypes of *Dichanthium*. Genetic similarity coefficients ranged from 0.67 to 0.92. Our results demonstrated the transferability of rice SSRs and their potential to evaluate the genetic relationships and comparative genomic studies in marvel grass.

Keywords: *Dichanthium*, SSRs, Transferability

1613 (P-295)

Molecular Characterization of Pop Corn Germplasm Using Microsatellite Markers

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Maize is one of the most important cereals providing energy to millions of people worldwide. Pop corn has emerged as one of the popular snacks item, and recorded ever increasing demand due to increased urbanization and industrialization. Pop corn grains possess hard endosperm and thick pericarp, and upon heating it forms large flakes. The knowledge of diversity in pop corn is useful for their genetic improvement through plant breeding. Pop corn germplasm base is quite narrow in India, and not much information about their genetic relationship is documented. Here we characterized a diverse set of 39 pop corn inbreds of exotic and indigenous origin using 60 microsatellite markers covering all 10 chromosomes. A total of 266 alleles were produced with a mean of 4.43 alleles per locus. Polymorphic information content ranged from 0.09 (*umc1352*) to 0.79 (*bnlg1396*) with a mean of 0.44. Across inbreds, Jaccard's dissimilarity coefficient varied from 0.44-0.93. Principal coordinate analysis also depicted diverse genetic nature of inbred lines. Cluster analysis grouped the inbreds into two major clusters. Cluster-I possessed 7 inbreds, while sub-cluster-IIA, -IIB and -IIC had 16, 13 and 2 inbreds, respectively. One inbred was found to be distinct from all other inbreds. The pop corn inbreds analyzed here thus possessed wide genetic variation, and can serve as valuable genetic resource in pop corn breeding programme.

Keywords: Diversity, Microsatellite Markers, Pop corn

1616 (P-296)

Development of Vitamin A Enriched Quality Protein Maize Germplasm through Introgression of β-carotene Hydroxylase and *Lycopene-ε-cyclase*

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Vitamin A deficiency is widely prevalent in India as staple crops are traditionally deficient in provitamin A (proA) carotenoids to meet dietary requirement. Natural variation for two key genes, *crtRB1* (β-carotene hydroxylase) and *lcyE* (*lycopene-ε-cyclase*) has been reported that cause high proA in maize. Though *crtRB1* gene has been exploited; effects of *lcyE* alone and in combination is yet to be studied in QPM genetic background. Here, favourable allele of both the genes was introgressed from HarvestPlus germplasm into parental lines (HKI161, HKI163; HKI193-1; HKI193-2) of four commercial QPM-hybrids. *lcyE* showed normal segregation in contrast to *crtRB1* gene. ProA varied from 0.64-22.64 µg/g (mean: 5.95 µg/g) in the BC$_2$F$_2$ generation across crosses. Of the nine genotypic classes, homozygous double recessive type recorded highest proA. One way ANOVA has confirmed the enormous effect of *crtRB1* on proA irrespective of genetic constitution of *lcyE* gene. The increase of proA in back cross (BC)-progenies having favourable *lcyE* allele was however low. Sequence comparison of *lcyE* favourable allele among indigenous and exotic inbreds identified nucleotide polymorphisms. Introgression of *crtRB1* and *lcyE* alleles resulted in enhancement of proA to a range of ~13-22 µg/g among the selected BC-progenies of four populations. Background effect of recipient parent genome (RPG) on proA was observed. SSR-based background selection resulted in recovery of ~89-92% RPG. These proA rich QPM genotypes would play significant role in achieving nutritional security of the country.

Keywordss: *CrtRB1*, *LcyE*, Provitamin A

1622 (P-297)

Evaluation and Characterization of Cowpea Genotypes for Fresh Pod Nutritional Quality and Yield Traits

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Cowpea (Vigna unguiculata L. Walp) is an important food legume grown in tropics and sub-tropics for enriching the daily diet with nutrition in rural masses and also served as nutritious fodder for livestock. In India and South East Asia, cowpea is mostly grown for immature tender pods and dry seed both and consumed as important nutritious vegetable as well as cheaper source of protein (20-25%) available in dry seeds which is a double/triple the amount of any cereals. Due to its good protein quality and high nutritional value especially rich in vitamins and minerals, cowpea is often referred to as the poor mans meat. Evaluation and, characterization of genotypes/ germplasm for existing variability with respect to maturity, fresh pod quality, yield traits and resistance to diseases and pests is prerequisite for the development of varieties that can increase the pod yield and productivity. Since, yield is a complex quantitative trait which is influenced by several yield contributing characters controlled by polygenes and environments, therefore, the knowledge about the nature and magnitude of variation in available breeding materials/ germplasm, the association of component traits with yield and their exact contribution through direct and indirect effects are very important for the improvement program. Genetic variability, heritability, genetic advance, correlation and path coefficient for 13 yield contributing traits and 5 biochemical nutritional quality traits were studied in 36 genotypes of cowpea. The study indicated existence of considerable amount of genetic variability for all the characters studied.

Keywords: Cowpea, *Vigna unguiculata*, Genetic variability, Morphological, Biochemical traits, Nutritional quality

1624 (P-298)

Molecular Characterization of *Sugary*- and *Shrunken*- based Germplasm using Microsatellite Markers for Improvement of Kernel Sweetness in Maize

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Sweet corn has emerged as popular choice due to its increased sweetness. Recessive *shrunken2* (*sh2*) on chromosome-3, and *sugary1* (*su1*) on chromosome-4, have been traditionally used in sweet corn cultivar development. Shrunken-based genotypes are called 'super sweet corn', and possessed increased shelf-life. Sugary types have attractive glossy appearance in kernels due to high water-soluble-phytoglycans. The germplasm base of sweet corn is narrow, and limited attention has been paid for its improvement in India. We developed a diverse set of *sh2sh2* and *su1su1* inbreds through introgression breeding. Further, inbreds with novel combination (*sh2sh2/su1su1*) have been developed by crossing shrunken and sugary inbreds. Characterization of these newly developed inbreds is vital to their effective utilization in the breeding programme. A set of 48 diverse sweet corn genotypes comprising of 24 *sh2sh2*, 16 *su1su1* and 8 *su1su1/sh2sh2* inbreds were characterized using microsatellite markers. 56 SSRs produced 213 alleles with an average of 3.8 alleles per locus. The average polymorphism information content was 0.50. Jaccard's dissimilarity was as high as 0.87, and principal coordinate analyses also depicted the diverse nature of inbreds. Cluster analyses grouped the inbreds into three major clusters. Inbreds with similar genotypes viz., *su1su1*-, *sh2sh2*- and *sh2sh2/ su1su1*- were in general together. These newly developed inbreds are valuable genetic resource, and hold immense significance in the sweet corn breeding programme. Large number of experimental crosses has been generated from selected inbreds, and evaluated at three sowing- and harvest-time. Promising hybrids with elevated sweetness, high -grain and -fodder yield have been identified.

Keywords: *Shrunken2, Sugary1,* Sweet corn

1630 (P-299)

Molecular Characterization of *shrunken2* Gene Encoding Large Subunit of *ADP-glucose pyrophosphorylase* for its Utilization in Sweet Corn Breeding

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Conservation of agro-biodiversity assumes great significance in crop improvement programme. Sweet corn has become very popular as a fresh- and processed- vegetable, and generates income and employment. In India, sweet corn germplasm is not well characterized, and information on genetic diversity of underlying *shrunken2* (*sh2*) gene affecting the starch metabolism is not available. We intended to characterize *sh2* alleles in diverse sweet corn germplasm for their utilization in the sweet corn breeding programme. The *sh2* gene is 7320 base pair long with 16 exons, and codes for large sub-unit of ADP-*glucose pyrophosphorylase*. Thirteen overlapping primers with each amplicon spanning 800-1000 bp were designed covering the entire *sh2*-gene. The markers were employed in six each of mutant (*sh2sh2*) and wild type (*Sh2Sh2*) inbreds. Molecular profiling generated 25 alleles with polymorphism information content (PIC) varying from 0.47 to 0.83 with a mean of 0.60. Three markers *viz*., MGU-RC11, MGU-RC4 and MGU-RC12 clearly distinguished the *sh2*-mutants from wild genotypes with PIC values being 0.89, 0.75 and 0.75; respectively. The study detected five unique alleles. Genetic dissimilarity ranged from 0.13 to 1.00 with an average of 0.54. Cluster analyses grouped 12 genotypes into three major clusters with a tendency of mutant and wild type inbreds being in different clusters. Principal coordinate analysis depicted the diverse nature of the genotypes consistent with the cluster analyses. The information on genetic relatedness would help in conservation of diverse and unique sweet corn germplasm. Further, the gene-based polymorphisms for *sh2* would be useful in marker-assisted selection for sweet corn traits.

Keywords: Gene-based marker, Maize, *Shrunken2*

1632 (P-300)

Trait-specific Genetic Resources of Leafy Vegetables for Conservation and Utilization

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Green leafy vegetables constitute a major part of any balanced diet and are good sources of vitamins and micronutrients, apart from containing numerous phyto-chemicals. These are the cheapest of all vegetables within the reach of poor man and receiving attention now days because of their high nutritional value, rapid growth, and adaptability to a wide range of climate and soil conditions. The base collection at ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR) consist ~ 7,000 accessions of different leafy vegetables. This vast gene pool is available to the breeders, but due to large size of the collection and lack of detailed information on unique traits, there has been minimum use of germplasm in breeding programmes to develop new varieties/hybrids. Hence, the trait-specific information from different sources was collected and collated to make a useful compilation for the breeders. The important leafy vegetables conserved in the genebank are *Amaranthus* spp., *Basella* spp., *Trigonella* spp., *Brassica* spp., *Hibiscus* spp., *Portulacca* spp., *Spinacia oleracea*, *Chenopodium album*, *Coriandum sativum Sesbania grandifolia*, *Moringa oleifera, Artiplex hortensis*, *Beta vulgaris* var *bengalensis*, etc. The details of promising accessions as sources of specific traits are documented and conserved in National Genebank (NGB) for utilization in crop improvement programme.

Keywords: Conservation, Leafy vegetables, Traits-specific germplasm, Utilization

1655 (P-301)

Genetic Diversity Patterns in Stem Rot Resistance Genotypes in *Corchorus Capsularis* L.

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Corchorus capsularis L. is a bast fibre crop having industrial applications due to its fine fibre, but the area under this crop is reducing due to poor fibre yield and susceptible to stem rot disease (caused by *Macrophomina phaseolina* (Goid). 76 diverse germplasm lines (indigenous, exotic, mutants and land races) were evaluated in RBD with three replications for fibre yield, stem rot resistance and genetic diversity. Each replication, five randomly selected plants were selected for stem rot inoculation and for fibre yield. Artificial stem inoculation method was used to screen for stem rot resistance and data was recorded eight days after inoculation by measuring the lesion length (in centimetres). CMU-49 (2.47 cm), CMU-9 (2.57 cm) and CIN 109 (3.06 cm) were resistant and CIN-001, CIN-002, CIN-003, CIN-005, CMU-2, CMU-43, CMU-50, CMU-52, CIJ-162 and CIJ-165 were moderately resistant (<5.5cm) but poor fibre yielders, whereas cultivars highly susceptible to stem rot but high fibre yielders. Disease responsive genotypes were used diversity analysis by using jute microsatellite markers. Out of 45 markers screened only 18 markers were reproducible which were used for diversity analysis. Diversity based on molecular markers grouped 76 germplasm lines into seven different clusters (A, B, C, D, E, F and G). Most of the genotypes were group into cluster 'G' and few land races, variety (Padma) and one exotic line (CIJ-151) grouped into A, B, C, D and E clusters. Diverse germplasm lines with disease resistance and high fibre yield will be useful in future resistant breeding programmes.

Keywords: Disease resistance, Diversity analysis, Resistance breeding

1657 (P-302)

Genetic Resources of *Cucumis melo* for Improvement of Nutritional Quality and Resistance to *Fusarium* Wilt

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Muskmelon is highly relished as dessert because of its attractive and unique aromatic musky flavour, sweet taste and being a rich source of vitamins and minerals. Genetic resources of *Cucumis melo* from 3 horticultural groups (*inodorous*, *catnaloupensis* and *momordica*) were augmented and evaluated at IARI, New Delhi for yield, fruit quality (TSS, acidity) and phytonutrients (P, K, Ca, Mg, Mn, Zn, Na, Cu, Fe, Vit. C, total carotenoids). High genetic variation for Fe, total carotenoids, Zn, Cu, Mg, Mn, K, Ca, Na, P and low variation for TSS, Vit. C and acidity were recorded among 60 genotypes. The first variety Pusa Sarda of *C. melo* var. *inodorous* from public sector in India was developed for protected cultivation. Pusa Madhurima for open field has unique lobed fruit shape. Inter varietal hybrid DMH-5 can be grown in open field condition which yield is significantly higher (25.2 t/ha), with TSS 12.8 ^{0}brix and improved post harvest life over Pusa Madhuras. *Fusarium* wilt resistance is a major challenge for melon breeders worldwide. Indian melon germplasm was utilized for development of resistant variety of muskmelon against different diseases in many parts of the world but limited efforts were made to utilize these genetic resources in India for identification of resistance gene and its introgression. Novel source of resistance from Indian snapmelon germplasm DSM-11-6 has been identified. Genetics of resistance has been studied in cross with susceptible parents Kashi Madhu and Hara Madhu and it was found to be a single dominant gene.

Keywords: Inheritance, Introgression, Muskmelon, Phytonutrient

1697 (P-303)

Evaluation of CIMMYTS advanced Wheat Pre Breeding Germplasm for Grain Yield and Yellow Rust Resistance in Punjab

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There is an alarming concern regarding narrow genetic base of modern day commercial cultivars. Breeders usually prefer advance breeding elite lines for developing new cultivars rather exploring and exploiting the rich genetic diversity available in wild relatives of wheat or landraces. To address this issues, a number of initiatives have been undertaken at global level to pursue pre breeding in wheat. A total of 1000 advanced pre breeding linesdeveloped at CIMMYT, Mexico were evaluated for yield under yellow rust epidemic in Punjab Agriculture University and for yield potential under protected conditions at BISA, India. These advanced lines constituted the linked top cross population (LTP) panels which included a series of top cross populations in linked through common elite parents in their pedigree(so called LTPs). Crop was raised using recommended package and practices for the timely sown irrigated environment and no chemical spray was done for controlling the rust at PAU so as to assess yield losses due to stripe rust. Over 87 genotypes yielded better or at par with local commercial checks at BISA whereas 46 genotypes out of these best 87 succumbed to stripe rust at PAU and showed approximately 20-50% yield losses. Only 41 genotypes out of 1000 lines were found to be significantly higher yielding rust resistant lines as compared to the local commercial checks at both locations. High yielding and disease resistant lines were selected and grown at off season location in Himalayas (Keylong, HP) for multiplication of seed. These genotypes will be followed up in varietal pipeline in coming crop season.

Keywords: Prebreeding, Wheat, Stripe Rust, Yield

1798 (P-304)

Evaluation of Native Shrubs and Climbers of Western Himalayas for Ornamental Usages

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The Indian Himalayan region is spread between 21^{O} 57' to 37^{O} 5' North latitude and 72^{O} 40' to 97^{O} 25' East longitude. Based on population features and vegetation elements Indian Himalayas is divided into Western Himalayas, Central Himalaya and the Eastern Himalayas. Himachal Pradesh, situated in the lap of Western Himalayas, is a rich bio-diversity of flora and fauna due to prevailing diverse climate and topography. The forests and valleys harbour a wide variety of plants which can be utilized for various ornamental and landscape purposes. Some plants are so beautiful, that these can be introduced as novelty items in commercial cultivation. But these plants have not been characterized and evaluated in field for commercial usage. In this study exploration surveys were conducted in different four agro-climatic zones/ areas of lower and mid himalayas of Himachal Pradesh during 2004-2008. Potential plants germplasm were selected and identified using herbariums and literature and propagules were collected from different areas for propagation which further conserved ex situ in the experimental farms of Department of Floriculture and Landscape Architecture, UHF, Nauni. Ten potential ornamental shrubs and climbers were propagated and then evaluated under mid hill conditions for various morphological and landscape characters and different ornamental usages e.g; Barleria cristata, Eranthemum pulchellum, Caryopteris bicolour, Reinwardtia indica Rosa brunonii, Hypericum oblongifolium, Jasminum humile, Inula cuspidata, Phlogacanthus pubinervius, Schefflera venulosa. These were characterized for their vegetative and floral traits such as plant form and architecture, plant growth & spread, number of branches, foliage and floral characters, number of flowers per plant, flowering period and possible landscape usages. Majority of the shrubs were found to be utilized as specimen, for shrubbery borders, mass plantations, some of them suitable for shady areas and production of pot plants etc.

Keywords: Himalayas, Evaluation, Native, Wild, Ornamental, Shrubs, Climbers, Landscape characters

1853 (P-305)

Plant Genetic Resources of Arid Legumes are the Sources of Useful Genes for Biotic Stress Resistance and High Yield

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The NBPGR Regional Station Jodhpur, established in 1965, has collected and conserved the germplasm of Arid legumes namely, mothbean (1839 acc.), Cowpea (2166 acc.), mungbean (2911 acc.) and cluster bean (7753 acc.) in its gene bank. This germplasm includes land races, obsolete varieties, wild forms and wild relatives, breeding lines, varieties in cultivation and genetic stocks and has primarily been collected from the hot arid and semi-arid regions of Rajasthan, Gujarat, Haryana and Maharashtra provinces of India. The 470 accessions of cowpea (*Vigna unguiculata* (L) Walp.), the 510 accessions of moth bean (*Vigna aconitifolia* (Jacq.)), and the 435 accessions of mung bean (*Vigna radiata* (L.) and 1103 accessions of cluster bean (*Cyamopsis tetragonoloba* (L)) were evaluated during *summer* and *kharif* seasons of the year 2012. The cultivated moth bean and its related species *Vigna trilobata* withstands drought but susceptible to a number of viral, fungal and bacterial diseases. The experiments got infected naturally by crinkle virus so severely that all accessions were wiped out by the virus, except two namely IC 39786 and IC 39822 which showed strong inbuilt genetic resistance. In the cowpea experiments, insects infestation was abounds and only one accession C-720 exhibited the strong genetic resistance to insects - leaf hopper, semi looper, aphids and jassids. An early maturing single plant (probably spontaneous mutant and named as NBPGR mung-150 was identified and harvested separately. The progenies of this single plant mature in just fifty days only and give high yield. The species of cultivated cluster bean accession namely *Cyamopsis tetragonoloba* (L.) and its wild relative *Cyamopsis senegalensis* and *Cyamopsis serrata* are being conserved by us. The cluster bean accession IC 421811-Sel.3 has determinate growth habit with photo-insensitivity and high yield potential.

Keywords: PGR, Arid Legumes, Useful Genes, Abiotic Stress, High Yield

1892 (P-306)

Evaluation of *Triticum dicoccoides* Germplasm of Wheat for Variation in Grain Length

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Increasing grain size of wheat continues to be a major breeding target because of its effect on yield. It is also one of the main components that distinguish the domesticated species of diploid wild einkorn and tetraploid emmer wheat from its wild ancestors. Due to the difficulty in quantifying this trait the phenotypic and genetic variation of wheat grain morphology is understudied.Grain length (GL) has been found to be one of the important traits being neglected in improving grain weight of wheat as compared to rice. Wild germplasm of wheat found to be excellent source of variation in grain length to be exploited in wheat grain improvement. In the present study 110accession of tetraploid T. diccocoides (AABB) accessions were evaluated for grain length andgrain width (GW)for three consecutive years. Grain length varies from 6.5 mm to 10.4 mm while grain width varies from 1.7mm to 3.6 mm in different accessions indicating wide variation of grain size.Significant positive correlation have been found between GL and GW in about 15-20 accessions with long grain indicating grain length could be contributing factor towards grain weight. Increase of grain length was studied in five accessionswithGL between 9mm-10mm(long grains) and five accessions having GLbetween 7mm-8mm (short grains) at regular intervals after anthesis. GLincreases from 15-18 days post anthesis (DPA) and thereafter decrease when changes to mature dry grain. In long grain accessions maximum gain in length is between 12DPA to 15DPA while in short grains accessions maximum gain of length is between 9DPA to 12DPA

Keywords: Wild emmer wheat, Yield components, Association analysis

1879 (P-307)

Evaluation of Germplasm of Organic Vegetable Crops

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The cultivars that produce higher yields with better quality and nutritional value, and agronomic importance come from diverse plant germplasm. To meet this need organic agriculture research program at Tennessee State University is conducting research trials of vegetable crops in organic management system. This paper presents yield and growth performance evaluation of sixty four cultivars of leafy greens, tomato and sweetpotato in organic management system. The experimental design was randomized block design with three replications in each cultivar. Plants of leafy greens spaced at 1' intervals within the rows and 1.5' between the rows, tomatoes were spaced at 2'within the rows and 3' in rows and sweetpotato slips planted at 1' spacing within rows and 4'between rows. Highest yielders in leafy greens were, 'Buttercrunch' lettuce at 31,756 lb/ac; 'White Russian' Kale at 10,956 lb/ac; 'Morris heading' Collard at 9,068 lb/ac; 'Rainbow chard' Swiss chard at 13,690 lb/ac; 'Love lies bleeding' Amaranth at 4,334 lb/ac and 'Green wave' Mustard green at 16,961 lb/ac. The results of the tomato cultivar yields ranged from a high of 25425lb/ac for hybrid Arbason F1 to a low of 3,141 lbs/ac for Hillbilly. In case of sweetpotato, higher total yields were measured in Carolina Ruby (34,790 lb/ac) of sweetpotato which had significantly greater weight than all cultivars tested. Continuing evaluation of diverse food crops and germplasm is critical to meeting future production challenges of these crops due to key source of income for farmers.

Keywords: Cultivar trials, Genetic diversity, Organic crop production, Tennessee, Vegetables

1884 (P-308)

Introgression of Cotton Leaf Curl Disease Resistance from *Gossypium armourianum* into *G. hirsutum*

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Gossypium hirsutum is the dominating species covering greater than 90% of cotton area worldwide. Cotton leaf curl disease (CLCuD) is the most serious menace affecting American cotton not only in the North Western Indian cotton growing states of Punjab, Haryana and Rajasthan but also Pakistan. More than 90% losses in seed cotton yield due to CLCuD have been reported in the susceptible upland cotton varieties. The disease causing virus complex is transmitted through whitefly. Great strides have been made for the development of American cotton cultivars resistant to CLCuD, however, continuous appearance of recombinant virus strains has rendered American cotton germplasm susceptible. Recently, we identified two novel sources of CLCuD resistance including a related non-progenitor wild cotton species *G. armourianum* (DD). An interspecific hybrid between *G. hirsutum* x *G. armourianum* was developed. A total of 15,898 flowers of this male-sterile hybrid were pollinated with *G. hirsutum* as the male parent resulting into the setting of five BC_1F_1 seeds at the rate of 0.031%. Four seeds germinated to produce BC_1F_1 plants. The backcross derivatives were screened for CLCuD at the phenotypic and molecular levels. Virus specific primers were used to amplify DNA from the samples. Two of the four BC_1F_1 plants were observed to be free from the disease and are being used in the backcrossing programme. These introgressed derivatives will play a crucial role in the development of CLCuD resistant American cotton cultivars.

Keywords: Wide hybridization, Gemini virus, Resistance breeding

1885 (P-309)

Development of Interspecific *Momordica* Species Hybrid: A Step towards Introgression of Root Knot Nematode Resistance

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Bitter gourd (*Momordica charantia*) is an important vegetable crop. This species bears edible fruits esteemed for their taste and medicinal properties. Root knot nematode is a serious threat to successful cultivation of bitter gourd and is reported to cause 38 to 48.2 % yield losses. Genetic resistance is the most viable option for the management of nematodes. Hence, identification of sources of nematode resistance is an important research activity at PAU and has led to the identification of several root knot nematode resistance lines of *Momordica balsamina* (varh karela). However, direct crosses between these species were not successful as fruit retention was very low (< 1%) and also the two F_1 seeds obtained resulted into albino seedlings, which later on died. In other cases, seeds were either hollow or contained shriveled embryos with papery cotyledons and did not germinate. Therefore, 19-21 day old embryos from *M. charantia* Acc. PAUBG-56 x *M. balsamina* Acc. MB-3 crosses were cultured on MS medium containing malt extract. Six interspecific *Momordica* species plants were produced at a frequency of 0.43%. However, all the plants were observed to be albino and eventually died. Bittergourd specific SSR markers were used to confirm the hybridity of interspecific *Momordica* species hybrids. These preliminary results indicate the presence of post-fertilization barrier(s) for the development of F_1 hybrid between these *Momordica* species.

Keywords: Wide hybridization, Embryo rescue, Resistance breeding

1928 (P-310)

G. Hirsutum Treasure at Surat

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Surat centre is the Main Cotton Research Station of Gujarat and has historical and so many first ever achievements. The extra ordinary achievement of Surat due to robust gene pool of *G.hirsutum, G.herbaceum* and *G.arboreum*. At present Surat have about 600 germplasm lines of *G.hirsutum*, more than 450 of *G.herbaceum* and 260 of *G.arboreum*. This paper will narrate only for *G.hirsutum* germplasm. Out of 600 germplasm lines, 141 had ability of 1500-2000 kg/ha seed cotton yield, 87 possess 2000-2500 kg/ha seed cotton yield and 33 had more than 2500 kg/ha seed cotton yield. The range of seed cotton yield varied from 349 to 4063 kg/ha. The genotype 9-9 had recorded highest seed cotton yield *i.e.* 4063 kg/ha. Considering the boll weight, nine lines exhibited more than 5.0 g boll weight, whereas EC-177-GRS-6159-134 and G-S-156 had recorded 5.5 g boll weight. With respect to seed index, 90 lines had noticed with more than 9.0 g seed index. The range of seed index was 5.0 to 11.0 g. Germplasm lines BC-68-1146-4-6-793, G-111-2 and Girja exhibited higher seed index (11.0 g).For ginning percentage, 74 lines possessed more than 40.0% ginning percentage. The range of ginning percentage was 27.2 to 43.7 % (EC-11-757(AC-134)). Looking to fibre length, 108 lines belong to medium, 239 belong to medium long and 149 lines belong to long staple fibre length. Variation in 2.5% span length was 21.5 to 32.7 mm (Acala-63-69). The bundle strength of gene pool suggested that the germplasm lines had 14.1 to 26.7 g/tex. Twelve lines had poor, 339 lines had low, 124 lines had average, 11 lines had good and two lines had excellence in fibre strength.

Keywords: *G. hirsutum*, Germplasm

Technical Session 4-B :

Science-led Innovation

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PGR and Genomics

509 (O-34)

Population Genetic Structure and Phylogenetic Relationships in Lentil Species as Revealed by Morphological and SSR Markers

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Genetic structure and relationships among 130 lentil accessions belonging to six taxa were studied to identify diverse and promising accessions for future breeding programmes and to analyze genetic relationships. Seven morphological traits and thirty-one polymorphic Simple Sequence Repeat (SSR) primers were used for this purpose. Results: Morphological traits grouped lentil accessions into five main clusters and appeared highly important in detecting variation across studied lentil taxa. At molecular level, 31 SSR primers amplified 139 polymorphic alleles in a range of 2-10 with an average of 4.48 alleles. The size of amplified alleles varied from 50 to 650 bp. Polymorphism Information Content (PIC) ranged from 0.02 to 0.85 with an average of 0.46. Neighbor-Joining tree grouped accessions and taxa broadly according to their taxonomic ranks except *L. culinaris* ssp. *Odemensis* which deviated from its group. Analysis of Molecular Variance (AMOVA) revealed that a major portion (82.0%) of genetic variance resided within species, while only 18% resided among species. Bayesian model-based STRUCTURE analysis assigned genotypes into five clusters and showed some admixture within individuals. Conclusion: The study revealed that Lens culinaris ssp. culinaris accessions of Ethiopian origin clustered separately, indicating its distinct lineage. Among the analyzed lentil species, *L. culinaris* ssp. *odemensis* seemed to have conserved

Keywords: Lentil, SSR markers, Structure, Phylogenetic relationships

1166 (O-35)

SNP Marker Based Genetic Diversity Study in Rice Germplasm of Arunachal Pradesh

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Rice genetic resource is the primary source for rice breeding and makes a concrete contribution to global wealth creation and food security. India is one of the centers of origin for rice and the nutritional security of the North-eastern states of India predominantly depends on rice. The NE region especially Arunachal Pradesh is considered to be one of the hot pockets of rice genetic resources in the world and also has diverse rice growing conditions as compared to other parts of the country. Genetic diversity of 662 rice accessions originating from the state of Arunachal Pradesh was assessed using 36 single nucleotide polymorphism (SNP) markers distributed across all 12 chromosome of rice genome. Polymorphic Information content (PIC) of SNP markers ranged from 0.006 to 0.375 and major allele frequency ranged from 0.51 to 0.99. Similarly, heterozygosity and gene diversity ranged from 0.003 to 0.162 and 0.006 to 0.49, respectively. The genetic relatedness was inferred using un- rooted Neighbor joining tree, which grouped all the genotypes in to three major clusters. AMOVA analysis showed that, among population level 21% and among individual level 58% diversity was present. Population structure from K=1 to K=20 were tested and Δk was found maximum at K=3. Principal Coordinate Analysis (PCoA) showed that accessions were getting distributed into three major groups which support the grouping obtained with population structure and un- rooted Neighbor joining tree.

Keywords: Rice, SNP markers, Genetic diversity

1783 (O-36)

Molecular Diversity in Pearl Millet Association Mapping Panel Revealed by Genomic and EST SSR Markers

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Pearl millet is fourth most important crop grown for food and fodder in arid and semi-arid regions of Asia and Africa. It is endowed with more Fe and Zn content in grains and can offer a better solution to nutritional security. Understanding genetic diversity in pearl millet for micronutrients is useful for selecting genotypes with high iron and zinc content in pearl millet breeding. The present study was undertaken with an association mapping panel covering 130 diverse pearl millet genotypes which were genotyped with 84 EST and 30 genomic polymorphic SSR markers covering the entire genome. A total of 296 alleles (212 from EST and 84 from genomic SSRs) were detected with 2.65 average allele number per locus (2.52 for EST and 2.8 for genomic SSRs). Genomic SSRs exhibited higher polymorphism and gene diversity compared to EST SSRs. Number of alleles ranged from 2 to 5(PSMP 2081) in genomic SSR, whereas, the range is 2 to 4 (IPES 0126, IPES 0200 and PGIRD 50) for EST-SSR. 130 genotypes were grouped into three clusters based on DARwin's neighbor-joining tree with distance dissimilarity matrix. All the maintainers except 5540B grouped into one cluster and restorers grouped into two different clusters. Fe and Zn rich lines are distributed in all the clusters. Since, grain Fe and Zn content are governed by additive gene action, genetically diverse maintainers and restorers which are rich in grain micronutrient can be used for further population improvement or hybrid development.

Keywords: Diversity, Fe, Pearl millet, SSR, Zn

328 (P-311)

Banana Genetic Resources of Northeast India and their Sustainable Production

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Northeast region (NER) of India harbours a high diversity of banana (*Musa* spp.) both in wild as well in the cultivated stands. Being located in the South East Asian region where banana originated, several unique and novel genetic resources are abundantly found however very few studies on the proper characterization have been reported. The objective of the study is to identify the existing banana genetic resources of the region, elucidation of their genomic groups and establishment of *in vitro* mass production of the local Cavendish banana A total of 38 banana cultivars have been identified and characterised into AA, BB, AB, AAA, ABB and ABBB groups. Efficient *in vitro* regeneration of the local Cavendish banana (AAA group) has been achieved using male flower as the explant. The knowledge generated from the study could be utilized for proper genetic identification of potential germplasm and large scale production of quality banana planting materials.

Keywords: Banana, Northeast India, Genetic resource, *In vitro* propagation

342 (P-312)

Identification of Medicinal Sedges of Cyperus Species using Rbcl Genetic Marker

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Sedges belonging to the genus *Cyperus* and family Cyperaceae are the most invasive weeds known, having spread out to a worldwide distribution in tropical and temperate regions. *Cyperus* spp. is well known for medicinal uses. It possess pharmacologically active substances such as Î±-cyperone, Î²-selinene, cyperene, cyperotundone, kobusone, isokobusone etc. To diagnose adulteration in medicinal formulations, authentication of particular medicinal plant using DNA barcodes overcome these problems. Consortium for the Barcode of Life (CBOL) Plant Working Group (2009) has recommended the core 2-locus combination of rbcL+matK as the plant barcode in order to provide a universal framework for the routine use. In the present study, a total of 27 samples of Cyperus species collected from places located in seven different states of India were subjected to morphological and molecular analysis. The data generated through molecular analysis were further used for phylogenetic analyses. The plant samples were belonging to nine different species under *Cyperus* genus. Among those, one plant each found unique to the species *Cyperus echinatus*, *C. tenuculmis* and *C. odoratus*, respectively. The Rubisco Large subunit (rbcL) barcodes varied in length from 300 to 347 bases. The barcodes specific to *C. rotundus* and *C. esculentus* were generated. The rbcL genetic marker can be used as DNA barcode for the identification of sedges having medicinal value. The rbcL marker also generated robust data to group 27 individuals of present study in to nine distinct species.

Keywords: DNA barcoding, *Cyperus* species, Rbcl genetic marker

387 (P-313)

Analysis of Genetic Variation of Some Non-Commercial Cultivars of *Musa* L. from Assam, India using ISSR Makers

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The genus *Musa* L. comprises of the cultivated bananas which are consumed by human being and animals as nutritious fruit since the dawn of civilization. The genus is found mainly in the tropical humid forests and plains and are considered to be originated from Southeast Asia. Adjacent to the southeast Asia, the agroclimatic condition of Assam in the northeastern part of India favors the growth of different varieties of *Musa*. Most of the cultivars are domesticated since long and for long time practice of hybridization at inter and intraspecific level by cultivators resulted in the occurrence of a number of cultivars in this region. Immense utilization of the fruits as nutritious food is prevalent among the localities of Assam. Also the people use the plant parts in their religious ceremonies or even sometimes the whole plant is seen to be used as a sign of good will. A study was undertaken to analyze the molecular diversity of 13 cultivars of *Musa* which are locally found and domesticated but have limited commercial importance in Assam, Northeast India based on Inter Simple Sequence Repeats (ISSR) markers. ISSR fingerprinting of these *Musa* genotypes was carried out by seven primers of ISSRs. ISSR primers produced total 62 amplified bands out of which 56 bands showed polymorphism. The genetic similarity index was prepared using Jaccard's similarity coefficient and the range of genetic similarity was from 0.28-0.77 with an average of 0.51.

Keywords: *Musa* cultivars, Non-commercial, ISSR markers, Assam

497 (P-314)

Cloning and Characterization a Gene Encoding NADP Dependent Malic Enzyme from Field Pea and its Possible Role in Resistance to Root-Knot Nematode *Meloidogyne* spp

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Among various productivity constraints in field pea (*Pisum sativum* L.*)*, root-knot nematode (RKN; *Meloidogyne* spp.) is a major constraint and is reported to cause upto 15% yield losses. The current study was undertaken to evaluate resistance of different field pea genotypes to RKN under pot culture conditions. The RKN inoculum level was 1 juveniles/cc soil and the genotypes were evaluated after 3 months of sowing based on gall index 1-5 scale. No genotype was found highly resistant or resistant against *M. javanica*. However, moderate resistant reaction was observed in a few genotypes viz; IPFD 11-10, IPFD 99-13, NDP 1200, RFP 2004, KPF 10-28, RFP 72, HFP 8909, HFP 715, PANT 244, KPFD 101, PANT 243, RFP 2009-3, KFD 1204, IPFD 13-2. The susceptible reaction was observed in IPFD 13-14, IPFD 12-17, PANT 42, IPFD 11-5, IPFD 13-4, IPF 2-17, IPFD 99-25 IPFD 12-8, IPFD 12-2, IPF 11-15 IPF 13-13, NDP 12-102 PANT 195, IPFD 5-19 IPFD 1-10 and IC 19002 genotypes. The NADP-dependent malic enzyme (ME) is one of the major genes conferring resistance to RKN in legumes. In present study partial sequence of putative NADP dependent Malic enzyme gene has been cloned and characterized. Thirty field pea genotypes showing moderate resistance/susceptible reaction were screened for *PsME* using PCR. Variations in PsME gene sequence and resistance/susceptibility reaction of pea genotypes have been discussed. Association of sequence variations in *PsME* and resistance/susceptibility reaction in pea would help in developing gene based marker for screening pea genotypes for root knot nematode resistance.

Keywords: Field pea, Malic acid enzyme, *Meloidogyne javanica*, Resistance

537 (P-315)

Population Structure and Adaptive Variability of Selected Indigenous Aromatic Rice Landraces from India

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The Indian sub-continent is home to a large number of indigenous aromatic landraces, which may serve as valuable genetic resources for future rice improvement to meet the ever growing demand for quality rice. In the era of high yielding modern varieties there is an urgent need to develop conservation strategies to protect the valuable aromatic landraces. Understanding the population structure and adaptive variability of landraces will be useful in this regard. To explore the genetic structure and diversity 256 individuals of 8 aromatic landraces were genotyped using 17 SSR markers. Sixty-nine alleles were recorded and none of them found common to all landraces. Twenty-six alleles were found unique to an individual landrace. Kala Joha from Assam was most diverse in terms of effective number of alleles, expected heterozygosity and Shannon's information index. Analysis of molecular variance (AMOVA) revealed maximum variation of 39.36% present among populations within groups followed by within groups (30.52%) and rest (30.12%) within populations. The adaptive variations among populations for various morphological traits revealed significant. Two way Mantel test showed that non-significant correlation (r=0.39) existed between phenotypic distance and genetic distance.

Keywords: Aromatic rice, Adaptive variations, Genetic diversity Population structure

661 (P-316)

Enrichment and Utilizations of Genomic Resources in Jute and Allied Fibre Crops

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Jute and Allied Fibres (JAF) are agricultural crops with a profitable commercial importance in India, Bangladesh and China. Jute, kenaf, ramie, flax and sunnhemp are included in the JAF crop group, which produces lingo-cellulosic composite bast (stem) fibre that is consumed in coarse textile industries for making yarn, sack, hessian and carpet backing cloth. One of the major interventions in up-liftment of JAF, is its genetic enhancement for superior quality fibres to meet diversified use requirement and profit maximization. Genomic resources in flax are available through the whole genome sequence, transcriptome and sizeable molecular markers, but these are limited in other JAF crops, such as in jute, kenaf, ramie and sunnhemp. The recent surge in efforts to enrich genomic resources in jute, kenaf, and ramie produced SNP markers and transcriptomic resources. We report here development of 2079 non-redundant EST-SSR markers, 6037 Potential Intron linked Polymorphic (PIP) markers and 101 long non-coding RNA (lncRNA) derived SSR markers (from 4147 lncRNA sequences), which may significantly aid in breeding programs. Among these markers, EST-SSR markers were integrated into a user-friendly web-database (jutemarkerdb.icar.org.in) for easy data accessibility. In flax 506 transcription factor derived EST-SSR and 75 lncRNA-SSR markers were developed and validated. We also developed a *de novo* assembly of RNA-seq data from Sunnhemp inflorescence resulting into 41727 unigenes and 9067 EST-SSR primers. The above findings are expected to produce a quantum enrichment in the genomic resources of JAFs and is expected to aid in efficient breeding programs.

Keywords: Jute and Allied fibres, Genomic resources, Molecular markers

678 (P-317)

Microsatellite Markers Based Hybridity Test and Evaluation of Opaque2 Introgressed Maize (*Zea Mays* L.) Hybrids For Quantitative and Quality Traits

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The genuineness of a hybrid is one of the most important characteristics of good quality seed. A total of 45 hybrids and their parents were analyzed using twelve microsatellite simple sequence repeat (SSR) markers. The hybrids could be clearly identified by using the SSR loci umc1066, umc2263, umc1030 and umc 2317 based on the banding pattern resolved on agarose gel (3%) and morphological markers. The results indicated that the hybrids showed significant variability for most of the traits studied. Among the F1 hybrids SC-8 yielded the highest grain yield per plant (170.77 g) followed by SC-30 (170.41 g), SC-24 (168.69 g) and SC-20 (161.96 g). Two F1 hybrids (SC-13 and SC-19) had high tryptophan content among all the hybrids. The range of phenotypic coefficient of variation was observed from 2.56 to 30.63 % and GCV ranged from 2.35 to 30.12 %. Heritability in broad sense was high (>80%) for days to 50% pollen shed, silking, 75% maturity, plant height, cob placement height, grain yield per plant, grains per row, protein content and tryptophan content. Grain yield per plant was found to be significant positively associated with plant height, cob placement height, 100-seed weight, cob length, cob girth, grains per row and protein content at genotypic level. The component characters viz., plant height, 100-seed weight, grains per row with grain yield per plant showed positive and significant correlation (0.6647, 0.8182 and 0.8314) and also exhibited positive and strong direct effects (0.3244, 1.0809 and 0.9167) on grain yield per plant. These identified potential genotypes can be further utilized in the maize breeding program.

Keywords: QPM, SSR, Hybridity

728 (P-318)

Screening and Validation of *Ty-1*, *Ty-3* Linked Markers in *Solanum Chilense* Accessions for Resistance to Tomato Leaf Curl Virus

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Tomato leaf curl virus (ToLCV) is the most destructive disease of tomato causing fruit yield losses up to 90-100%. Most of the cutivated tomato varieties/cultivars are susceptible to ToLCV. The ToLCV resistance genes have been introgressed into cultivated tomato varieties mostly from its two wild relatives *Solanum chilense* and *S. habrochaites*. There are six resistance genes *Ty-1*, *Ty-2, Ty-3*, *Ty-4*, *ty-5* and *Ty-6* which are being practically utilized in breeding programmes. Seven *S.chilense* accessions (LA 1938, LA2773, LA2748, LA 1930, LA2879, LA2748, LA2778, LA1932, LA1958) were screened under field conditions to find a new source of resistance. All the accessions were found resistant to ToLCNDV. *Ty-1*, *Ty-1/Ty-3* linked five each of sequence based markers (WU_M17, WUR_M25, WU_M27, WU_M29, WU_M31) and five SCAR markers (P6-25-F2, FLUW-25F, UF_TY3-P19, Ualty3a, Ualty3b) were validated with all the accessions for identification of novel allels for ToLCV resistance breeding programme. The markers WU_M29, P6-25-F2, FLUW-25F, UF_TY3-P19, Ualty3a, Ualty3b were polymorphic among the accessions. In accessions LA2879 and LA1969, marker P6-25-F2 showed that two alleles of *Ty-1* and *Ty-3* were present as compared to presence of source of single gene *Ty-1*/*Ty-3* in other accessions. The marker and field screening results showed that accessions LA1938, LA2778 and LA2879 carries novel alleles resistant to ToLCNDV, potential source for introgression of ToLCNDV which can serve as resistant genes into commercial tomato varieties.

Keywords: Tomato Leaf Curl Virus, *Solanum chilense*, Molecular markers, Resistance breeding

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930 (P-319)

Population Structure and Genetic Diversity among Named Wheat Landraces using Microsatellite (SSR) Markers

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Platform for improvement of crop plants is largely setup by the genetic variability studies. The North Western Himalayan region is rich in wheat landraces, which may serve as valuable genetic resources for future wheat improvement to meet the ever growing demand of climate change. In the era of high yielding modern varieties there is an urgent need to develop conservation strategies to protect the valuable landraces. Understanding the population structure and adaptive variability of landraces will be useful in this regard. This will also help in studying reliability/ consistency in farmer naming of wheat landraces. For assessment of genetic diversity and measuring population genetic parameters 24 individual of each and every eight important named landraces from Garhwal and Kumaon divisions of Uttarakhand state were genotyped by using 16 polymorphic SSR primer pairs. A total of 52 alleles were identified in all landrace populations with an average of 3.25 alleles per loci. A total of 14 rare alleles occurring with frequency lesser than 0.05, were recorded in landraces from Kumaon and Garhwal division of Uttarakhand with maximum in Mundari landrace while Lal Mundiya with no rare allele. The highest mean value of Shannon's information index, observed number of allele and expected heterozygosity were recorded in Safed Mundia, which belongs to Garhwal division. Analysis of molecular variance (AMOVA) revealed that maximum variation was contributed by among populations (71.38%) followed by within populations (34.47%). Among groups there was negative value (-5.86%).

Keywords: Wheat landrace, Population structure, Genetic diversity, Safed mundia

1158 (P-320)

Development, Identification and Validation of CAPS Marker for SHELL Trait Governing Dura, Pisifera and Tenera Fruit Forms in Oil Palm

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Exploiting oil palm biodiversity for identification of suitable molecular markers using advanced science and technological options paves way for oil palm crop improvement. Identification of desired fruit type is a major asset to the breeders for applications in breeding, seed certification and to reduce time, space and money spent on identification of fruit form. In the present study, we developed Sh gene specific primer pairs and bulk segregant analysis was done using 300 genomic and 8 genic SSR markers. We identified one cleaved amplified polymorphic site (CAPS) marker for oil palm fruit type which produced two alleles (280 and 250bp) in dura, three alleles in tenera (550, 280, and 250bp) and one allele in pisifera genotypes (550bp). The shell allele sequencing results showed that two snips were present, of which snip2 contributed for variation of fruit forms. The nucleotide 'A' was present in only dura genotypes, where as 'T' was present only in pisifera genotypes, which in turn led to the change of amino acid lysine to aspargine. The identified CAPS marker was validated on 300 dura, 25 pisifera and 80 tenera genotypes, 80 dura/ pisifera cross progenies and 60 lines of tenera/ tenera cross progeny. The identified CAPS marker facilitates selection and timely distribution of desirable high yielding tenera sprouts to the farmers instead of waiting for 4-5 years. This saves a lot of land, time and money which will be a major breakthrough to the oil palm community.

Keywords: CAPS marker, Marker assisted selection, Oil palm, Shell gene

1170 (P-321)

Genetic Diversity Study in *Andrographis Paniculata* using Scot and CBDP Markers

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India, being a major mega diversity center, has immense biological wealth marked by species, their genetic diversity and remarkable ecosystem. This rich biological diversity is matched equally by rich cultural diversity and health traditions. Most of the recorded angiospermic plants from India are reportedly used for medicinal purposes. *Andrographis paniculata* is a popular antipyretic and hepatoprotective drug, used as traditional medicine in India. For effective conservation and optimum genetic amelioration, gene targeted molecular markers, i.e. Start codon targeted (SCoT) and CAAT box derived polymorphic (CBDP) markers were used to assess genetic variability among thirty nine accessions of *Andrographis* collected from different agro-ecological regions of India. The average proportion of polymorphic loci across twenty-two SCoT and nineteen CBDP primers were 74% and 82%, respectively. Polymorphic information content (PIC) estimated for SCoT and CBDP primers ranged from 0.09 to 0.48 and 0.30 to 0.46, with an average value of 0.34 and 0.41 per primer. The resolving power for SCoT and CBDP primers ranged from 2.36 to 10.54 and 1.39 to 13.15 per primer, respectively. Unweighted pair group method with arithmetic mean (UPGMA) based grouping of 39 accessions using two marker system did not show any correlation with their agro-ecological regions. Population structure based analysis with SCoT and CBDP marker data divided total 39 accessions into four and three populations, respectively.

Keywords: *Andrographis,* CBDP markers, Genetic diversity, Population structure, SCoT markers

1245 (P-322)

Identification of SSR Markers Linked to Short Stature of Oil Palm (*Elaeis guineensis* Jacq.)

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Short stature of oil palm plant facilitates easy harvesting and extends economic yield period of the palm by 5 years or so. Thus, identification of molecular markers for plant height is important trait to introgress reduced vertical growth trait into high yielding genotypes. Hence, in the present study we selected eight each of dwarf, tall and dwarf with good yield palms for bulk segregant analysis. The genomic DNA of these selected palms were isolated and bulked for molecular analysis. With an aim to identify the molecular markers, ten EST based SSR markers were designed from oil palm asparagine synthase-related sequences, and coco nut AGAMOUS-like sequences. The BSA analysis was done with 400 SSR markers among three bulks DNA. A total of 50 SSR markers were able to find polymorphism between the bulks of dwarf, tall and dwarf with good yield. However, only two SSR markers (mEgCIR3328 and mEgCIR0059) were able to clearly differentiate the dwarf and dwarf with good yield individual genotypes from tall genotypes. The UPGMA dendrogram grouped the selected genotypes into three major groups according to the stature of oil palm genotypes. Cluster A consisted of dwarf genotypes, B cluster comprised of dwarf with good yield genotypes, whereas cluster C had tall genotypes. The identified markers also showed differentiation between the tall and dwarf progeny obtained from the dwarf/ dwarf cross. Hence, fine mapping of major QTLs is required for further validation and for marker assisted selection to differentiate the dwarf with tall genotypes.

Keywords: Bulk segregant analysis, Oil palm, SSR markers, Short stature

1314 (P-323)

Development of A and B Genome Specific Markers in Banana

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Banana has originated from two important ancestors, *Musa acuminate* (AA) and *M. balbisiana* (BB). The combination of these ancestors led to a great diversity belonging to varied genomic groups (AAA, AB, AAB, ABB, BB etc). The accuracy on genomic constitution of banana genotypes based on taxonomic score cards is limited as these morphological characters are highly influenced by environment, age and developmental stage of the plants. Thus assigning the genomic constitution based on taxonomic score card in complement with the genome specific markers will be the accurate one. The genome specific markers will also facilitate in the banana breeding program to confirm the integration of B and/or A genome in the hybrids developed between two different genomes (AA and BB). Thus in the present study efforts were taken to develop the genome specific marker using various molecular markers. As a result, two markers namely SSR 4 (obtained from banana EST-SSR marker), chitinase (obtained from SSH clones) have been developed as it could clearly differentiate A and B genome. These markers were validated in the progenies of Karpuravalli (ABB) x Pisang Jajee (AA) and confirmed through morpho-taxonomic characterization and flowcytometry analysis. These two markers have an advantage over existing genome specific marker (ITS marker) as the polymorphism could be detected with a single step (PCR) whereas ITS marker needs two steps (PCR +digestion). These genome specific marker facilitate the banana germplasm curator and breeder for assigning the genomic status of newly collected/unknown germplasm accessions and selecting the desirable progenies with respect to their genomic status at seedling stage itself.

Keywords: Banana Genome, Breeding, ITS marker, SSR marker

1322 (P-324)

DNA Profiling of Plantain Clones using ISSR Markers

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Banana has become the most important food fruit crop, which is available all through the year and remains to be the potential energy source to mankind and financial source to the farming community. Presently, the tissue culture multiplication has given rise to a large number of elite clones. Such clones are morphologically very similar at the early stages and farmers find it difficult to identify the same. The morphological similarity also poses problem to the tissue culture companies in the correct identification, multiplication and supply of the required clone to the farming community. In southern India, farmers are quite often disappointed by supply of Nendran in the name of Swarnamukhi or Quintal Nendran which are superior in terms of yield. This necessitated the development of DNA profiles for all plantain clones. A total of eleven ISSR primers were used to detect DNA polymorphism among sixteen clones of plantain. A total of 223 fragments were amplified whose size ranged from 200 bp to 2700 bp in size. 93.79% polymorphism was observed in the present study. The study was also able to generate clone specific bands for all the plantain clones tested except for Nijokhome, False Horn plantain and Mysore Eathen. They could be converted into SCAR markers for use in clonal identification. The specific markers would also serve as reference for use in genetic fidelity testing of the plantain clones and thereby help in overcoming the limitations faced by the companies and farmers.

Keywords: DNA fingerprints, Genetic fidelity, ISSR markers, Plantains

1332 (P-325)

Development of Simple Sequence Repeat (SSR) Markers in Kodo Millet (*Paspalum scrobiculatum* L.)

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Kodo millet (*Paspalum scrobiculatum var. scrobiculatum*) also known as rice grass, is one of the nutritional security crops due to its high- quality protein, high anti-oxidant activity and excellent fiber content. The crop is very important in Indian context as it is the only country where it is primarily cultivated as a grain whereas in Africa, it is grown wild as *Paspalum scrobiculatum var. commersonii*. The crop is also known for its drought tolerance and can be grown in moisture deficient lands. Kodo millet is morphologically highly variable and molecular marker based studies would play an important role in evaluating genetic diversity useful for marker-assisted selection based breeding for kodo millet improvement. Simple sequence repeat (SSR) markers are the markers of choice due to their high level of potential polymorphism, locus-specificity, multi-allelic, co-dominance, high abundance, wide genome coverage and reproducibility. In the present study out of twenty eight, fourteen SSR markers were developed in *Paspalum scrobiculatum* through cross-species transferability from *Paspalum notatum* and *Paspalum atratum* species of the genus *Paspalum*. The markers developed were validated in ninety six accessions of kodo millet from twelve different regions (Andhra Pradesh, Karnataka, Kerala, Tamil Nadu, Bihar, Chhattisgarh, Gujarat, Madhya Pradesh, Maharashtra, Odisha, Uttar Pradesh and West Bengal) of India. Present study is the first report of SSR marker development in *Paspalum scrobiculatum* and the markers developed would serve as potential markers to study this crop at molecular level.

Keywords: Kodo millet, Marker development

1345 (P-326)

Genetic Diversity Analysis of *Momordica subangulata* subsp. *renigera* (Teasel Gourd) Collections from Eastern India Using ISSR Markers

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Teasel gourd is a semi-domesticated vegetable crop of eastern and north-eastern India. It is the second most important vegetable of genus *Momordica* grown for its fruits. Although sufficient diversity exists in teasel gourd, it has never been estimated using molecular markers. In the present study one hundred anchored ISSR primers were screened for identification of primers useful for amplification in teasel gourd. Fifty primers were identified and these were used for diversity analysis among seventy two accessions collected from the states of Orissa (16), Tripura (30), Mizoram (19) and Assam (7). A total of 504 markers were amplified, of which 464 markers (92.1%) were polymorphic. An average of 10.1 markers were amplified per primer with the primer UBC869 and UBC826 amplifying five (minimum) and sixteen (maximum) bands respectively. The primer UBC888 had the maximum resolving power while the primer UBC844 had the lowest resolving power. The average heterozygosity detected was 0.28. As observed by the Nei's gene diversity index, the accessions from Tripura were most diverse followed by those from Mizoram. Maximum number of markers detected polymorphism among the accessions from Tripura (83%) followed by Mizoram (76.8%), Orissa (66.2%) and Assam (60%). The present study indicates that ISSR markers detect moderate genetic diversity in the accessions of teasel gourd collected from Tripura, Mizoram, Orissa and Assam.

Keywords: Diversity analysis, Polymorphism, Semi-domesticated

1375 (P-327)

Diversity of *Luffa* Species in India: Prospects for Future Utilization

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The genus *Luffa* (Miller) is one of the most important and widely adapted vegetable of the humid tropics with several health benefits. There are nine species of Luffa, of which seven are found in India. Among them the edible species are— *Luffa acutangula*, *Luffa cylindrica* and *Luffa hermaphrodita*. These species are cross compatible which makes them amenable to traits transferability for genetic enhancement of *Luffa* species utilizing the prevailing diversity. *Luffa hermaphrodita* (locally known as Satputia) is characterized by short viny growth, earliness and most importantly, bears small smooth fruits in clusters. These traits can be utilized to enhance the genetic architecture of *Luffa acutangula* and *Luffa cylindrica* as they are commercially cultivated. To assess the genetic diversity in *Luffa* species, both phenotypic and genotypic approaches have been employed. Morphological characteristics of 40 *Luffa* accessions were recorded for both qualitative and quantitative traits during spring summer season, 2016. For genotypic analysis, PCR based markers i.e. ISSR and EST –SSR (developed using NGS approach from the sponge gourd leaf transcriptome) were used for molecular diversity study. Of the 191 EST- based SSR markers of sponge gourd tested across the accessions, 132 EST showed band amplification indicating likelihood of markers transferability across the species. The 20 ISSR primers tested produced clear and polymorphic bands in most of the accessions. The genotypes showing maximum diversity will be utilized for heterosis breeding to generate transgressive segregants and improved cultivars in the future.

Keywords: *Luffa*, Satputia, Transcriptomic SSRs, Genetic diversity

1423 (P-328)

Genetic Diversity Assessment in White Clover (*Trifolium repens* L.) Accessions using SSR Markers

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White clover (*Trifolium repens* L.) is an allopolyploid (2n = 4x = 32) and outcrossing species in the bean family Fabaceae and is used as a cool season forage legume worldwide. Many improvements have been achieved in white clover using conventional breeding approach. However, supplementing these conventional approaches with molecular markers can significantly accelerate breeding and selection efficiency. In the present study, genetic diversity analysis in 72 white clover accessions was carried out using 15 microsatellite markers. Based on this preliminary study, the average similarity among all the accessions was found to be 68%. The similarity values ranged from 38 to 97%. Cluster analysis separated the single accession of *Trifolium alexandrinum,* included as an outlier*,* as the most distinct. Also three red clover accessions formed a separate group. All rest of the accessions except three could be grouped into three main clusters, each with varying number of accessions. Principal co-ordinate analysis revealed that the first three co-ordinates accounted for 40% of the total variation, whereas the total variation explained by all the components accounted for 25% of the variation in the material under study.

Keywords: Genetic diversity, White clover, SSR markers

1432 (P-329)

Genetic Diversity in Indian Cotton (*Gossypium hirsutum* L.) Cultivars Using Microsatellite Markers and Comparison of Diversity Patterns

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Cotton is major fiber yielding cash crop of India. The genetic diversity has been analyzed in 96 cotton genotypes. PCR-based molecular marker techniques such as Simple Sequence Repeat (SSR) and Inter Simple Sequence Repeat (ISSR) were used for genetic diversity assessment of 96 genotypes and for making a comparison of diversity pattern among different groups. The 31 SSR and 4 ISSR primers generated 75 and 23 markers, respectively. The Polymorphism Information Content (PIC) value of SSR and ISSR primers was found to be 0.47 and 0.78, respectively. On the basis of statistical parameters such as per cent polymorphism, PIC, Resolving Power (RP) and Marker Index (MI) eight primers were found to be useful. Cluster analysis revealed two main clusters for the G. hirsutum genotypes at 65% genetic similarity. Further, principal co-ordinate analysis substantiated the cluster analysis. A comparison of genetic diversity patterns between Bt versus Non- Bt, Varieties versus Parental lines, Bt hybrids versus Non-Bt hybrids and Varieties versus Bt-hybrids showed that there were no significant differneces between these group-wise comparisons. The findings might be useful to the breeders engaged in cotton improvement for selecting diverse parents for hybridization programmes.

Keywords: Genetic diversity, Gossypium hirsutum, SSR markers

1444 (P-330)

The Microsatellite Distribution across Linkage Groups of Sesame (*Sesamum indicum* L.)

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Sesame is an ancient diploid (2n) dicotyledonous oil seed crop belonging to family Pedaliaceae. It is cultivated in the tropical and sub-tropical regions of the world by poor and marginal farmers. Sesame, as a source of high quality oil is valued for its stability, nutritional value and resistance to rancidity and is often referred to as the “Queen of oil seeds”. Molecular breeding in sesame is still at infancy due to limited number of SSR markers available and the low level of polymorphism exhibited by them. In the present study we developed physical map of SSRs using whole genome linkage group wise assembly of Sesame. As a whole the distribution of di, tri, tetra, penta and hexa nucleotide repeats on 16 linkage groups is 33%, 16%, 23%, 5%, and 3% respectively. Compound SSRs account for nearly 18%. Microsatellites were more abundant in linkage group 3 followed by linkage group 6 and 8. Linkage group 16 consists of least number of SSRs when compared to all others. Even though the distribution of SSRs varies from one linkage group to other the density is almost similar in all linkage groups. The physical map developed will be highly useful in cultivar identification and diversity analysis so as to improve the genetic potential of the crop.

Keywords: Assembly, Microsatellites, Physical map

1488 (P-331)

Identification of Resistance Sources for Important Diseases of Wheat from Germplasm Resources Deploying Molecular Markers for the Mitigation of Climate Change

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Wheat (*Triticum aestivum L.)* is a crop of global significance and increase in its production is very much essential to meet the demand of ever increasing population. Foliar diseases like rust, powdery mildew and spot blotch cause considerable damage to the crop and affect wheat yields. Climatic changes have led to the resurgence of new races of rust pathogens as well as movement of pathogens to the new areas. Five new pathotypes of stripe rust (*Puccinia striiformis)* namely, 46S117, 110S119, 238S119, 110S247 and 110S84 have been identified recently, which are cause of concern as the north western plains zone (NWPZ) of India, considered to be the nation’s wheat bowl, is prone to stripe rust. Similarly incidence of spot blotch (*Bipolaris sorokiniana)* is increasing in NWPZ where this was not a major disease. Indigenous and exotic germplasm accessions received from NBPGR, New Delhi and CIMMYT, Mexico were subjected to screening for rust and spot blotch under epiphytotic conditions. The accessions showing resistance were subjected to molecular characterization with gene linked markers viz., *Xpsp3000* and *Xgwm11* for Yr10, *Xgwm175* and *Xgwm273* for Yr15; *Cslv34* for Lr34/Yr18/Sr57/Pm38; *Xwmc719* for Lr46/Yr29/Pm39 for stripe and leaf rusts and powdery mildew, and *Xgwm148* for spot blotch. The findings of the study were very encouraging as accessions were found possessing single as well as multiple resistant genes. The accessions possessing multiple resistant genes could be used in hybridization for pyramiding of genes using marker assisted breeding for the development of wheat varieties possessing durable disease resistance.

Keywords: Biotic stress, Climate change, Germplasm, Molecular markers, Wheat

1501 (P-332)

Molecular Characterization of Maize Landraces Cultivated in North-Western Himalayan Region using Microsatellite Markers

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Maize is an important cereal crop of North-western Himalayan region of India with wide-ranging and diversified uses. The traditional farmers of this region still cultivate landraces maintained by their ancestors which represent an extraordinary genetic resource of the crop. These landraces differ in many traits like agronomic and nutritional characteristics, prolificacy, biotic and abiotic stress resistance and maturity. However, the reports on the molecular characterization of maize landraces collected from north-western Himalayan region are scarce. Only a very small proportion of maize germplasm has been utilized in breeding programmes. Modern agriculture involving the adoption of new commercial hybrid varieties and changes in land use pattern is leading to genetic erosion which further necessitates the characterization of huge gene reservoir of available maize populations. The present study was carried out to conduct molecular characterization of 142 landraces collected from the farmers of different districts of Himachal Pradesh using 10 polymorphic SSR markers distributed across the maize genome. A total of 45 alleles with molecular weight ranging between 65 and 260 base pairs were obtained. Polymorphic information content ranged between 0.37 and 0.71 with a mean value of 0.60. Mean expected heterozygosity was 0.58. Cluster analysis was performed on the basis of Jacccard's similarity coefficient to deduce the relationships among the landraces. The results indicated a fair amount of genetic diversity among the landraces representing a gene reservoir that could be useful in maize breeding programmes in India.

Keywords: Landraces, Microsatellite markers, Heterozygosity

1509 (P-333)

Diversity in Lucerne (*Medicago Sativa* L.) Germplasm for Morphology, Yield and Molecular Markers and their Correlations

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Lucerne is important legume forage grown worldwide due to its high nutritive value, yield potential, quality and highly contrasting environments. Estimation of genetic diversity in germplasm is important criteria in breeding programmes which is done based on phenotypic characters, biochemical and molecular markers. Thirty one accessions of Lucerne collected from traditional growing areas of Maharashtra and Gujarat were evaluated for morphological, yield characters, molecular markers and correlated with national check RL-88. The results of morphological & yield characters indicated wide range of variation within the accessions. The accession RLG 08-1 recorded significant differences for plant height, no. of tillers per plant, internodal length, green fodder, dry matter & crude protein yields ($P<0.05$) over RL-88. Green fodder yield was positively correlated with plant height ($r=0.72$), no. of tillers per plant ($r=0.71$) and internodal length ($r=0.71$) similarly dry matter yield also positively correlated with these characters ($r= 0.70, 0.69, 0.70$) respectively. Leaf stem ratio was negatively correlated with green fodder, dry matter and crude protein yields. The data was analyzed by Principal Component (PC) analysis which demonstrated that the first two PCs contributed to 93.7 per cent of total variance among the accessions. The accession RLG 08-1 was found distinct among the accessions. Initially thirty two Inter Simple Sequence Repeats (ISSRs) markers were screened and thirteen markers showed 82.8 per cent polymorphism. The dendrogram revealed slight geographical structuring for BAL accessions and RLG 08-1 was diverse from all other accessions whereas, no mantel correlation was observed between morphology, yield and molecular characters.

Keywords: Accession, Correlation, Diversity, ISSRs, Morphology

1582 (P-334)

Molecular Characterization of Maize Genotypes using Microsatellite Markers Associated with QTLs for High Kernel -Fe and -Zn

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Deficiency of -Fe and -Zn in diet has been recognized as one of the major problems affecting the world populations. Natural genetic resource rich in -Fe and -Zn provides a sustainable- and cost- effective solution to alleviate micronutrient malnutrition. Maize being the leading staple assumes great significance as a target crop for biofortification. In the present study, a diverse set of 20- maize inbreds (for Fe and Zn) were used for molecular characterization using 39- SSRs linked to QTLs identified in the exotic and indigenous genetic background. Among the inbreds, kernel Fe ranged from 30.0-46.1 mg/kg, while the same was 18.9-39.6 mg/kg for Zn. A total of 95 alleles were produced with a mean of 2.4 alleles per locus. PIC values ranged from 0.15 (*bnlg339*) to 0.72 (*umc1957*) with a mean of 0.43. Across inbreds, Jaccard's dissimilarity coefficients varied from 0.30-0.85. Principal coordinate analysis depicted diverse genetic nature of inbred lines. Cluster analysis grouped the inbreds into three major clusters for inbreds varying for Fe and Zn. The study identified selected inbreds to (i) develop heterotic hybrids high in micronutrients, (ii) accumulate favourable loci for high micronutrients, and (iii) generate new mapping populations for identifying QTLs in locally adapted germplasm. The information generated here would help the maize biofortification programme.

Keywords: Iron, Microsatellite markers, Zinc

1591 (P-335)

Characterization of Indian Maize Germplasm for Kernel A-Tocopherol using Functional Markers

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Vitamin E or tocopherol is an essential micronutrient for reproduction; and quenches free radicals in cell membrane which further protects from cardiovascular disease, Alzheimer disease and neurological disorders. Food and nutrition guidelines recommend 15 mg/day of vitamin E for both adults and teenagers. Among different isomers, α-tocopherol is most biologically active form of vitamin E. Maize is an important staple food crop, and major proportion (~80%) of total tocopherol in maize is constituted by γ-tocopherol that possesses low vitamin E activity. Hence, biofortification of maize with enhanced kernel α-tocopherol assumes great significance. Favourable allele of γ-tocopherol methyl transferase (*VTE4*) gene is reported to enhance accumulation of α-tocopherol by 3.2 fold. Gene-based markers (*InDel7* and *InDel118*) has been developed that helps in rapid identification of α-tocopherol rich genotypes without intensive biochemical assay. Here, a set of 160 inbreds of indigenous and exotic origin were screened for favourable alleles of *InDel7* and *InDel118* using gene-based markers. Of which 9 was found positive for *InDel118*, 83 for *InDel7* and 15 had favourable alleles for both. Four Indian elite QPM inbreds (HKI161, HKI163, HKI193-1 and HKI193-2) parents of four commercial QPM hybrids had unfavourable allele for both the *InDels* and possessed low α-tocopherol (6-8 ppm). The exotic inbred with favourable allele for both the *InDels* and high α-tocopherol (>20 ppm) identified was used as donor for enhancement of α-tocopherol in these QPM inbreds through marker-assisted backcross breeding. Besides, these positive lines can also be used to diversify the Indian maize germplasm for kernel α-tocopherol.

Keywords: α-tocopherol, Functional marker, Maize

1595 (P-336)

Utilizing the Exotic Germplasm for Development of Multi-Vitamin Rich Sweet Corn Genotypes through Marker-Assisted Breeding

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Deficiency of vitamin -A and -E poses serious health concern among preschool children and pregnant women. Natural mutants have been identified and gene-based markers were reported for β-carotene hydroxylase (*crtRB1*) and γ-tocopherol methyl transferase (*VTE4*) in exotic germplasm that causes higher accumulation of provitamin -A and -E in maize kernel, respectively. Sweet corn consumed both as fresh and processed vegetables; is an important source of fiber, minerals, and vitamins. Sweet corn kernels with recessive *shrunken2* (*sh2*) accumulate high amount of reducing sugars and sucrose than normal maize. Here, three elite sweet corn inbreds viz., SWT-16, SWT-17 and SWT-18 (parents of hybrids ASKH1 and ASKH2) were used as recurrent parent (RP) to introgress favourable alleles of *crtRB1* and *VTE4* using exotic inbred as donor. F_1s were tested for heterozygosity and were backcrossed to respective RP. Individual plants heterozygous for *crtRB1* and *VTE4* were selected in BC_1F_1, and were backcrossed to RP to generate BC_2F_1. About 14.58% progenies of SWT-16, 17.02% of SWT-17 and 4.16% of SWT-18 showed heterozygosity for *crtRB1* and *VTE4*, and homozygosity for *sh2* in BC_1F_1. Foreground selection in BC_2F_1 identified heterozygous plants that were selfed to generate BC_2F_2. More than 100 polymorphic SSRs have been used for background selection for recovery of RP genome. Progenies with *crtRB1*, *VTE4* and *sh2* in homozygous conditions would serve as novel genetic resource in the breeding programme, and help in developing multi-vitamin rich sweet corn genotypes.

Keywords: α-tocopherol, β-carotene, Sweet corn

1691 (P-337)

Haplotype analyses of *Phosphorus uptake 1* (*Pup1*) in Indian Rice Germplasm and its Implications on Phosphorus Deficiency Tolerance

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Improving P uptake and use in rice varieties can help reduce P fertilizers use, thereby addressing scarcity, rising P fertiliser cost, soil P deficiency increase and mitigating P pollution in high input areas. *Phosphorus uptake 1* (*Pup1*) locus in rice has been mapped which imparts low P tolerance, however, its structure in Indian rice germplasm is largely unknown. Therefore, haplotype analysis of *Pup1* was carried out in a set of 88 rice germplasm lines including Indian and few exotic rice lines, through genotyping with markers interspersed in *Pup1* region. The genotypes were screened at seedling stage under -P (0 ppm) and +P (10 ppm) in hydroponic culture. The genotypes showed significant phenotypic variation in P response under two P regimes. Root length showed significant low P response in the germplasm and based on phenotype performance, genotypes were grouped into three groups namely -P responders, +P responders and insensitives. The conserved region in *Pup1* was highly fragmented with 39.4% germplasm showing Kasalath *Pup1* haplotype. Due to fragmentation, the marker trait association of *Pup1* haplotypes was poor. The region encompassed by markers K46K1, K46-2 and K46-3 containing Os*PSTOL1* gene was key region that conformed low P response. Several Basmati genotypes possessed large proportion of Kasalath *Pup 1* alleles, which is a matter of evolutionary interest. It was observed that the Os*PSTOL1* gene is the driving factor for low P tolerance qualifying it for use rice improvement program and several indigenous sources have been identified, which can be used as the donor.

Keywords: *Phosphorus uptake 1*, Haplotype analysis, Deficiency tolerance, Rice germplasm

1921 (P-338)

Analysis of Molecular Diversity in Grain Amaranth Germplasm using STMS Markers

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Highly nutritious grain amaranths can help achieve nutritional security. At the same time it can solve the problems of changing climatic conditions with its wider adaptability and climate resilient nature. This has brought the long neglected crop much attention globally. Development of improved varieties of *Amaranthus* spp. require diverse germplasm. Morphological markers have been in use since long but they are considered as weak identifiers due to environmental influence. For meaningful understanding of genetic diversity use of molecular markers is highly relevant. STMS analysis of 120 accessions of grain amaranth comprising of 94 accessions of *Amaranthus hypochondriacus,* 13 of *Amaranthus cruentus,* 10 of *A. caudatus,* and one each of *Amaranthus edulis, Amaranthus dubius* and *Amaranthus hybridus,* was undertaken. Ten STMS markers with optimum amplification, good polymorphism and reproducibility were selected for characterization after screening the germplasm with 53 markers. Diversity analysis indicated high genetic diversity and strong population substructure (Fst-0.6). *A. hypochondriacus* and *A. cruentus* showed maximum and *A. edulis* showed minimum genetic diversity. UPGMA dendrogram and PCA analysis indicated presence of three major cluster. Six species were categorised into 16 groups on the basis of source. However no association was observed between source and clustering pattern. Structure analysis also indicated presence of only 10 putative clusters instead of 16 clusters. Diverse genotype were identified which can be used in improvement programme. Highly informative markers which can be used in molecular characterization and diversity analysis were also identified.

Keywords: *Amaranthus*, Diversity Analysis, Molecular Characterization, STMS

1772 (P-339)

Analysis of Population Structure and Assessment of Genetic Diversity in *Momordica* Accessions using Microsatellite (SSR) Markers

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The present investigation was carried out for studying genetic diversity and genetic relatedness among 51 bitter gourd lines using 61 SSR markers. Among 61 SSR primers screened, 30 were polymorphic and highly informative to differentiate these genotypes. Based on genotyping, a moderate to high level of genetic diversity was observed with a total of 101 alleles. The PIC values were ranged from 0.038 for BG_SSR-8 to 0.723 for SSR marker S-24 with an average of 0.429. The number of alleles was ranged from 2 to 5 with an average of 3.3 alleles per locus and heterozygosity was ranged from 0.02 to 0.24 suggesting a wide variation among 51 bitter gourd accessions. The UPGMA cluster analysis results showed that these accessions could be grouped into 3 major clusters. The cluster-I comprises of 4 small fruited type genotypes which are commercially cultivated in central and eastern India. Cluster-II comprises of 35 genotypes which were abundant and diverse group consisting of medium to long size fruited genotypes. Cluster III comprises of 12 genotypes with long and extra long fruited genotypes. The STRUCTURE analysis result was also in accordance with clustering method of UPGMA tree and principal coordinate analysis (PCoA). Therefore these polymorphic SSR markers will have potential applications in assessment of genetic diversity, molecular fingerprinting, and genetic mapping in *Momordica* species for economic traits. From this study the knowledge generated in terms of levels of gene diversity and population structure of bitter gourd germplasm, will be helpful in improvement of bitter gourd.

Keywords: *Momordica charantia*, Population Structure; Genetic Diversity, SSR Markers

1796 (P-340)

Gene Expression Analysis in Tolerant and Susceptible Banana Cultivars Under Drought Stress

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Banana is an important fruit crop to resource-poor farmers in marginal areas, where its production faces drought stress constraints. Present study quantified gene expression in tolerant and susceptible banana cultivars under drought stress, which identified candidate drought-tolerance genes. One drought-tolerant (*Monthan*, ABB, cooking variety) and one drought-susceptible (*Amritsagar*, AAA, dessert variety) banana cultivar were grown in glasshouse under well-watered and water-stressed conditions. Total RNA was extracted from control as well as stressed leaves after 20 days of stress followed by cDNA synthesis. Quantitative RT-PCR was performed for ten selected genes on three biological replicates for each treatment (stress and control) for each cultivar (*Monthan* and *Amritsagar*). The qRT-PCR reactions were normalized with the banana actin gene as a reference for all comparisons. The $\Delta\Delta$CT method of relative gene quantification was used to make the various comparisons of relative gene expression. All the ten genes were confirmed as being drought responsive in banana. Two genes were identified as candidate drought-tolerance genes, as one of them (*MaEXP*) was exclusively up-regulated in the drought-tolerant cultivar; while the other (*MaStpkNAK*) was exclusively down-regulated. Present study identified several drought responsive genes in banana which will be highly useful for the ongoing banana improvement efforts.

Keywords: Banana, Candidate genes, Drought tolerance, *Musa*

1825 (P-341)

Resistance Gene Analogue Polymorphism (RGAP) in Sugarcane for Developing Biotic Stress-Related Resistance

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Sugarcane is an important commercial crop of India. It suffers from various biotic and abiotic stresses during its crop cycle. Biotic stress related damage in plants could be managed by incorporating disease resistance in cultivated genepool through plant resistance genes resources (R-genes). Resistance gene analogues (RGAs) are members of multigene families related to stress response pathways that regulate enhancement of stress tolerance in crop plants and reveal polymorphism among different genotypes upon PCR amplification. Therefore, our objective was to develop PCR based resistance gene analogue polymorphism (RGAP) markers to provide candidate genes and QTL for disease resistance in sugarcane. In order to develop RGAP markers, fifty five degenerate primers designed from the highly conserved motifs of resistance genes were employed to amplify the genomic DNA of twenty nine sugarcane genotypes including cultivated & wild species and commercial hybrids. Thirty-four primers were successfully amplified resolving 1-6 amplified bands for each primer. The highest numbers of RGAP markers were observed in clones of wild species as compared to the cultivated sugarcane. The reason may be that the cultivated species have major proportion of chromosomes from *S. officinarum* and most biotic/ abiotic resistance genes are derived from wild species *S. spontaneum*. The markers obtained in this study were considered to be related to biotic stresses. The results indicated that these primers may be considered as potential resistance gene analogue polymorphism (RGAP) markers that should be taken into consideration to develop stress related resistance genotypes *via* crosses between wild types and cultivated elite cultivars.

Keywords: Red rot, RGA, *Saccharum*

1886 (P-342)

Identification of Genomic Regions Associated to Shoot Fly Tolerance in Maize

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Shoot fly (*Atherigonanaqvii*) is a major insect of maize causing yield losses up to 45 per cent. The insect resistance in maize is complex and quantitative in nature. Therefore, the present study was undertaken using 107 $F_{2:3}$ families from the cross between CM143 as the resistant (female) parent and CM144 as the susceptible (male) parentand data was recorded at different time intervals of inoculation. The disease reaction data showed normal distribution clearly indicating that the inheritance of shoot fly resistance in CM143 is under the control of quantitative loci. $F_{2:3}$ families alongwith parents were evaluated for various component traits (like deadheart, oviposition, leaf injury, leaf dimensions, seedling vigor, leaf glossiness etc.) that could be involved in shoot fly resistance. Parental polymorphism survey was done with 643SSR markers and 195 were found to be polymorphic. A linkage map of 1181.11 cM length was constructed with 105 polymorphic SSR markers on 107 F_2 individuals. Both genotypic data and mean values of phenotypic data of each component trait was analysed using QTL cartographer and QTLs on chromosome 1, 2, 4 and 9 were detected for various component traits explaining phenotypic variance from 2.15 to 19.43 per cent with LOD score ranging from 2.6 to 5.83. The QTL detected on chromosome 9 for oviposition and deadheart in the present study is syntenic to regions of chromosome 10 of sorghum which was also accounted for deadheart and oviposition. Fine mapping of identified QTL regions may provide useful information of genes underlying quantitative shoot fly resistance that can be further used in for genetic and breeding studies.

Keywords: Biotic stress, *Zea mays*, MAS

1887 (P-343)

Candidate Gene Expression Profiling under Waterlogging Stress in Maize

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Water logging is a serious constraint for maize production and causes an average yield loss of 25-30 per cent almost every year. The metabolic and cellular adaptations in the form of induction of anaerobic proteins and miRNA targets have been identified in maize roots at earlier hours of water logging stress. The present investigation was undertaken to study the expression of anaerobic polypeptides and miRNA targets at later hours of stress in maize roots (24h to 96h). The plant material consisted of two inbred lines viz. I110 (susceptible) & I172 (tolerant).Water logging stress was imposed for 10 days in two replications at V7 (7 leaf) stage and third replication was treated as control. The data on various morpho-physiological and yield contributing traits i.e. plant height, root length, chlorophyll content, leaf area, root dry weight, shoot dry weight, grain weight and cob weight were recorded. Water logging tolerance coefficient was found higher for tolerant lineas compared to susceptible line. For transcriptome profiling, selected gene transcripts of anaerobic polypeptides and miRNA target genes were quantified by qRT-PCR. The study revealed that some of the genes were initially activated, and then suppressed at the late hours or vice versa.Mostly the susceptible line showed response at late hours of stress while tolerant line showed response at earlier hours of stress. The maximum fold change expression was observed for ubiquitin activating enzyme (UaeE1), putative MAPK (Pm) and pyruvate kinase (Pk) in tolerant genotype I172. Poly (ADP-ribose) polymerase (PARP), MiR171 target and catalase showed higher expression in susceptible line as compared to tolerant line. Most of miRNA target was downregulated in tolerant line that suggests the overexpression of corresponding mRNAs and further provide the morphological and metabolic adaptations. Overexpression of most of miRNA targets in susceptible line lead to oxygen consumption under oxygen limited conditions that might provide short term adaptation but decrease their long term fitness and making them susceptible to waterlogging. Cluster analysis revealed that all differentially expressed genes clustered into five groups according to their expression profiles.The differential expression patterns of anaerobic polypeptides and miRNAtargets suggested that these are active participants in water stress responsive mechanisms.

Keywords: Abiotic stress, *Zea mays*, micro-RNA

1908 (P-344)

Mapping of QTL for Southern Leaf Blight Resistance in Maize (*Zea mays* L.)

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Southern leaf blight (SLB) caused by necrotrophic pathogen *Drechslera maydis* is a pre-flowering disease causing major yield losses up to 40 per cent in maize. The SLB disease resistance in maize is complex and quantitative in nature which can be additive or recessive in effect. Therefore, the present study was undertaken using 220 F_8 RILs from the cross between LM5 as the resistant (female) parent and CM140 as the susceptible (male) parent. The SLB disease reaction data was recorded using scale 1-9 at different time intervals after 15, 30 and 45 days of inoculation. The F_8 RILs along with parental lines LM5 and CM140 were also evaluated for phenotypic traits like days to anthesis (DTA), days to silking (DTS) and anthesissilking interval (ASI) as these traits could be influenced by the disease. The disease reaction data taken at different time intervals of inoculation showed progress of disease with increase in relative humidity and the disease reaction fitted into normal frequency distribution clearly indicating that the inheritance of SLB in LM5 is under the control of polygenes. A linkage map of 730.13 cM length was constructed with 80 polymorphic SSR markers on 110 RILs. The putative QTL for SLB resistance and flowering traits were detected on chromosome 3, 7, 8 and 9 respectively. The major QTLon chromosome 8 explained more than 15 per cent of phenotypic variance with LOD 3.6. SLB resistance QTL co-localised with flowering traits QTL which indicates that the SLB development had an effect on flowering traits. The identified regions were again narrowed down by applying more 30 SSR markers in addition to 80 polymorphic markers to identify the QTL for SLB resistance. The probable QTL were detected on chromosomes 3 and 8, which are the hot spot region for SLB disease resistance as also reported earlier.

Keywords: *Drechslera maydis,* SLB, SSR markers, QTL, *Zea mays* L.

170 (P-345)

Genetic diversity in the Wheat Grain Transcriptome

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Bread wheat (*Triticum aestivum* L.), an allohexaploid with three sub-genomes (A, B and D) has the largest genome (17Gb) among the three major cereals maize, wheat, and rice that feed human populations. Wheat grain proteins, especially gluten proteins with their unique polymerizing nature, are responsible for the visco-elastic property of dough that gives wheat a special place among the cereals. Whole grain transcriptome sequencing was performed for 35 globally diverse bread wheat genotypes during early and late grain filling stages, at 14 and 30 days-post-anthesis respectively. Genes expressed differentially across all genotypes during wheat grain development were identified through RNA-Seq analysis. Genes that had statistically significant differences in expression were selected with the help of mean- and count-based statistical analyses using a false discovery rate (FDR) cut-off value at 0.01. In total, 26,477 genes were differentially expressed between the early and late grain filling stages. These genes were functional annotated and mapped to KEGG pathways. This revealed differential patterns of expression for different metabolic pathways during early and late grain filling. Major findings were: 1) metabolic pathway vary between early and late grain filling; 2) some metabolic pathways are unique at early and late grain filling, while some differentially dominate across grain filling; and 3) novel metabolic pathways for yield improvement were identified.

Keywords: Transcriptome, NGS, Wheat, Ontogeny, Diversity

926 (P-346)

Potential of Rice Landrace in a Cross Between Local Cultivar Tulaipanji and Ranjit (HYV) through Analysis of Genomic Introgression Based on SNPs Variations Revealed by GBS System

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Tulaipanji is a local rice cultivar of Uttar Dinajpur district of West Bengal. It is famous for its aroma and grain quality with some kinds of medicinal value. It needs minimum input (fertilizer and water) for cultivation, because Tulaipanji is a drought avoidance local landrace. Local rice landrace Tulaipanji was crossed with Ranjit (HYV) and two distinct lines were identified from the progenies- one line with awns and aroma traits and the other without awns and aroma. Genotyping-by-sequencing (GBS) approach of NGS (Illumina) was used for discovering and genotyping SNPs in progeny and parental lines. Total number of polymorphic SNPs identified was 52,810 and InDels was 4,327 at read depth 10 based on reference genome MSU7. Among these 16,490 were intergeneric, 7,812 were inside gene, and 4,435 were intronic. Phylogenetically, rice cultivar Tulaipanji (aromatic local landrace) was closer to reference genome MSU7. Based on recurrent parent genome analysis (RPG), 92.52% was introgressed into progeny-awn from parent Tulaipanji and 7.48% from parent Ranjit. Whereas, progeny-awnless carried 89.19% allelic count from parent Ranjit and only 10.81% from parent Tulaipanji at this fifth generation of RIL lines. These SNPs variation may be linked to the phenotypic traits of drought avoidance and can be utilized in crop improvement program through genomic selection to develop climate ready rice varieties. These results suggest that adding a high density of SNP markers to a mapping population through GBS has a great value for numerous applications in rice breeding and genetics research.

Keywords: Drought tolerance, Genomic introgression, Local Rice Tulaipanji, RIL F5 lines, SNPs by GBSs.

1911 (P-347)

Genetic Diversity and Evolutionary Analysis of HKT1 Gene in Bread Wheat and its Progenitor Species

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Salinity tolerance is confined to plants with specific physio-morphological adaptations such as halophytes. However certain non-halophyte species also retains the characteristics of salinity tolerance due to the presence of specific genes, which renders these plant species to survive on salt affected area. One of the gene families, which confer salinity tolerance, is *HKT*. There are two groups of genes in *HKT* family and the gene *HKT1;5* belongs to group I category, was sequenced and analyzed in diverse wheat varieties, progenitor species and ditlelosomic lines in order to understand its diversity and evolutionary significance. Genomic analysis in bread wheat revealed the presence of four alleles and the analysis in wild relatives *T. monococcum* and *A. tauschii* showed the presence of two major alleles or two major paralogous genes and sub-alleles. The comparative genomics with model plant *A. thaliana* revealed the higher conservation of this gene, particularly in coding part between monocots and dicots. The presence of multiple copies was observed among the wild relatives, particularly in *A. speltoides* and one its allele was shown to have an altered amino acid sequence within exon1 region. Higher conservation of this gene from bread wheat with diltelosomic line possessing 4DL chromosome and durum wheat with ditelosomic line possessing 4DS chromosome, revealed the evolutionary importance of this gene, which present in multiple copies among the homeologous chromosomes of bread wheat.

963 (P-348)

Transcriptome Analysis for Adult Plant Leaf Rust Resistance in Wheat

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Leaf rust is one of the major devastating disease of wheat caused by *Puccinia triticina*. To sudy the genes expressed against leaf rust pathogen, we performed transcriptome analysis of genotype CSP44 carrying a recessive adult plant resistance (APR) gene *Lr*48. RNA sequencing led to the identification of more than 7000 differentially expressed genes induced due to pathogen invasion in compatible/incompatible rust reactions in the host. The genes were studied for their ontology in terms of biological processes, their cellular components and molecular function. The *in-silico* analysis of these genes has suggested their specific roles in the signal transduction pathways. Based on their role in important metabolic pathways, approximately 70-80 genes were selected for their validation using qRT-PCR. The study revealed the higher expression of endopeptidases, chaperones, corepressors and transcription factors involved in gene regulation after pathogen inoculation. Upregulation of defense mechanisms involving heme binding oxidoreductases, peroxidases, secondary metabolic pathway enzymes and signal transduction pathway genes was observed following pathogen inoculation during both pre-adult (compatible) and adult plant (incompatible) stages. *De Novo* assembly of the contigs revealed some novel genes for the first time. We could observe around 953 differentially expressed genes from *Puccinia* species during transcriptome analysis. The pathogen specific genes are being validated for their expression and possible interactions with the host. This will provide better insights into the complex resistance signaling pathways.

Keywords: Adult plant resistance, Leaf rust, qRT-PCR and Transcriptome

Technical Session 4-C :

Science-led Innovation

Concurrent Session :

PGR Informatics

202 (O-37)

India as a Crucible to Develop Integrated Information Systems

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An organized digital information system provides fair and just opportunity for all to access. PGR Informatics manages (creation, storage, retrieval and presentation) and analyses (discovery, exploration and extraction) diverse information (facts, figures, statistics, knowledge and news). National Bureau of Plant Genetic Resources (NBPGR) is the nodal organization in India for managing plant genetic resources. NBPGR has established robust documentation systems and databases to facilitate genebank management. A web-based open-access resource *PGR Portal* was developed for everyone to retrieve accession level information. Recently, in collaboration with NBPGR scientists, other applications like *PGR Map, Genebank Dashboard, PGR Clim, IP-PGR, CWR Portal, Herbarium Portal, National Rice Resource Database, Genetics and Genomics of Vigna and Phaseolus, Inventory of Registered Germplasm*, etc. have been developed and are being tested. Fragmentation of data; task of linking past, present and future electronic data; dynamic nature of evaluation trait data descriptors/states; and inclusion of cutting edge data and technologies (GIS and Genomics) make developing an integrated PGR information system demanding. Apparently the benefits are incalculable but implementation complicated. India's geographical size, number of languages and dialects; agro-ecological variations; number of cultivated plants and their diversity; and institutions, personnel involved in data generation and handling make the collation and digitization of data on PGRFA pertaining to the relevant articles of Treaty, CBD, SMTA and GPA, a gigantic task rivaling some of the regional and global efforts. The challenges and successes are expected to make the experience richer in terms of *fair and just opportunity for all* in spirit and letter.

Keywords: Documentation, Information system, PGR Informatics, Portal

600 (O-38)

Mulberry Genome Network: An Interactive Web Platform for *Morus* Specific Genetic and Genomic Resources

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Mulberry productivity is the key determinant for success and sustainability of sericulture. With the advent of recent technologies, vast amount of genomic, metabolomic and phenomic data of the crop was generated or being generated at the Institute and across the globe. Besides, big data pertaining to mulberry - genic x environmental interactions are recorded at different locations necessitating the development of models for crop performance. There are few databases related to the crop in the public domain. There is a need for integration of the databases on a single platform for archiving and utilization of data by high speed computational analysis. In this direction, a Mulberry Genome Network (MGN) has been developed as a centralized platform for mulberry-omics integrated with innovative genetic tools, futuristic goals and network forum. The data contents are analysed and organized from in-house research projects and databases. These data are categorized and stored efficiently on a centralized system in relational tables using the MySQL and web interfaced using HTML, PHP, Javascript *etc*. The network is developed as a curated and integrated web-based database providing easier access with hyper-linking of related databases such as Mulberry Germplasm Database (MGD), MorusDB, MulSatDB, *etc*. The platform is also integrated with programs such as BLAST, CLUSTALW, Primer3Plus, Cmap *etc*., along with useful graphical tools for analysis. The user-friendly interface will be helpful to the scientists and researchers for utilization of crop resources and genomic information with opportunities to share data among the stake holders. It is publicly accessible through http://btismysore.in/mgn

Keywords: Big data, Crop modelling, Genetic tools, Mulberry genome network

1182 (O-39)

Modelling Distribution of Neglected and Underutilize Fruit Species in Sri Lanka for Sustainable Utilization

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Although Sri Lanka is rich in diversity of fruit species (i.e. 237 species belong to 56 families), only a very few species are cultivated commercially. Hundreds of lesser known fruit species are grown naturally countrywide in marginal environments. The task of evaluating genetic diversity of these species with lesser information is a problem central to biodiversity research. Distribution of 28 neglected and underutilized fruit tree species were modelled using 2976 location data collected from field investigations, different field research stations and herbarium records. Data were used with DIVA-GIS and FloraMap software for development of tree distribution maps and potential area maps. As a priority species Wood-Apple (*Limonia acidissima*) was selected to model with Maxent using 220 presence-only location data as a function of seven environment variables. The predicted range of *L. acidissima* is mainly north western and north central provinces in Sri Lanka. Temperature seasonality (bio 4) and precipitation in wettest quarter (bio 16) appeared to be the highest contributing variables to the final *L. acidissima* model formulation. The findings of this study is important not only for predicting the potential distribution of neglected and underutilized species but also as important information predicting the high potential environmental variables for distribution of these species in Sri Lanka.

Keywords: *Limonia acidissima*, Neglected and underutilized fruit species, Maxent, Species distribution modelling

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44 (P-349)

DIVA-GIS Based Diversity Analysis of Maize Inbred Lines under Temperate conditions

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DIVA-GIS enables identification of the diverse sources and possible regions for use in crop improvement. A set of 100 maize inbred lines both indigenously developed as well as procured from various national and international sources were evaluated for three years during 2012-14. DIVA-GIS version 7.5 was used for mapping diversity and statistical analysis of traits viz., plant height, days to silking, days to tasseling, days to maturity, ASI, ear height, EPP, grain weight, grain yield, kernel rows and protein content. Inbred lines were found to be diverse for all the traits except for EPP and they have been sourced from Northern and Southern parts of India. High Shannon diversity index with maximum range of 2.17-3.0, 2.25-3.0, 2.36-3.0, 2.4-4.0, 2.0-3.0, and 2.2-3.0 have been recorded for the traits plant height, ear height, grain weight, grain yield, Kernel row and protein content respectively. Inbred lines were found to be diverse for all the traits except for EPP and they have been sourced from Northern and Southern parts of India while for EPP which has recorded less diversity index range of 0.4-1.0 is sourced from South India. Interestingly, less diverse inbred lines for all the eleven quantitative traits have been sourced from Indo-gangetic plains as indicated in diversity grid maps. Maximum diversity indices recorded for ASI, days to silking, days to tasseling, maturity are in the range of 0.97-2.0, 1.528-2.0, 1.516-2.0 and 1.528-2.0 respectively. Grid maps developed by DIVA-GIS tool can be used for identifying sources of novel traits to combat climate change.

Keywords: DIVA-GIS, Diversity, Inbred, Maize

190 (P-350)

Decision Support Database of Maize Inbred Germplasm for Aiding Selection of Potential Lines for Hybrid Development

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Enhanced production and productivity in maize have largely credited to development and adoption of Single Cross Hybrid (SCH), which involves breeding of inbred lines, hybridization between selected inbred lines, and evaluation of experimental crosses and identification of most productive and adapted hybrids. Selection of parental lines is the most crucial step, which is initially based on combination of phenotypic traits possessed by different inbred lines. In order to support and assist breeders in choosing potential parental lines, a decision support database has been developed. The database houses data of 300 inbred lines of 13 traits *viz*. time of anthesis, time of silk emergence, density of spikelets, number of kernel rows, number of kernels per row, grain type, plant height, ear placement height, anthocyanin colouration at base of glume, anthocyanin colouration of anthers, grain colour , kernel row arrangement and 1000-kernel weight. The database was developed using the latest version of Drupal (7.34); Hypertext Preprocessor (PHP) was used for frontend development and database (backend) was developed in My Structured Query Language (MySql). The database allows selection of various inbred lines with different permutations and combinations of the 13 traits along with high-quality images of the tassels and the cobs. The database is being demonstrated for its features and applications. This database, which is a systematic documentation of the maize inbred germplasm, would be helpful for breeders in the selection of parental lines based on needs and requirements of various research programmes.

Keywords: Database, Decision support, Germplasm, Hybrid development, Maize

251 (P-351)

Genome-Wide SNP Analysis Reveals only a Moderate Level of Molecular Diversity in Castor

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Castor (*Ricinus communis* L.) is a highly valuable oilseed crop. The oil and its derivatives are used in manufacturing of several industrial products. It is a monotypic species under Euphorbiaceae family and mostly cross pollinated (aided by wind) though self- pollination does occur. Morphological diversity in castor is highly impressive. However, the status of molecular diversity in castor remains inconclusive. Earlier studies based on molecular markers showed low to moderate level of genetic diversity in castor but those studies had limitations in terms of the number of loci analyzed and the number/representation of the genetic materials used. In this study, we analyzed the molecular diversity in castor by genotyping a panel of 314 representative genotypes (comprised of core germplasm, commercial cultivars and advanced breeding lines) using 5,038 genome-wide SNP loci covering over 85 per cent of the genome. The average polymorphism information content of SNPs was 0.279. The observed heterozygosity across the castor genotypes was 0.11, indicating that the genotypes were near homozygous lines. The expected heterozygosity (gene diversity) was only 0.351, supporting the moderate level of molecular diversity in castor. The absence of definite population structure in the genotype panel underpinned the possibility of free gene flow. It is surprising that excellent phenotypic diversity in castor was not reflected at the molecular level. One possibility is that most of the phenotypic variations in castor may be due to the epigenetic mechanisms, which need to be explored.

Keywords: *Ricinus communis* L., Molecular diversity, SNP genotyping

311 (P-352)

Pigeonpea (*Cajanus cajan*) Collection Status, Diversity Distribution Mapping and Gap analysis using GIS tools

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Pigeonpea [*Cajanus cajan* (L.) Millspaugh] an important food legume, predominantly cultivated in tropical and sub-tropical regions of Asia and Africa. So far 2,967 accessions of pigeonpea have been collected often in collaborative mode by ICAR-NBPGR (1976 to 2015) from different agro-ecological regions of the country. A total of 2,456 accessions having essential geographic details (state, district, village, latitude and longitude) were screened. Considering the representation of diversity from all surveyed states in India, Madhya Pradesh (438), Jharkhand (387), Andhra Pradesh (326), Telangana (253), Bihar (249), Gujarat (230), Uttar Pradesh (188) and Maharashtra (178) exhibited maximum germplasm collections. Analysis of data revealed that about 86 landraces (with distinct names) were collected from 14 states and all are conserved under long term storage (LTS). In regard to crop wild relative of pigeonpea, six accessions of *C. cajanifolius* collected from Odisha (3 accns) and Andhra Pradesh (3 accns) and 46 accessions of *C. scarabaeoides* from Maharashtra, Odisha, Tripura and Uttarakhand were collected. Mapping of trait-specific germplasm (107 accessions) identified few areas – *viz.* south eastern coastal region of Andhra Pradesh, north-eastern part of Maharashtra and north-western part of Bihar showing maximum diversity of promising germplasm. However, mapping through fine grid method trait-specific germplasm identified from Akola area (Maharashtra) for pod bearing length; Srikakulam area (Andhra Pradesh) for bold seed and Hyderabad area (Telangana) for high pod number. Based on gaps identified in collections and diversity mapping, unexplored / underexplored areas identified for future pigeonpea germplasm collections have been discussed in present paper.

Keywords: *Cajanus cajan*, Collection, Diversity distribution, Crop wild relative, Trait-specific germplasm, GIS

364 (P-353)

Assessing Potential Pockets *vis a vis* Climate Suitability for Sustainable Cultivation of Yardlong Bean in Andhra Pradesh and Odisha

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Vigna unguiculata (L.) Walp. ssp. *sesquipedalis* Verdc. (Yardlong bean) is one of the important vegetable legumes throughout the tropics/subtropics of Asia. Yardlong beans are mainly a warm-season crop, vigorous climbing annuals and will survive extreme humidity and heat. Edible pods which belong to vegetable form of cowpea are very crisp, tender and delicious. The long beans are cut into shorter sections and cooked like common green beans. These yardlong beans are being grown in a few pockets in Andhra Pradesh and Odisha states of India. In view of its nutritional quality, the crop needs to be grown in larger areas. We have used Maxent version 3.3.3k and DIVA-GIS to identify the potential pockets *vis a vis* climate suitability in these two states. Presence points (38) of beans were collected during an exploration mission in these regions. Bioclim_2.5 arc min grids were used for current and future climates. Ecological niche models generated for present and future climatic models indicated that parts of East Godavari, West Godavari, Visakhapatnam, Vizianagaram, Srikakulam districts of Andhra Pradesh, Yanam of Puducherry and Koraput, Ganjam, Puri and Cuttack districts of Odisha are the high probable areas (0.58-1.0) for the sustainable cultivation of yardlong bean in the light of climate change. Precipitation of wettest quarter (28.8), Temperature seasonality (11.7), Isothermality (8.7), Mean diurnal range (8.0), Annual mean temperature(7.9), Precipitation of driest quarter (7.9), Precipitation seasonality (6.8), Precipitation of coldest quarter (6.7), are major bioclimatic variables contributing to the climatic models. Accordingly, proper strategies to be framed for sustainable cultivation in the identified districts.

Keywords: DIVA-GIS, Ecological niche models, MaxEnt

582 (P-354)

Genebank Information Management System at NBPGR, New Delhi, India

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Advancements in digitization of data for efficient management is utmost important for ensuring the reliable and quick retrieval of the data. Most of the global genebanks have developed their information systems in dynamic and flexible manner to maintain the integrity and quick retrieval for multitude of purposes. To cater the national needs and to keep updated in international arena, NBPGR has developed an in-house PGR Informatics System which includes Genebank Information Management System (GBIMS) where all information pertaining to the genebank collections. For documentation of genebank holdings we are using Information System Based on the MS-SQL Server and net technology for retrieval of genebank information (web based) programme which is accessible at http://database_rx/NBPGR/. In this system the system administrator can create multiple accounts with role-based access. Curators can manage their data themselves and print various reports along with the customized queries. The major partners in the NBPGR genebank information network include 10 regional stations, 59 National Active Germplasm Sites (NAGS), National Research Centres, All India Coordinated Crop Improvement Projects and State Agriculture Universities (SAUs). At present GBIMS stores information on a total of 4 20,316 germplasm accessions of 1778 crop species on 22 genebank descriptors (crop name, botanical name, national ID, collector no., other id, germination, moisture, seed quantity, donor institute.) including 8 descriptors states to define the biological status of the collections. The data base is monitored periodically and as per need, advance descriptors are added to facilitate smooth flow and effective dissemination of information to the scientific community.

Keywords: Genebank management, Information management system

652 (P-355)

PGRdup – An R Package to Facilitate Discovery of Probable Duplicates from Plant Genetic Resources Collections in Genebanks

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Globally ~7.4 million plant germplasm accessions are held in more than 1,750 genebanks. Considerable duplication (70-75%) exists both within and between these collections (FAO, 2010). Long-term conservation of orthodox seeds being an expensive affair, duplicate accessions consume valuable resources without adding to the value of the collection. Moreover, this also adds to the cost of characterization and evaluation of germplasm to facilitate their end use. Similarity in passport data associated with germplasm accessions can shed light on the extent of redundancy in collections. An R package 'PGRdup' was developed to facilitate the search for probable duplicate accessions in germplasm collections using passport databases. Primarily this package implements a workflow designed to fetch sets of germplasm accessions with similar passport data particularly in fields associated with accession names within or across passport databases. It offers a suite of functions for data pre-processing, creation of a searchable Keyword in Context (KWIC) index of keywords associated with accession records and the identification of probable duplicate sets by fuzzy, phonetic and semantic matching of keywords. It also has functions to enable the user to review, modify, validate and visualize the probable duplicate sets retrieved. Although, it may not imply 100% genetic identity of accessions, information on accessions with similar passport data can be utilized for prioritization of accessions for resource intensive conservation activities.

Keywords: PGR Informatics, Duplicate accessions, PGR databases, Passport data

702 (P-356)

Diversity Assessment in *Abelmoschus tuberculatus*: A DIVA-GIS Study

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The Indian sub-continent is an important centre of diversity for both wild and cultivated okra. *Abelmoschus tuberculatus* Pal and HB Singh, a wild relative of Okra is endemic to India and have been identified as potential source of desirable gene for YVMV and fruit borer which can be useful in okra breeding programme. Variability from north western, central Indian and adjoining regions of India has not been studied for agro-morphological and biotic stresses. Fifty eight accessions belonging to Gujarat, Madhya Pradesh, Rajasthan, Maharashtra and Telangana were used in the experiment and grown in an augmented block design during the *rainy* seasons of 2014-15 and 2015-2016 at Akola, India. Nine qualitative and ten quantitative traits were recorded. DIVA – GIS version 7.5 and SAS Enterprise Guide 4.3 were used for diversity and statistical analyses, respectively. Significant variability was observed in qualitative and quantitative traits. High coefficient of variation was observed in fruit per plant (52.56 %) followed by first fruit producing node (46.03 %), first flowering node (43.8 %), and number of seeds per fruit (38.82) suggesting existence of diversity in these traits. Dendrogram (Wards method) articulated two clusters comprising 21 and 37 genotypes. DIVA-GIS grid maps generated for diversity analysis in *A. tuberculatus* indicated that the Central Indian region was diversity rich pocket. The wild species as such have not been found to be of any commercial importance as vegetables. However, they possess certain useful characters which may be worth introducing into the cultivated species for future crop improvement programmes.

Keywords: DIVA-GIS, Diversity analysis, Wild okra

909 (P-357)

PGR Map: A Web Based Tool for Map Based Access to PGR Information

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PGR Map application aims to provide map based interface to obtain information on collection and conservation of crop species that are part of the Indian National Genebank holdings. The user friendly interface provides three search options viz. (i) “What’s around me” maps the current location of the users device and reverts with the details of the accessions collected from that location in India. (ii) “Search the map” retrieves details of accessions collected from a location in India on a simple click or tap on the map. (iii) “Search for species” maps the collection sites of a crop species selected by the user. PGR map is compatible with touch based mobile and computing devices. It provides easy and quick access to germplasm information and is expected to enhance it’s utilization. It has been developed to assist policy makers, researchers and students to easily access the details of conserved crop species of India. Details of the interactive system will be presented. The application is available at http://pgrinformatics.nbpgr.ernet.in/pgrmap/

Keywords: Access, Map based interface, PGR

998 (P-358)

PGR Portal - A Gateway to Plant Genetic Resources in India

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Indian Council of Agricultural Research-National Bureau of Plant Genetic Resources (ICAR-NBPGR) is the nodal organization in India for acquisition and management of indigenous and exotic plant genetic resources for food and agriculture, and to carry out related research and human resource development, for sustainable growth of agriculture. The National Genebank at ICAR-NBPGR conserves about 400,000 accessions belonging to about 1800 crop species. The PGR Portal is a web based application that provides information about germplasm accessions conserved in the National Genebank. The principle objective of the PGR Portal is to facilitate the utilization of germplasm accessions in crop improvement programmes through enhanced access to information. The Portal is accessible at http://pgrportal.nbpgr.ernet.in/ and also through "PGR Portal" link on ICAR website www.icar.org.in. Users can access the Portal through either structured simple search or free-text search. Characterization data is also accessible to any user; however, database and gap-analysis applications are available for internal users. The Portal has been accessed by users around the world.

Keywords: Plant genetic resources, PGR portal, Genebank, Characterization, Conservation

1102 (P-359)

National Rice Resource Database

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Indian National Gene Bank conserves more than 1000,000 accessions of rice on long term basis usefulness of these accessions can be realised only through their characterisation and evaluation. With this objective 15,000 unique rice germplasm were characterised and evaluated at five locations Varanasi, Cuttak, Raipur, Karnal and Hyderabad for three seasons (2009-2010, 2010-2011, 2011-2012). A rice database has been developed for rice genotypic and phenotypic information resource of unique rice accessions 15,000 (Indigenous-13733, Exotic-1267) from National Gene Bank were characterized for 30 morphological characters —19 qualitative and 11 quantitative characters characterization Data (5 locations, 3 seasons and 13.5 lakh data points), evaluation data for (10 traits: 7 biotic and 3 abiotic; 2 years), molecular marker data (36 HvSSR markers) and rice core set of 1548 accessions has been developed using powercore. The CMS based Rice database web portal has been hosted with set of data analysis applications to browse and search rice database graphically and portal can serve more than 200 online web users request simultaneously. As a result, establishment of rice database may act as a rice knowledge platform to enhance information utilization to farmers, breeders and research community. National Rice Resource Database is available for public access. Point a browser to the link www.nbpgr.ernet.in/nrrd

Keywords: Informatics, Rice characterisation, Rice core collection, Rice database

1168 (P-360)

In-sillico Characterization of Phosphoglucose Isomerase (PGI) gene in *Triticum Aestivum*

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The food security is major concern in India; hence, it is necessary to devise certain strategies to enhance the food grain production, and support, the exponentially growing population. Phosphoglucose isomerase enzyme, also known as Glucose-6-Phosphate isomerase(GPI), has major role glucogenesis i.e. starch synthesis. It has also been reported, that there is 50% reduction in starch synthesis with 50% reduction in PGI enzyme, which leads to reduction in grain size. Hence, characterization of the PGI gene is important to know in detail about its role in starch synthesis. The protein sequence of PGI enzyme of wheat (Triticum aestivum) was downloaded from the protein database of NCBI, and analyzed to find the respective gene in T. aestivum. Three homologous gene copies of PGI were found, which were present on 1A, 1B and 1D chromosome of Triticum aestivum. The orthologous gene copies were also traced in grass family. Multiple Sequence Alignment tool was used for gene as well as protein sequences analyse in homologous as well as orthologous copies of PGI. The sequence difference in PGI gene in grass family was analyzed and phylogenetic tree were constructed. To further study the gene sequence, gene structure (introns and exons) of homologous as well as orthologous PGI were manually constructed. Finally, to analyse the structure and function of the homologous and orthologous genes, 3D protein structure were predicted with the help of I-Tasser software which helped in understanding the mode of action of different PGI genes.

Keywords: *Triticum aestivum*, Wheat, PGI, Starch synthesis

1567 (P-361)

Application on Digital Herbarium of Weed Seeds Intercepted in Imported Germplasm

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National Bureau of Plant Genetic Resources (NBPGR), New Delhi is the nodal agency that facilitates exchange of plant germplasm meant for research between India and different countries. It has the power to carry out quarantine of the plant germplasm including transgenic imported for research purpose. To ensure effective implementation of Plant Quarantine (Regulation of Import into India) Order 2003, it is essential that all imported seed samples are free from weeds of quarantine importance. Seeds imported to the country can be a threat towards the agricultural aspect if they are weeds and not thoroughly checked. It can spread in larger areas and may affect the ecosystem, which can be hazardous to human as well as animals. In view of the importance of detecting weed seed an application has been developed as Digital Herbarium of Weed Seeds Intercepted in Imported Germplasm. This application has been developed using Visual Basic 2008 and SQL Server 2008 R2 softwares. It is intended to store information of weed seeds and a search system has been developed to search weed seeds according to the common name, botanical name and distribution of weed across the globe. The data entry form is meant for storing the data and picture of weeds with following fields viz: common name, scientific name family, status, distribution, description. This application would be a great help for referring information related to weed seeds imported in germplasm and will be an asset to the organisation.

Keywords: Digital, Herbarium, Weed, Seed, Imported germplasm

1724 (P-362)

Phyto-Geographical Distribution and Species Richness of *Corchorus* in India

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The genus *Corchorus* is widely distributed in tropical and sub-tropical countries including India. Spatial data available with passport information of a total of 2856 accessions of *Corchorus* accessions analysed with the help of DIVA-GIS. Most of *Corchorus* species are found pandemic in distribution with differential habitat preferences in the country. Combine geographical, edaphic and precipitation based distribution profile of *Corchorus* demonstrated multilayer genotypic and environmental interactions that led to differential spatial distribution of the species. The highest species concentration is found in Tamil Nadu, followed by Gujarat, Rajasthan, Madhya Pradesh and Maharashtra. Complementarity analysis showed that the major diversity hotspots are found in Tamil Nadu followed by Gujarat. Moreover, ethnobotanical applications of the genus show its long association with prevailing ethnic communities. The information generated in the present study enhanced our understanding about distribution and anthropogenic threat perception of *Corchorus* plant genetic resources in relation to environmental factors. The information will prove guider for future collection and conservation strategies for the genus in India with potential to extrapolate globally.

Keywords: *Corchorus*, Phyto-geographical distribution, Species richness, Diversity, Conservation

1801 (P-363)

SeriPort: Bridging Sericulture to Informatics

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Data science has revolutionized wide array of fields like biology, biomedicine, agriculture, sericulture, etc. Sericulture, a major agro-based industry is one of the areas of our interest. It involves rearing diverse silkworms which have interactions with their food plants, pests, pathogens, etc. and have great economic significance. Scientific research in seri-related field has resulted in the development of various databases comprising a wide array of datasets. SeriPort, a web-portal has been developed by our laboratory to systematically categorize the seri-informatics web-resources. Around 70 databases classified as 22 silkworm databases, 23 host plant databases, 01 pest & pathogen database and 24 combined databases have been appended to SeriPort. Additionally, sericulture industries/ organizations, literature related to genome, proteome, transcriptome of seri-resources, have been incorporated in the portal. It has a user-friendly interface, an in-built search engine and various webpages describing each database briefly. It aims to provide easy access to the web-resources available in cyberspace which remain hidden due to invisibility in search results. It is expected that the portal will enable the researchers working in seri-related area to quickly search, analyze and construct new databases thus bridging the gaps in this field. The portal is available at URL http://www.seriport.in/.

Keywords: Database, Sericulture, Seri-Informatics, SeriPort, Silkworm

Technical Session 4-D :

Science-led Innovation

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Animal and Aquatic Genetic Resources

288 (O-40)

Status, Potential and Challenges to the Important Fish Germplasm *viz-à-viz* Aquaculture and Fishery Management in Coldwater Region, India

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Coldwater fisheries occupy an important place in fisheries sector of India. The country is bestowed with vast and varied hill fishery resources which are spread over the Himalayan and peninsular regions as upland rivers, streams, high and low altitude natural lakes and reservoirs. The present exploitation of fishery resources in upland Himalayan regions comes mainly from capture fisheries, though fish production through culture practices is gaining momentum. Indigenous fish species such as mahseer, snow trout and carps living within the Himalayan region form an important aquatic resource for the development of fisheries and aquaculture besides the introduced trout (*Oncorhynchus mykiss and Salmo trutta*) and carps (*Cyprinus carpio, Ctenopharyngodon idella and Hypophthalmichthys molitrix).* Experiences available within upland areas in India suggest there is potential for aquaculture and fisheries development by using locally available fish species to contribute to rural development and poverty alleviation. The major fish species in the Himalayan region are the cyprinids *Tor putitora, Neolissocheilus hexagonolepis, Schizothorax richardsonii, Schizothoraithys progastus, Schizothoraithys esocinus, S. niger, Labeo dero, Labeo dyochelius* etc. These significantly important coldwater/hill fishery resources in terms of gene pool are suitable for food, sport and ornamental value and thus we consistently made efforts to the development of scientific methodologies for their propagation and management. The paper presents recent technological innovations as well as some environmental, socio-economic, research and development aspects to be considered in the perspectives of coldwater aquaculture and fisheries in the hill states of Himalayan region, India.

Keywords: Himalayan fish germplasm, Culture, Management, Propagation

1626 (O-41)

Biodiversity *vis-à-vis* Oceanography: Few Case Studies Indicate Ecosystem Responses as a Major Factor Governing Fish Distribution in Space and Time

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Fish distribution along the western Indian coastal waters indicates a bias for pelagic-planktivores to the southern coast and carnivores to the northern coast. Southwest coast of India is an upwelling zone rich in phytoplankton dominated by diatoms during summer monsoon. The landing centre observation data since 1985 clearly indicate a dominance of Indian oil sardine (*Sardinella longiceps*) in this upwelling zone. The physiological activity of the fish is also tuned to the arrival of summer monsoon. A resting season is expected with the retrieval of monsoon in this area. Further north of our coastal waters we see that the dominant group of fishes includes the Sciaenids popularly known by the name ‘Ghol’ (*Protonibea diacanthus*), ‘Koth’ (*Otolithoides biauritus*) and ‘Dhoma’ (*Johnius dussumieri*). These fishes seem to flourish on the winter productivity in the northern coastal waters. The winter primary productivity in southern waters is not good enough to support carnivores with physiological active season during the winter. The productivity differences in the coastal waters in time and space and the oceanographic features supporting these could be studied from a synoptic scale with the help of satellite remote sensing and geographical information system. In this study we have utilized the various open sources remote sensing data to identify the oceanographic responses and the physical forcing that govern the distributional preferences of some dominant marine fish species.

Keywords: Fisheries, Physiology, Satellite remote sensing, Summer, Winter

604 (O-42)

Habitat Mapping of Deccani Breed of Sheep using Remote Sensing Variables: Implications for Breed Conservation and Disease Resistance

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Indian subcontinent is having rich source of Indigenous livestock breeds. Adaptation of various breeds to different agro climatic conditions has led to bio-diversity of sheep breeds which need to be conserved. Indigenous breeds contribute significantly to the livelihood of large proportion of small and marginal farmers and landless labourers. Bluetongue is an economically important midge-borne disease, caused by the bluetongue virus (BTV, Reoviridae: Orbivirus) and affects domestic and wild ruminants worldwide. BTV causes high morbidity and mortality resulting in huge economic losses to subsistence farmers. Past outbreaks of BT in India were detected mainly in crossbred and exotic breeds of sheep, whilst local breeds are considered to be relatively resistant.Remotely sensed variable have been used in the past to map global distribution of livestock. In this study a Non-Linear Discriminant analysis (NLDA) was carried out using temporal Fourier transformed remotely sensed variables as potential predictors of Deccan breed distribution and compared with the risk map of bluetongue. Village wise Deccani breed data for Andhra Pradesh was obtained from the DADF. Predictive performance was characterised using different accuracy statistics (sensitivity, specificity and kappa). Stepwise variable selection was carried out using the corrected Akaike Information Criterion (AICc).The habitat mapping resulted in suitability map for Deccani breed of sheep in South India. The map can be useful in planning conservation and also to introduce the breed in areas which are environmentally suitable for this breed. The potential of Deccani breed with respect to disease resistance and conservation planning is discussed.

Keywords: Bluetongue virus, Conservation, Deccani breed, Habitat, Modelling

845 (O-43)

Cytogenetic and Mitochondrial D-Loop Sequence based Characterization of Buffaloes of Odisha State in India

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Livestock biodiversity of Odisha state in India is reflected in almost all domesticated animals, reared to serve the needs of resource poor farmers. Odisha is well known for diverse buffalo genetic resources, catering to not only milk production but also as an important draft animal as well. Two buffalo populations of Odisha state, Chilika and Kalahandi have been recognized and included among the thirteen registered breeds recently. Chilika buffaloes are reared around the Chilika Lake, Asia's largest brackish water lake, remaining an important part of the Chilika ecology. Odisha buffaloes are kept under extensive system, Chilika having unique behavior of feeding on weeds submerged in the salty water of lake, purely maintained on grazing. Though low producers, they have unique milk products' properties that includes longer shelf-life of curd, unique taste etc. In this study, we used the cytogenetic constitution analysis and mitochondrial D-loop sequencing to explore the Odisha buffalos' riverine/swamp status and find their evolutionary relationships with other riverine and swamp buffaloes of India. Blood samples were collected from Chilika, Kalahandi and Paralakhemundi buffaloes at different locations of breeding tracts and cytogenetic screening resulted in identification of three swamp-riverine hybrid animals among Chilika, showing typical 49 chromosomes number with one large metacentric chromosome arising due to fusion of chromosomes 4 and 9, typical of hybrids. Both Kalahandi and Paralakhemundi being riverine type with 50 chromosomes. Mitochondrial D-loop sequencing of Chilika, Kalahandi and Paralakhemundi buffaloes of Odisha and haplotype sharing indicates, these three breeds/populations phylogenetically closer to Assamese buffaloes.

Keywords: Buffalo, Odisha, Mitochondrial D-loop sequence, Cytogenetic analysis

1342 (P-364)

Molecular, Cellular and Transcriptomic Evidences of Superior Heat Tolerance Potential of Indian Native Cattle

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In an attempt to undertake comparative evaluation of Sahiwal cows (Bos Indicus), Karan Fries cows (Cross-bred), Holstein Friesian cows (Exotic cattle) and Murrah buffaloes (*Bubalus Bubalis*) towards heat stress tolerance, large set of cellular and molecular data was generated across different temperature humidity index and seasons. The study involved 192 PBMCs and serum samples representing 10-12 healthy heifers collected at different THI i.e., 70, 75, 80, 85 and 90. Comparative cell proliferation rate of PBMCs, HSPs levels in serum, haematological, biochemical indices and transcriptome profiling of PBMCs across different cattle types and buffaloes was accomplished across different THI and seasons. The substantial inhibition of cell proliferation data was observed in Holstein and Karan Fries PBMCs at higher thermal stress. The serum level of three major chaperons (HSP70, HSP90 and HSP27) was relatively higher in Holstein Friesian and Karan Fries cows. Similarly, the transcriptional pattern of HSP27, HSP40, HSP60, HSP70 and HSP90 mRNA was relatively high in PBMCs of Holstein Friesian cows during peak summer. On the other hand, HSP transcripts in Sahiwal cows showed minimum change in expression with change in season. Comparative genome wide transcriptome analysis of PBMCs indicated difference in transcriptome signature of breeds in response to summer stress. The analysis revealed several heat responsive genes and pathways impacted to summer stress. Such study will be helpful in providing scientific basis that our indigenous cattle breeds have superior tolerance to heat stress and would be better in combating climatic change.

Keywords: Heat tolerance, Indian native cattle, Molecular and Cellular data, Transcriptomics

1800 (P-365)

Mining of Genome Wide Variations in Indian Native Cattle using High throughput Genotype by Sequencing Approach

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Genotyping-by-sequencing (GBS) has recently emerged as a promising genomic approach for exploring genetic diversity on a genome-wide scale. It provides a rapid, high-throughput, and cost-effective tool for a genome-wide analysis of genetic diversity and above that does not require a reference genome for single nucleotide polymorphism (SNP) discovery. In the present study, a total of 21.3 GB (GBS) data including 213217765 single reads (100bp) and 21321776500 bases was generated on 122 samples representing 8 diverse breeds from different agro climatic regions. After QC filtration, SNP were discovered using Linux based pipeline TASSEL. Amongst the clean SNps, 85001 were intragenic while rests (87495) were in the intergenic (introns or regulatory elements) regions. The observed alleles were compared across Ladakhi cattle from cold arid region with Sahiwal cattle from arid, RedKandhari cattle from tropical wet and dry region and Holstein Friesian (HF) from temperate region. The maximum number of unique SNPs were observed for Sahiwal (110945) followed by Red Kandhari (8826) and Ladakhi (8229) cattle while HF showed minimum number of unique SNPs. These SNPs can serve as candidate alleles conferring themotolerance for the climatic conditions of the specific zone. Phylogenic tree drawn on the basis of identified SNPs revealed the close grouping of breeds from similar agroclimatic zone. Sahiwal, Tharparkar, Hariana and Gir from semiarid region were grouped closely while RedKandhari and Ongole from tropical wet and dry region grouped together. Ladakhi cattle from cold arid region and HF, a tuarine breed from temperate region were placed in separate clusters.

Keywords: GBS, Genetic relationship, Ladakhi cattle, SNPs

532 (P-366)

Status of Small Indigenous Fishes of River Gandak

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Fishes occupy important place in overall aquatic biodiversity and play vital role in ecological harmony of aquatic ecosystem. Among 765 native freshwater fishes (NBFGR), about 450 may be categorized as Small Indigenous Fishes (SIFs) in India. The Upper, Middle and Lower stretch of river have been surveyed to enlist SIFs (≤25 cm) during 2014 - 2015 for assessing diversity, abundance and conservation status. A total of 65 species were recorded by fishing with cast net and modified barrier net, of these 45 species were SIFs belonging to 16 families and 6 orders, and the rest 20 species were non-SIFs. Among SIFs, 13, 3 and 29 species have been considered as food, ornamental and food-ornamental value respectively. Shannon's diversity index (H') indicated better SIFs diversity in Lower (2.8) followed by Middle (2.7) and Upper (2.5) stretch. The highest number of species/taxa were recorded under the family Cyprinidae (38%) while order Siluriformes (6 families) represented maximum numbers of families. The most abundant species recorded was *Aspidoparia morar* (21%). The conservation status of SIF species recorded as Least Concern (91%), Near Threatened (5%) and Not Evaluated (4%) as per IUCN Red List (version; 2015-4). The study revealed that River Gandak support rich diversity of SIFs with similar distribution pattern among surveyed stretches, and none of the recorded SIFs falls under threatened category. However, better management strategies such as controlled harvest and scientific fishing policies will ensure sustainable exploitation and conservation of SIFs in the River Gandak.

Keywords: Small indigenous fish, River gandak, Conservation status

581 (P-367)

Evaluation of Annual Trends for Milk Production and Age at First Calving of the HF × Sahiwal Crosses in India

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To determine the effectiveness of breeding programme, it is very much essential to evaluate the genetic trends in dairy cattle population. The present study was aimed to estimate the genetic change in the performance of Frieswal (HF×Sahiwal) cattle, which is one of the crossbred cattle strain developed in India with 5/8 Holstein Friesian inheritance. First lactation records of 8839 Frieswal cows from 37 Military Farms, over a period of 24 years (1989 to 2012) sired by 107 sires were analyzed to estimate genetic and phenotypic trends for first lactation 300 day milk yield (300DMY) and age at first calving (AFC). Variance components were estimated from single trait animal model analysis by REML method using WOMBAT software. The overall mean of 300DMY and AFC were 2840.820±7.623kg and 979.066±1.852 days, respectively. The heritability estimates of 300DMY and AFC were 0.047±0.017 and 0.039±0.013, respectively. Breeding values of the 107 sires were also evaluated and 52 sires exceeded the herd average. Top ten per cent of the bulls had 4.22 to 8.43 per cent genetic superiority over the population. The phenotypic and genetic trends for AFC were -6.250 ±1.950 and 0.356±0.104, respectively. The decline in the phenotypic trend in the AFC might be due to the managemental interventions. The phenotypic and genetic trends for 300DMY were 2.426± 6.933and 0.626±0.308 kg, respectively. So it can be concluded that the implementation of breeding programme has resulted in the improvement, but to a limited extent and more efforts are required in selection and management to achieve the target.

Keywords: AFC, Frieswal, Genetic trend, Heritability, Milk production

654 (P-368)

Delineating Y-Chromosome Variations in Indian Native Cattle Breeds and Crossbred Population

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The paternally inherited Y chromosome markers have been used widely in population genetic studies to trace paternal lineages, to understand differences in migration pattern and populations admixture in animals. In the absence of crossing over, Y-chromosomal markers in the non-recombining male-specific region (MSY) are mostly transmitted as haplotype. Recent studies of five polymorphic sites on DDX3Y, UTY and ZFY genes of bull MSY assisted in the identification of three haplogroups (Y1, Y2 and Y3) in contemporary cattle. Here we report the screening of five SNPs (ZFY9- 120> C/T; ZFY10- 655> C/T; DDX3Y1- 425>C/T; DDX3Y7 -123>C/T and UTY19-423>C/A) on bull MSY employing optimized and validated allele-specific PCR (AS-PCR) protocols. We identified all the three haplogroups (Y1, Y2 and Y3) by screening 181 bulls from 10 native cattle breeds (Gir, Kankrej, Khillar, Mewati, Nagori, Nimari, Rathi, Sahiwal, Tharparkar, Malnad Gidda) and 50 HF crossbred animals using standardized AS-PCR. Y1 and Y2 were restricted to HF crossbred bulls with a frequency of 0.98 and 0.02, respectively. The high frequency of Y1 haplogroup is possibly due to the occurrence of Y1 lineage predominantly in HF bulls. All the native cattle breeds were observed to have pure indicine type (Y3). These cost effective AS-PCR protocols may be useful for reliable and accurate genotyping of Y-SNPs in diverse native cattle breeds, exotic and crossbred cattle populations. Moreover, genotyping of Y-specific microsatellite markers has shown additional variability in Indian native cattle breeds and resulted splitting of Y3 into additional haplotypes for the first time.

Keywords: MSY, Pseudoautosomal region, Y-haplotype

873 (P-369)

Mining of SSRs from the Brain and Gonads of *C. batrachus* (Linnaeus, 1758) using RNASeq Data

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Clarias batrachus is a commercially important catfish, which is listed in IUCN Red List under endangered category. However, limited genomic resources available for this species are one of the major constraints for its conservation, management and genetic improvement programs. SSR markers are widely used for numbers of applications, i.e. population genetics, conservation biology and evolutionary studies etc. Whole genome and transcriptome data are being used recently as a powerful platform for development of SSR markers. In the present study, the transcriptome data of *C. batrachus,* generated from ovary, testis, male brain and female brain were assembled separately using Trinity software. The transcripts, thus, obtained were pooled and made non-redundant datasets. The SSRs were further mined from the non-redundant transcripts. Mono repeats were found to be abundant (51%) followed by di (35.3%), tri (10%), tetra (2.70%), penta (0.2%) and hexa repeats (0.007%). These transcripts were further mapped on to the *C. batrachus* genome and only those SSRs were mined which were present in both transcriptome and genome after the removal of mono and complex SSR and the primer were identified using Primer3. This resulted in identification of 19,046 uniquely *in silico* amplified SSRs on to the genome of *C. batrachus*. The annotation of SSRs associated with some of the important traits, *viz*. embryogenesis, growth, immune and neural related functions resulted in identification of 66, 231, 88 and 126 SSR, respectively.

Keywords: *Clarias batrachus*, SSR, Transcriptome

950 (P-370)

Evaluation of Prolificacy in Different Crossbred Ewes (GMM and Avishaan)

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A breeding scheme was initiated at ICAR-CSWRI to introgress fecundity Booroola gene from Garole(G) to Malpura(M) sheep. GMM crosses (25%G&75%M) inheritance were produced. To overcome lower pre-weaning growth of GMM, Patanwadi(P) inheritance was introduced and Avishaan was developed. Lambing records of 1082 GMM (2006-16) and 265 Avishaan (2010-16) were analysed. Overall percentage of single, twins, triplets and quadruplet lambing in GMM were 47.97, 46.86, 4.80 and 0.37% with litter size at birth being 1.58. In Avishaan, the corresponding figures were 53.58, 43.40, 2.64 and 0.38% with litter size at birth being 1.50. During the current year 2015-16, corresponding figures were 21.31, 62.30, 13.93 and 2.46% with litter size at birth of 1.98 were observed in GMM , whereas in Avishaan these were 42.86, 54.14, 2.26 and 0.75% with litter size at birth being 1.61. Results revealed that FecB++ GMM ewes had litter size of 1.09 whereas FecB B+ ewes had a litter size of 1.65. There is gain of 0.56 litter due to introgression of one copy of gene. FecBBB ewes had a litter size of 1.87 and there is gain of 0.22 litter due to additional copy in GMM. FecB++ Avishaan ewes had litter size of 1.07 whereas FecBB+ ewes had a litter size of 1.67. Gain of 0.60 litter due to one copy of gene. Carrier FecBBB ewes had a litter size of 2.09 resulting in gain of 0.42 litter due to additional copy of gene in Avishaan. Results indicated introgression of fecundity gene resulted in increased prolificacy.

Keywords: Booroola, Fecundity, Litter size, Prolificacy, Sheep

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992 (P-371)

Exploration of Novel SNPs in BMPR1B, BMP15 and GDF9 Genes for Association with Prolificacy in Seven Indian Goat Breeds

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Developing countries produce approximately 97% of the total amount of goat meat produced in the world, reflecting the great importance of goat meat to feed millions of people in these countries. Improvement of reproductive traits such as prolificacy could help to meet the nutritional needs of growing human population in the coming decades. In recent years, many studies on the genetics of prolificacy in small ruminants have highlighted the importance of candidate genes for fecundity in affecting ovulation rate and litter size through different mechanisms. In the present study, six novel SNPs in three candidate genes for prolificacy (BMPR1B, BMP15 and GDF9) were genotyped in seven breeds of Indian goats to evaluate their association with litter size. Tetra primer ARMS-PCR and PCR-RFLP based protocols were developed for genotyping six novel SNPs viz. T(-242)C in BMPR1B, G735A and C808G in BMP15 and C818T, A959C and G1189A in GDF9 gene. The effect of breed was highly significant ($p \leq 0.01$) on litter size but the effect of genotype was non-significant. The effect of parity on litter size was also significant in the prolific Black Bengal breed. The litter size differences observed between breeds are attributed to breed differences. Novel mutations observed at different loci in GDF9, BMP15 and BMPR1B genes do not contribute to the reproductive capability of the investigated breeds. Further studies with more number of breeds and animals exploring association of these novel SNPs with reproductive traits may be fruitful.

Keywords: Prolificacy, Indian goats, GDF9, BMP15, BMPR1B

1136 (P-372)

Studies on Genetic Diversity of Marwari Goat for Myostatin (*MSTN*) Gene

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Myostatin (*MSTN*) or Growth and Differentiation Factor (GDF-8) gene plays an important regulatory role in the muscle growth of the animals. The Marwari goat breed of Rajasthan is a well known meat breed of India characterized by faster growth and breeding efficiency under the tropical climatic conditions. Therefore the present study was conducted on 120 unrelated Marwari goats to assess the genetic variations present at exon 1 of *MSTN* gene through polymerase chain reaction- single strand conformation polymorphism (PCR-SSCP) technique. Genomic DNA was extracted from whole blood through spin column method using blood genomic DNA isolation kit. PCRs were performed to amplify exon 1 of *MSTN* gene using sequence specific primer designed from MSTN gene sequence (Gene bank accession no. DQ167575). 8% non-denaturing polyacrylamide gel electrophoresis (PAGE) was carried out to resolve the different banding pattern of amplified PCR products. Genotyping was performed according to the band pattern. The result indicated similar conformation pattern in all the samples investigated which could be indicative of absence of mutation in the exon 1 of the *MSTN* gene of Marwari goat. The monomorphic pattern detected for this locus in the present study is suggestive of fixation of this locus in Marwari goat. The unique pattern detected for Marwari goat could be used to identify Marwari breed from other native breeds of goats. However a study on large number of goats should be conducted before reaching a definite conclusion.

Keywords: Marwari goat, Myostatin gene, PCR-SSCP.

1599 (P-373)

Hypolipidemic and Hypocholesteremic Effect of Indian Ginseng "*Withania Somnifera*" in Normal and Synbiotic Supplemented Broiler Chickens

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Withania or Ashwagandha is well known for its hypolipidemic and cholesterol lowering effect. Keeping in view, the meat food security and growing concern about meat quality, the present study was designed to observe the hypolipidemic and hypocholesteremic effect of *Withania somnifera* either alone or in combination of growth promoter 'synbiotic' in broilers. A 42 day feeding trial was conducted under standard feeding and managemental conditions with broiler starter (0-21 days) and finisher (21-42 days) ration on 360 day old Vencobb broiler chicks randomly divided into 8 treatment groups (T_1-T_8) with three replicates of 15 chicks each. The T_1 group was kept as control whereas T_2, T_3 and T_4 were supplemented with 0.5%, 1% and 1.5% Withania root powder; T_5 and T_6 were supplemented with 0.025% and 0.050% synbiotic and T_7 and T_8 were fed on diet containing 0.25% Withania+0.025% synbiotic and 0.50% Withania+0.05% synbiotic, respectively. Serum was separated aseptically from blood (2ml) collected from brachial vein (two chicks/replicate) after 28 days of trial. Total cholesterol, triglycerides and high density lipoprotein (HDL) were estimated as per standard protocol. Low density lipoprotein (LDL) was estimated as per Friedwald's formula. The serum HDL, total cholesterol, triglycerides and LDL ranged from 44.17 (T_1, T_5) to 56.33 (T_4); 116.5 (T_8) to 137.33 (T_1); 46.5 (T_4) to 72.67 (T_1) and 51.67 (T_8) to 78.63 (T_1) mg/dl, respectively. Significant increase in serum HDL and reduction in serum cholesterol, triglycerides and LDL were observed with the supplementation of *W. somnifera* root powder. The study concluded that optimum performance could be achieved at 0.5% level of Withania in the presence of o.o5% synbiotic.

Keywords: Broiler, *Withania*, Synbiotics, HDL, Cholesterol

1612 (P-374)

In Silico Characterization and Evolutionary Analysis of Glutamine Synthase (glula) Protein of Teleosts

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Glutamine synthase has pivotal role in cell metabolism and function. In teleosts, the activity of Glutamine synthase is higher in brain than other tissues. In some fish species, brain Glutamine synthase activity and mRNA demonstrates for increase response to ammonia exposure, on the contrary in other species the increase in brain glutamine is accompanied by the decrease in glutamate. This overall reduction in brain glutamate suggests that ammonia toxicity in some fish species is partly mediated by an over activation of the glutamate NMDA receptors. In the proposed study, Glutamine synthase (glula) amino acid sequence of *Danio rerio* was retrieved from NCBI and used as a reference sequence. Blastp analysis was done with default value for all other parameters and E-value ($\leq e^{-10}$). A total of 37amino acid sequences from the top hits were downloaded in the FASTA format for *in silico* analysis. Physico-chemical analyses of these amino acid sequences revealed the most abundant amino acid residues, which were Ala, Leu, Ile, Ser, and Val. Analysis of the protein sequence domains showed the constant identification of Gln_synt_c domains and detection of three motifs. Phylogenetic analysis using MEGA 5.1 of Glutamine synthase proteins from Teleost, amphibian and mammals provided that these vertebrates are closely related to each other.

Keywords: Glutamine synthase, *Insilico*, Phylogeny, Teleost, Ammonia toxicity

1710 (P-375)

Strategy for Genetic Conservation of Bikaneri Camel for *Myostatin* Gene

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Myostatin (*MSTN*) or growth and differentiation factor 8 is a member of the transforming growth factor-β superfamily that plays an important role in the regulation of muscle growth. The camel popularly referred as “ship of the desert” is well known for its transportation and load carrying capacity in the desert ecosystem. Keeping in view, the dwindling population of the state animal “Camel” in Rajasthan, the present study was undertaken to characterize the Bikaneri breed of camel through PCR RFLP genotyping for growth affecting myostatin (*MSTN*) gene. A total of 25 blood samples from unrelated Bikaneri camel were randomly collected from different regions of Bikaner (Rajasthan), India. Genomic DNA was extracted from whole blood using blood DNA isolation kit based on spin column method as per standard protocol. The quality of extracted genomic DNA was checked on 0.8% agarose gel. The exon 2 of *MSTN* gene was amplified using homolog region of caprine *MSTN* primers designed from GenBank (Accession No. AB077206). The amplified 375 bp region of the exon2 of camel *MSTN* gene was digested with *Hae* III restriction enzyme at 37C for overnight. The genetic variability in exon 2 of *MSTN* gene in Bikaneri camel was assessed on 8% polyacrylamide gel electrophoresis to detect the different genotypic pattern. All the digested samples showed m allele with two fragments of 88 and 287 bp. The study concluded that all the animals were monomorphic and genotyped homozygous “mm” for the locus studied. The result showed the suitability of PCR RFLP for evaluating genetic variability and the information could be utilized in formulation of breeding plan to conserve this genetic resource.

Keywords: Bikaneri camel, *Myostatin*, PCR RFLP

1734 (P-376)

Linkage Disequilibrium and Haplotype Block Structure in Indian Milch Cattle

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To estimate genome-wide levels of linkage disequilibrium (LD) and to understand haplotype block structure in Sahiwal, Gir and Tharparkar cattle breeds, present investigation was undertaken using data generated with the IlluminaBovineHD BeadChip. The maximum average LD; measured by r^2 varied from 0.57 in Tharparkar to 0.59 in Gir cattle at a distance of 0-1 kb and minimum average value of r^2 varied between 0.17 in Sahiwal and 0.19 in Gir at distance of 200-300 kb, which indicated decline in r^2 value with increase in SNP pair distances. The magnitude and pattern of r^2 value of these cattle at different distances remains almost similar, indicating higher persistency of LD among these cattle. The joint population of all these cattle breeds resulted in maximum r^2 value of 0.53 at a distance of 0-1kb and minimum of 0.11 at 200-300 kb and beyond, which again revealed higher persistence of LD in the cattle breeds. Considering a threshold of useful LD value = 0.20 for estimation of genomic breeding value, the markers at physical genomic distance of 30-40 kb can be utilized for estimation of GBV in these cattle. A total of 14, 27 and 24% of SNPs were clustered into haplotype blocks in Sahiwal, Tharparkar and Gir cattle, respectively. The investigation presented first high density linkage disequilibrium map and haplotype block structure in Indian milch cattle breeds with possibility of undertaking genome-wide association studies. Further investigation of haplotype blocks may lead to identification of signatures of recent positive selection.

Keywords: Cattle, Genome, Haplotype block, India, Linkage disequilibrium

1739 (P-377)

Genomic Resources for Hypoxia Tolerance in Indian Catfish, *Clarias Magur* (Hamilton1822)

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The Indian catfish *Clarias magur* being bottom dwellers and inhabitant of marshy lands and aquatic bodies is frequently exposed to hypoxia or low dissolved oxygen conditions. In natural conditions it tolerates hypoxia in part by using its air-breathing capacity. However, molecular processes facilitating its adaptation to hypoxia were remains largely unexplored. This study was undertaken to generate the molecular resources to explore the probable mechanism of hypoxia tolerance in this important catfish species. The tissues studied are involved in metabolic regulation, growth, homeostasis, immune function and locomotion. The analysis employed the construction of twelve suppression subtractive hybridized cDNA libraries (six forward and six reverse) from six tissues of C. magur under experimental hypoxic and normoxic conditions to identify differentially expressed genes under normoxia and hypoxia. Annotation and pathways analysis of differentially expressed ESTs showed their involvement in a vast majority processes affecting metabolism, cellular processes, signal transduction and/or immune related functions. Additionally, 18 potential novel genes, were identified. Eight EST-SSR loci were found to be under positive selection, out of 68 identified. Thus, this study provides a valuable genomic resource in C. magur to study the molecular underpinnings of its adaptation to hypoxic environments as well as to assist studies on functional genomics, mapping and future genome projects.

Keywords: Genomic, Resources, Hypoxia, Tolerance, Catfish

1753 (P-378)

Development of Novel SSR Markers in Great Snakehead, *Channa Marulius* (Hamilton, 1822) for Utilization in Conservation Programs

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Channa species are widely recognized as economically and conservation-important species in southern and southeastern Asia. The great snakehead, Channa marulius is the fastest growing among murrels, a table delicacy and is promising high value aquaculture species. The limited knowledge of molecular markers and genetic diversity of wild populations of C. marulius are an impediment in developing the management strategies. The Simple Sequence Repeats (SSR) are considered to be among the best markers for genetic stock identification. The present study was undertaken to isolate and validate SSR loci; and assess genetic diversity from wild populations of *C. marilius*. The 524 novel SSR markers were developed through an enriched genomic library using pre-cloning selective hybridization approach. A total 154 primers yielded scorable amplicons of which 19 valid loci exhibited polymorphism. Genotype data of 67 individuals from three distinct natural riverine populations (Godavari, Mahanadi, and Teesta) of India was generated to assess the suitability for determining intraspecific genetic variation. The PIC values ranged from 0.366 to 0.831, which indicated moderate-to-high range of informativeness. Wrights fixation index (Fst) values ranged from 0.326 to 0.567 suggesting moderate level of genetic differentiation. Inter-specific cross-priming of SSR loci revealed successful amplification (20-60%) of heterologous loci in five related species. Results of preliminary observation demonstrated that these novel loci were promising for population genetic variation studies in C. marulius and could provide potential markers for at least three congeners.

Keywords: Simple sequence repeat (SSR), *Channa marulius*, Genetic diversity

1755 (P-379)

Development of mtDNA Character-Based Molecular Identification Key for Scombrids from Indian Waters

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Scombrids are one of the most economically and socially important marine species belongs to family Scombridae. Scombrids comprises 51 species and possess wide distribution across tropical, subtropical and temperate waters. 16 species occurrence has been reported in Indian water, which form an important fishery resources of the country. The group contributes a total production of 3, 75,481 tones, constitutes 10% of the total fishery, with high domestic and export value (CMFRI, 2015). Accurate identification of species and distinguishing it from closely related ones is important for fisheries management perspective. In the present study, the character based molecular identification keys for 17 species of scombrids occurring in Indian waters, were screened in-silico form data set comprises 603 mitochondrial COI sequences, using Barcoding with LOGic (BLOG: 2.0) tool. BLOG works based on logic formula, which identify the specific location of key diagnostic nucleotide for each species in a defined sets. COI analysis of scombrids occurring in Indian waters, revealed the nucleotide divergences value ranged from 2 to 22%. BLOG: 2 analysis clearly distinguished scombrid fish species from each other with 100 % true positive value and uncovered 39 unambiguous molecular keys, capable of distinguishing all reference taxa under study. These diagnostic molecular keys have the potential for translation into customised DNA chips, will have profound impacts on the species identification in all forms. The development of species specific molecular signatures and key diagnostic nucleotides for each species will be helpful in effective management of these important resources in the region.

Keywords: Indian waters, Molecular identification key, mtDNA, Scombrids

1765 (P-380)

The Complete Mitochondrial Genome of the Olive barb, *Systomus sarana sarana* and its Phylogenetic Status

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Systomus sarana sarana commonly known as olive barb is an important food and ornamental fish; and widely distributed in South East Asian countries. In India, it has wider occurrence throughout India except peninsular region (Talwar and Jhingran, 1991). The mitogenomic resource is important for comparative genome studies as well as phylogenetic reconstruction. In present study, the complete mitochondrial genome of olive barb was sequenced and annotated. The high quality genomic DNA was amplified into long 7-8kb overlapping amplicons which were used for library preparation using Ultra™ DNA Library Prep Kit. These libraries were sequenced through next generation sequencing (NGS) platform Illumina HiSeq 2500. The whole mitogenome of *S. sarana sarana* was 16.5kbp in length and consisted of 13 protein coding genes, 22 transfer RNAs (tRNA) and 2 ribosomal RNA (rRNA) and a non-coding region (D-loop). The positions of protein-coding genes and two rRNA genes were identified by sequence homology to other known Cypriniformes sequences in the GenBank. All tRNA genes were located and folded into their proposed clover-leaf structures. The overall base compostion of the mitogenome was comparable to other carps. Phylogenetic relatedness was ascertained using mitogenomes of 30 related fish species from NCBI. The clustering pattern indicated that the results were in line with the conventional classification. In conclusion, the mitogenome of *S. sarana sarana* was sequenced, annotated and its taxonomic status was confirmed.

Keywords: Mitogenome, NGS, *Systomus sarana sarana*

1775 (P-381)

Spatial Pattern of the Hard Corals of Mithapur Reef, Gujarat

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Coral reefs are one of the most ancient and dynamic ecosystems of India. Hard corals (*Scleractinia*), forms the one of the major building blocks of Coral reef ecosystems. Habitat distribution maps are often the core spatially consistent data set on which marine reserve networks are designed. Till date, the extend of hard coral distribution along the Saurashtra coast are less studied. This study records the spatial pattern of hard corals along the Mithapur coast, which lies in the northern part of Saurashtra, Gujarat and maps it over a GIS platform. Photo quadrant method was employed to study the occurrence and coverage of different species of Scleractinians. Distribution maps were created with help of ArcGIS 10.1, which revealed the spatial pattern of occurrence of each species. Overall hard coral presence was found more towards seaward side and along margins of the subtidal creeks. Distribution of some of the major species revealed that species such as Porites lutea, Porites lichen, Porites compressa and Acanthastrea hillae were found more towards northern side while Gonisatrea, Cyphastrea serailia and Favia favus were additional towards southern side of the study area. Survey also recorded feeble bleaching occurrence along the region. Database on the extend of distribution of Hard corals, which are protected under the Wild Life Protection Act 1972, Govt. of India, can help in taking proactive conservative measures in the current scenario of climate change and anthropogenic interventions.

Keywords: Distribution, *Scleractinia*, Saurashtra coast

Technical Session 4-E :

Science-led Innovation

Concurrent Session :

Microbial and Insect Genetic Resources

759 (O-44)

A Preliminary Study on Abundance of Selected Soil Organisms in Prominent Landuse Systems at Mid Country of Sri Lanka

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Information on below ground bio diversity is very meagre for Sri Lankan context. Hence a preliminary study was carried out in Udakumbura area (7°23'0" North latitude and 80°30'0" East longitude) to understand abundance of major belowground organisms in few representative landuse systems namely, Kandyan Home garden (HG), natural forest (NF), agro-chemical used conventional field (CL) and conventional field fallowed for period of one year (FF). Highest abundance of earthworms (78 individuals m^{-2}) was observed in NF followed by HG (73 individual m^{-2}). Least abundance (1 individual m^{-2}) was observed in CL. A strong positive correlation ($r = 0.79$) was observed between earthworm abundance and the soil moisture content. Highest abundance of free-living nematodes in NF was observed ($<0.05p$). Arbuscular Mycorrhizal Fungi spore density ranged from 148-243 spores in 50 g of soil, with the highest count occurring in the NF and FF. The higher number of bacteria colonies (2.4×10^4 cfu g^{-1}) and lower number of colonies (5.5×10^3cfu g^{-1}) was observed in NF and CL respectively. The highest amount of soil organic matter (5.94 %) was recorded in the NF whereas the lowest (1.66 %) was in the FF. Landuse practices have substantial effects on the abundance and diversity of the belowground organisms. Even if the Kandyan home garden was considered as a non-chemical perennial crop field, the abundance and diversity of belowground organisms was lower than the natural forest possibly due to the disturbances to the micro climate. Out of several organisms, earthworms seem to be more sensitive to agricultural practices.

Keywords: Belowground, Biodiversity, Kandyan home garden

1491 (O-45)

Soil Metaproteomics: A Novel Tool for Deciphering Functional Diversity from Environmental Samples

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Metaproteomics is a study of all proteins recovered directly from environmental samples at a given time and provides a direct evidence of functional diversity and structure among microbial community present in niches. Although potentially powerful, the use of metaproteomic analyses for the study of complex environmental consortia especially from soil is still in its infancy. Due to chemical composition and complexity of soil samples the exhaustive methods of extraction of metaproteome is a major challenge. Among several methodological challenges few are i) predominance of humic acids and phenolic compounds present in soil sample which hinder in downstream process, ii) the presence of low proteins in soil samples, iii) type of samples and spatial distribution, microbial diversity and dynamics of soil community, iv) sometime extracellular enzyme of microbial community strongly adhere onto soil minerals. Thus, there is need to develop a reliable method to extract metaproteome from soil. The aim of the present study was to evaluate the existing metaproteome extraction protocols and to develop and standardize a fast and reliable method for extraction of metaproteome from soil samples. The extracted protein were precipitated with either 10% TCA overnight at 4ºC or 0.1M ammonium acetate in methanol overnight at -20ºC. The protein pellet was dissolved in 0.5M TEAB buffer. The protein after 1D-SDS-PAGE evaluation was quantified, trypsinized and analyzed with LC/MS. The mass spectra were searched against the NCBInr using the software Spectrum Mill. The resultant data will be used to analysis the community function in detail.

Keywords: Metaproteomics, Metaproteome extraction, Functional diversity

1688 (O-46)

Draft Genome of a Phosphate Solubilizing Bacterium *Burkholderia Cenocepacia* PS27

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Burkholderia cenocepacia PS27 (earlier known as *Pseudomonas striata* PS27*)* is an efficient P bio-inoculant widely used by the farmers on variety of crop plants throughout India. It is capable of solubilizing 24-58.4% TCP and 5.26% MRP. Genome sequencing was done to understand mechanisms responsible for P solubilization. The genome sequence was obtained by PacBio sequencing technology and assembled in 4 contigs (7607708 bp) through denovo genome assembly methodology. The strain PS27 has three chromosomes and one large plasmid. Annotation of genes resulted in total 7035 gene which include 6911 CDS, 18 rRNA, 24 misc rRNA, 81 tRNA and 1 tmRNA. It also has 1483 genes for hypothetical proteins and 2302 unique genes. Further characterization of genes showed that it has genes for phosphate metabolism (pQQ cluster; *pqq*EDCB) and phosphate transportation (*pstS, pstC, pstA, pstB, phoU, phoR, phoB* and *phoH*), osmoregulation (glycine-betaine; *opuCA*, *opuCB* & *opuCC*), osmoprotectant (*osm*F, *yeh*Y, *yeh*X, *yeh*W). Strain PS27 has few unique genes like octopine metabolism (*occP, occM, occQ* & *occT*). It also has gene for 2-hydroxy muconate-semialdehyde hydrolase, which participates in 5 different metabolic pathways like Benzoate degradation, Toluene and xylene degradation, Carbazole degradation and Styrene degradation and *pcpB* which participate in pentachlorophenol oxidation. These results and analysis support the acceptance of strain PS27 as an efficient P-solubilizer, able to neutralize the osmotic stress and to transform the organic waste. This genome analysis will help to find out the regulatory mechanisms present in the bacterial cell.

Keywords: Genome analysis, Phosphate solubilization, Gene mining, Osmoregulation

1699 (P-382)

A Thermophilic Microbial Machine

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With the expansion of new chemical and physical methods being used for the synthesis of nanoparticles, concern for environmental contamination are also emerged as the chemical methods produce large amount of hazardous by products. Thus, now there is a need for microbe mediated synthesis process that includes a clean, non-toxic and eco-friendly method of nanoparticle synthesis. The objective was to find out a bacterial strain for synthesis of silver nanoparticles at high temperature. A bacterial strain NBLCHUR14 was isolated from hot water spring of Chumathang, Ladakh, India. Strain was Gram positive, able to grow upto 72 °C and have high growth rate at 42 °C. Strain NBLCHUR14 was used for the synthesis of Silver-nanoparticles at three different temperatures (37, 42 and 50 °C) with 100, 200, 300, 400 and 500 mili moles of Silver nitrate. Nanoparticles obtained were characterized and used for screening of antibacterial and antifungal analysis. Results concluded that strain NBLCHUR14 produced silver nanoparticles efficiently at high temperature. The strain was also screened for various industrially important extracellular enzymes viz; protease, amylase, lipase, cellulose and pectinase and showed positive production of all the enzymes at 55 °C. Thus strain NBLCHUR14, could be utilized to synthesize industrially important enzymes and biological Silver-nanoparticles in non-toxic manner.

Keywords: Nanoparticle, Thermophile, Enzymes, Hot Springs

Technical Session 5 :

Quarantine, Biosafety and Biosecurity Issues

1942 (O-47)

Trade and Biodiversity

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While trade is often regarded as one of the main causes for the loss of biodiversity due to its role in the global movement of pests and diseases, it is also a crucial driver for the preservation of biodiversity as it compels governments and economic operators to implement measures to protect agricultural productive capacity and to consider biodiversity as an economic asset and a working capital. Numerous endemic disease agents wreak havoc on such staples as cassava, maize, rice and wheat, and inflict substantial losses on pastures, threatening the livelihoods of vulnerable farmers and severely undermining the calorie intake and the nutritional status of millions in developing countries. These damages are exacerbated by climate change that increases pest and disease pressures due alterations in the host-pathogen-vector interactions thereby leading to more frequent outbreaks and upsurges; and the continuous appearance of new pathogens that are resistant to agrochemicals. Increased application of pesticides leads to loss of biodiversity due to their devastating impacts on natural enemies, soil fauna and pollinators. These threats are exacerbated by man-caused introductions of invasive alien species that severely undermine the sustainability of farming systems leaving producers helpless towards these unfamiliar invaders against which no traditional management practices work. The WTO Agreement on the Application of Sanitary and Phytosanitary (SPS) Measures ensures the safe transboundary movement of goods, including foodstuffs. It aims to limit the risk of introduction, through the trade pathway, of pathogens that could otherwise severely damage plant, animal and human health or the environment. Importing plants, animals and their products requires a science-based risk assessment to design adequate risk management measures that guarantee the freedom of imported products from quarantine pests and diseases.

1218 (O-48)

Biosecurity Policies Influencing International Exchange of PGR

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Biosecurity policies facilitate transboundary exchange of PGR by preventing introduction of pests into new areas. Although, international exchange of PGR has contributed significantly towards crop improvement, many pests have moved across countries. Most countries regulate import due to the pest risk posed by such imports. Presently, under the Convention on Biological Diversity (CBD) and World Trade Organization (WTO), international exchange of PGR has been transformed. WTO promotes trade by undertaking quarantine while CBD aims at protection and conservation of biodiversity. National regulations related to biosecurity influence safe international movement of PGR. PGR exchanged under ITPGRFA is also governed by respective national biosecurity regulations. The Plant Quarantine (Regulation for Import into India) Order (2003) and its amendments complies with the SPS Agreement of WTO. The National Seed Policy (2002) emphasizes on excluding pests in national seed production programmes. The Insecticides Act (1968) emphasizes on safety of human beings and animals from new molecules. Protection of Plant Variety and Farmers' Rights Act (2001) provides for protection of plants/ environment while Biological Diversity Act (2002) needs to regulate in-country movement of infected/ infested material. Environment Protection Act (1986) needs provisions for Invasive Alien Species, and exchange of genetically modifies PGR in compliance with Cartagena Protocol on Biosafety. Under such a fragmented national system, national legislations need to be in harmony with each other while complying with international norms. The establishment of National Agricultural Biosecurity Authority, Biosafety Regulatory Authority of India and enactment of Seed Bill need to be top priority for holistic biosecurity.

Keywords: Biosecurity, Policies, Exchange, Plant genetic resources

1219 (O-49)

Tuta absoluta: A New Invasive Alien Insect Pest of Solanaceous Crops in India– Threat Assessment and Management Options

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The tomato pinborer, *Tuta absoluta* (Gelichiidae: Lepidoptera), originated from Peru is one of the most devastating insect pests of tomato in the countries it has invaded so far. Invasion of this insect was first detected in India during October 2014 from tomato fields in Pune, Maharashtra. *Tuta absoluta* has the ability to reduce yield and fruit quality of tomato grown in green house and open field conditions. Severely attacked tomato fruits lose their commercial value. The present study critically assessed its spread to new areas, damage potential on its host plants and management options. The monitoring data revealed that this invasive pest has now established permanently in almost all the tomato growing regions of the country sparing few locations. The damage assessment on tomato revealed upto 64.8% leaf damage and 92.3 % fruit damage in certain areas. On potato, upto 23.2% leaf damage due to *T. absoluta* feeding has been quantified. Under net house studies, the *T. absoluta* has been found to prefer an array of solanaceous hosts plants either for egg laying or larval feeding. The tomato was the most preferred host followed by potato and egg plant among the cultivated host plants screened. The bio-intensive management options viz., monitoring of the adults by sex pheromone lures, release of *Trichogramma* spp., to destroy the eggs and use of botanical and *Bacillus thuringensis* formulations in addition to insecticides for the management of larval populations have been found effective for the management of *T. absoluta*.

Keywords: *Tuta absoluta*, Invasive pest, Solanaceous crops

1451 (O-50)

Biosecuring Import of Transgenic Crops Germplasm into India under Quarantine Umbrella

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Presently, in India, import of transgenic planting material is permitted only for research as per Plant Quarantine (Regulation of Import into India) Order 2003. ICAR-NBPGR, a nodal agency to issue Import Permit and undertake quarantine of imported transgenic planting material has established a National Containment/ Quarantine Facility (CL-4) to biosecure import of transgenics. During 2010-15, imported transgenic samples (4,336) comprising *Arabidopsis thaliana*, *Brassica oleracea*, *Eucalyptus camaldulensis*, *Glycine max*, *Gossypium hirsutum*, *Solanum lycopersicon, Mannihot esculenta, Nicotiana tabacum, Oryza sativa and Zea mays* with various transgenic elements/ traits from different countries were analysed for associated pest risk and processed for quarantine clearance. Quarantine processing including X-ray radiography of *G. hirsutum* and *Z. mays* resulted in interception of pests of quarantine significance. These included fungi: *Bipolaris maydis, Fusarium verticillioides and Rhizoctonia solani* on *Z. mays; B. oryzae, B. sorokiniana, F. verticillioides and Sarocladium oryzae* on *O. sativa; Phoma sorghina* on *A. thaliana*; Viruses: High plains virus (HPV), Maize chlorotic mottle virus (MCMV), Maize dwarf mosaic virus (MDMV) and Wheat streak mosaic virus (WSMV) on Z. mays; Insects: Sitophilus oryzae and Sitotroga cerealella in O. sativa. Of these, HPV, MCMV and WSMV are not yet reported from India. Infested/ infected material was salvaged. All rice samples were given mandatory hot water treatment. In addition, as per legislative requirement, all transgenic lines were also tested to ensure the absence of embryogenesis deactivator gene. Interception of different pests has biosecured our fields against the ravages of exotic pests, which otherwise would have caused severe losses.

Keywords: Transgenic germplasm, Quarantine, Biosecurity

1515 (O-51)

Role of Viral Diagnostics in Quarantine for Plant Genetic Resources and Preparedness

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International exchange of plant genetic resources (PGR) and trade play an important role in the long-distance dissemination of destructive viruses/strains, which could be a threat to agrobiodiversity. ICAR-NBPGR has been empowered for quarantine of imported PGR including transgenics for research purposes. Adopting a workable strategy of post-entry quarantine growing followed by use of combination of detection techniques viz., electron microscopy, ELISA and RT-PCR, 38 viruses of great economic and quarantine importance were intercepted in imported PGR in the last 15 years. The interceptions include 16 viruses not yet reported from India viz., *Barley stripe mosaic virus*, *Bean mild mosaic virus, Bean pod mottle virus*, *Broad bean mottle virus, Broad bean stain virus, Broad bean true mosaic virus*, *Cherry leaf roll virus*, *Cowpea mottle virus, Cowpea severe mosaic virus,* High plains virus, *Maize chlorotic mottle virus*, *Pea enation mosaic virus*, *Peanut sunt virus*, *Raspberry ringspot virus, Tomato ringspot virus* and *Wheat streak mosaic virus*. Besides, 19 viruses not known to occur on particular host(s) in India were intercepted and 20 viruses were intercepted in germplasm imported from CGIAR centres. Some of the intercepted viruses are not known to occur in India, but their potential vectors exist and also congenial conditions to multiply and spread destructive exotic viruses/strains. India also need to establish a strong network of interconnected accredited laboratories to quickly diagnose new viruses/strains; enhance surveillance capacity and develop early warning systems. This makes it imperative that India should put in place a “National Plant Biosecurity Diagnostic Network” to enhance preparedness.

Keywords: Viruses, Diagnostics, Quarantine, PGR

1527 (O-52)

Comparative Study of the Reproductive Biology of Gorse (*Ulex Europaeus*) in the Mount Lofty Ranges of South Australia and Central Highlands of Sri Lanka

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Gorse (*Ulex europaeus* L.) is an extremely competitive invasive plant that makes tremendous impact on native biodiversity and agricultural wealth. Several traits, namely fruit:flower ratio, seed production per pod, pod predation and the density of seeds in the soil seed bank were examined in two climatically distinct regions in its invasive range, South Australia and Sri Lanka. Results suggest that the reproductive success of gorse in Sri Lanka, in terms of fruit:flower ratio, is less than that of gorse plants in South Australia. Results also suggest that gorse populations in Sri Lanka had significantly higher seed numbers per pod compared with gorse in South Australia ($z = 3.758$, $P < 0.001$). However, given the similarity of medians this result must be interpreted cautiously. Predation of pods was negligible in the study sites in both countries during the period of study. We also observed a highly significant difference ($z = 15.470$, $P< 0.001$) in the density of gorse seeds in the top 5 cm layer of the seed bank between 3 m away from shrubs and under gorse shrubs. The estimated density of gorse seeds under shrubs in Sri Lanka was 2141 / m^2 which was 1.5 times higher than that of South Australia. The findings of this study provide some baseline information for managers to design programs for control of gorse. Also it reveals that the contributions of traits that influence the reproductive success of gorse could vary among countries in the invasive range.

Keywords: Fruit:flower ratio, Predation, Seed Bank density, Seed production, *Ulex europaeus*

1767 (O-53)

Cyprinid herpesvirus-2: Widespread Occurrence in Goldfish Populations in India

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Cyprinid herpesvirus-2 (CyHV-2), a member of the genus Cyprinivirus in family Herpesviridae, is a pathogen of goldfish, Carassius auratus and Prussian carp, C. gibelio. CyHV-2 causes a disease known as herpesviral haematopoietic necrosis (HVHN), which is responsible for heavy mortality in goldfish. The disease occurs during the spring and autumn when temperature of water ranges from 15-25 oC. Originally described from Japan in 1992, the disease has been reported from USA, Taiwan, Australia, New Zealand, UK, Switzerland, Italy, China and recently from India. Subsequent to first report of the disease outbreak from the country in 2014 under National Surveillance Programme for Aquatic Animal Diseases, samples of goldfish were collected from aquarium shops in Uttar Pradesh, West Bengal, Chhattisgarh, Uttarakhand and Andhra Pradesh, and screened for CyHV-2. The results indicate that the virus is quite widespread in goldfish populations. Importantly, the virus was detected in clinically normal goldfish, in addition to its detection in goldfish exhibiting clinical signs of HVHN. Therefore, it is reasonable to assume that movement of fish with subclinical infection is responsible for widespread occurrence of the virus. As no vaccine is currently available for the control of HVHN, therefore, on-farm control strategy should focus on biosecurity measures, surveillance and good husbandry practices. The biosecurity measures viz. secure water supply, use of quarantine and establishing virus-free populations of goldfish, etc. can be useful in preventing the spread of the virus.

Keywords: Cyprinid herpesvirus-2, Goldfish, Biosecurity, Surveillance

1764 (P-383)

Aquaculture & Biosecurity Concern in India: Search for Exotics.

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Since 1950s onwards, Govt. of India initiated steps to import aquaculturally important exotic fish species to improve India's aquaculture production. Blue revolution in India took off in 1971 with the launching of nationwide demonstration on composite culture. The introduction of polyculture techniques with exotic species had a huge impact in national aquaculture expansion. Though use of exotic fishes contributed significantly to aquaculture production, in due course, many species were illegally introduced in India by the farmers and fish hobbyists. Some of these fishes escaped to natural water bodies, posing threat to our ecological niche. Many of the exotic fishes are either highly adaptable to our environment, the threat posed by the species are of great concern, as some of these fishes look similar with other species in the same family. A critical aspect of monitoring of these exotic species is the ability to accurately identify any specimen to the species level, which is highly essential for early detection system. DNA barcodes using COI gene helps in rapid identification of the species. In the present study we accurately identified four exotic fish species *Oreochromis mossambicus* (Tilapia), *Pangasianodon hypophthalmus* (Malyasian catfish), *Piaractus brachypomus* (Pacu) and *Clarias gariepinus* (African catfish) collected from various natural water bodies, using COI gene amplification and by comparing the sequences with available information in the NCBI sequence database. Early detection and identification of the species will help the planners to comply with Aichi target, to control or eradicate the invasive alien species from our waters.

Keywords: Aquaculture, Biosecurity, Exotic fish, Barcoding, COI.

74 (P-384)

Incidence of Enzootic Bovine Haematuria in Cattle of Himachal Pradesh and Survey of Ferns in the Endemic Areas

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Enzootic bovine haematuria (EBH) is an economically important chronic disease of hill cattle characterized by intermittent presence of blood in urine, and is caused by malignant lesions in urinary bladder. The disease is a serious malady in several countries, including India and is incurable. EBH is caused primarily by chronic ingestion of bracken and other ferns, as the cattle graze or when ferns are used as a bedding material. The carcinogen in bracken is ptaquiloside (PT). It is suggested that high incidence of EBH occurs in areas where concentration of PT in ferns is high, whereas no disease is observed in areas where PT content is low. In Himachal Pradesh, surveys of the ferns in endemic areas like Lag valley, Kullu; Barot valley and Jhanjheli, Mandi; Tissa, Chamba; Fagu and Theog, Shimla were conducted and the samples were identified and digitalized. The major ferns identified included, *Pteris vittata, Onchyium contiguum*, *Dryopteris nigropaleacea*, *Woodwardia unigemmata*, *Polystichum squarrosum*, *Thelypteris dentate*, *Diplazium maximum*, *Pseudocyclosorus canus*, *Hypolepis punctata, Pseudophegopteris pyrrorhachis, Asplenium indicum, Adiantum venustum* and *Osmunda claytoniana.* Ptaquiloside isolation from these ferns would provide information about their role in carcinogenesis. Data on the incidence of EBH (collected from Department of Animal Husbandry, HP) during a period of 5 years (from 2009-13) showed a large number of cases in district Kullu (2,839), Mandi (1,439), Shimla (697), Sirmaur (300) and Kinnaur (122). Studies on the amelioration of fern toxicity in guinea pig laboratory animal model are in progress.

Keywords: EBH, Ferns, Himachal Pradesh, Ptaquiloside

200 (P-385)

Evaluation of *Nesidiocoris tenuis* (Reuter) (Hemiptera: Miridae) Preying on Invasive Insect Pest *Tuta absoluta* (Meyrick) (Lepidoptera: Gelechiidae) in Tomato

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Increased global trade in agriculture and transfer of plant materials have increased the risk of introduction of exotic pests (Satyanarayana and Satyagopal, 2013). Recently, in India severe incidence by the invasive insect pest, the South American tomato pinworm, *Tuta absoluta* (Meyrick) (Lepidoptera: Gelechiidae) was reported for the first time infesting tomato crop in Pune, Maharashtra. Later infestation was reported in the states of Karnataka,Tamil Nadu, Gujarat & Andhra Pradesh (Ballal et al., 2016). A large population of zoophytophagous mirid, *Nesidiocoris tenuis* was observed to be associated with *T. absoluta* in the infested fields. A net house experiment was conducted to evaluate *N. tenuis* on *Tuta* infested tomato plants. The aim was to ascertain if releases of *N. tenuis* could reduce *Tuta* infestation or due to its phytophagous nature it could lead to significant damage of tomato plants. The treatments comprised of A) release of *N. tenuis* on *Tuta* infested plants and B) releases of *N. tenuis* on uninfested plants and C) *Tuta* infested plants were maintained as control. Results indicated that number of *Tuta* eggs and the % mined area were significantly lesser in treatment with *N. tenuis*. Number of necrotic rings per plant caused by *N. tenuis* was significantly lesser (1.59) in *Tuta* infested plants treated with *N. tenuis* compared to uninfested plants (3.45). It was also recorded that number of necrotic rings per plant increased with decreasing *Tuta* population. Further studies are needed to investigate the precise role of *N.tenuis* as a natural mortality factor of *T. absoluta* in field situations.

Keywords: *Nesidiocoris tenuis*, Necrotic rings, Tomato, *Tuta absoluta*, Zoophytophagous

249 (P-386)

Invasive Western Flower Thrips, *Frankliniella Occidentalis* (Pergande) (Thripidae: Thysanoptera): A Potential Pest and Tospovirus Vector

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The western flower thrips, *Frankliniella occidentalis* (Pergande), is a major polyphagous pest of agricultural and horticultural crops worldwide and one of the most destructive pest species in the order Thysanoptera (Rugman-Jones et al. 2010). It was first described in 1895 from specimens collected in California, USA (Pergande, 1895). From India, it has been reported for the first time based on specimens collected from tomato (Kaomud Tyagi and Vikas Kumar, 2015). Extensive surveys were carried out in Karnataka and Tamilnadu at monthly intervals from September, 2015 to June, 2016 for surveillance of spread of *F. occidentalis* to identify the potential distribution of the pest for delimiting or cordoning the area to initiate management measures. Different methods (standard beating and yellow pan traps) were used for sample collection from various ecosystems. But the species was not traced from any of the collected samples from Karnataka not even from Bangalore, from where the first specimens were collected. In February, 2016 however, 9 females and one male of *F. occidentalis* were collected on *Erythrina* sp. from Ooty in the Nilgiris, Western Ghats, Tamil Nadu. Apart from direct feeding damage, western flower thrips is one of the important vector of tospo viruses causing high economic loss worldwide (Wijkamp et al. 1995). Therefore, the report of this economically important species in India is a serious problem and a concern for quarantine authorities. Considering its economic importance as a serious pest and vector of tospoviruses, occurrence of *F. occidentalis* in other parts of India need systematic monitoring.

Keywords: *Frankliniella occidentalis*, Invasive thrips, Thysanoptera, Western flower thrips

1207 (P-387)

Identification of High-Risk Agro-Ecological Regions Using Species Distribution Modeling

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Invasive species may cause considerable impact on agriculture and food security. *Mimosa pigra, Annona glabra, Lantana camara, Prosopis juliflora* and *Parthenium histerophorus* are considered as priority invasive species in Sri Lanka. The potential areas of these species are not available for land managers for timely control and management actions. This study has modelled the suitable climate area for these invasive species under current climate scenarios using Maxent model. The discrimination capacities of these distributional models were determined by calculating the area under the receiver operating characteristic curve (AUC) criterion. The resulting models were found to have good discrimination ability of presence and absence, with very high AUC values of 0.888, 0.989, 0.910, 0.821 and 0.998 for *M. pigra, A. glabra, L. camara, P. juliflora* and *P. histerophorus* respectively. The study identified highly responding variables for the model prediction of each species. The maxent predictions were compared with predictions received using several other algorithms (glm, bioclim and domain) in R interphase and received quite similar pattern. Maxent predictions were overlaid on agro-ecological map of Sri Lanka and high-risk agro-ecological regions were identified for the five species considered. Resulting maps can be a useful tool for land managers to take information based decisions for control and management programs. They can be used in public awareness campaigns to enlist local communities in the management of existing infestations and the prevention of further invasion.

Keywords: Invasive Species, Maxent, Species Distribution Modeling

1333 (P-388)

Salvaging of White Tip Nematode Infected Paddy Germplasm by Hot Water Treatment

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ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR) plays an important role in exchange and conservation of plant germplasm. Every year large number of paddy samples meant for research purpose are received at ICAR-NBPGR for its quarantine processing. White tip nematode of rice, *Aphelenchoides besseyi* was intercepted in paddy seeds imported from Bangladesh, China, Japan, Philippines, USA and Vietnam. *A. besseyi* is one of the major seed borne pests of paddy therefore considered as a quarantine pest by several countries. This nematode cause considerable yield losses to the paddy in Brazil (50%), China (10-50%), India (20%). *A. besseyi* could survive several years in infected paddy seeds and serves as a source of primary inoculum for further spread and establishment in pest free areas. The nematode causes white tip disease in paddy, affects plant growth and vigor which results in less number of grains per panicle, abnormal elongation of panicles and chaffiness of florets. During last three years (2013-2015), a total of 473 samples of paddy were found infected with *A. besseyi*. All the imported paddy samples were subjected to hot water treatment (HWT) at 52°C for 30 min. After HWT, the seeds from infected samples were water soaked, split opened and observed for presence of *A. besseyi* and to see the efficacy of HWT in salvaging of *A. besseyi* infected paddy. This concept of re-examination of seeds from infected samples after HWT is therefore useful for confirmation of elimination of *A. bessyi* and to prevent an introduction of its exotic population.

Keywords: *Aphelenchoides besseyi*, Hot water treatment, Paddy, Quarantine

1336 (P-389)

Exotic Weed Seeds Intercepted in Barley Germplasm: A Concern of Biodiversity

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International trade is a major route by which non-indigenous organism are introduced into new habitats. some of the alien species become invasive when they are introduced deliberately or unintentionally outside their natural habitats into new areas where they express the capability to establish, invade and outcompete native species. About 40% of the species in the Indian flora are alien, of which 25% are invasive. Contamination of weed seeds in imported crop seeds are the major causes of invasive alien plant invasion. Invasive species cause loss of biodiversity including species extinctions, and changes in ecosystem function. Thus, invasive species are a serious hindrance to conservation and sustainable use of biodiversity. In view of the above, barley (*Hordeum vulgare*) seeds imported from Morocco were screened for weed seeds especially for the presence of exotic weed seeds. A total of 9688 samples of barley (*Hordeum vulgare*) seeds were imported from Morocco by the India office of ICARDA through ICAR-National Bureau of Plant Genetic Resources in October, 2015. Each sample was spread in a thin uniform layer on a clean white drawing sheet and examined with the help of magnifying lens. All weed seeds were collected and then segregated into different types on the basis of their shape, size, colour, texture and presence of any attachment. Percentage incidence on number basis, viability and weed risk assessment score of different weed species were determined. A total of 12 weed species were intercepted in 861 samples. Among 12 species, 05 species namely *Avena barbata*; *Centaurea melitensis*; *Convolvulus erubescens; Echium plantagineum* and *Galium tricornutum* are exotic to India and remaining 07 species are reported from India. It is evident that all the weed seeds were found viable. Weed Risk Assessment score was recorded between 08 and 15 for all exotic weeds and revealed that all intercepted exotic weeds have potential to become problematic weeds in India.

Keywords: Barley, Biodiversity, Germplasm, Weed seed

1454 (P-390)

Capacity Building of Enforcement Agencies for Transboundary Movement of LMOs in India

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The growing demand for food requires safeguarding agrobiodiversity for future food production, and genetic diversity for ecosystem resilience. Living modified organisms (LMOs) is one of the strategies to keep pace with increasing food demand. Cartagena Protocol on Biosafety (CPB) specifically focuses on transboundary movement of LMOs resulting from modern biotechnology that may have adverse effects on biological diversity and risks to human health. Capacity building of enforcement agencies- plant quarantine and customs officials, first line of defense for transboundary movement of LMOs was undertaken by ICAR-NBPGR to enable them to fulfil requirements of CPB Article 18: handling, transport, packaging and identification of LMOs. In India, ICAR-NBPGR is the nodal organization for management of plant genetic resources (PGR) including transgenics is vested with authority to issue Import Permit and Phytosanitary Certificate and undertake quarantine of PGR meant for research. The Bureau organized seven Training Workshops on *Strengthening Capacities of Plant Quarantine and Customs officials for Transboundary Movement of LMOs* supported by UNEP-GEF under Phase II Capacity Building Project on Biosafety, implemented by MoEF&CC. Four training workshops for Customs officials were organized at National Academy of Customs, Excise and Narcotics (NACEN), Faridabad and its Regional Training Institutes at Chennai, Mumbai and Kolkata. Three Workshops for Plant Quarantine Officials across the country were organized at ICAR-NBPGR, New Delhi. A total of 113 customs and 43 plant quarantine officials were trained throughout the country. Based on recommendations of workshops, an Interactive Meeting of both the enforcement agencies was also organized and important recommendations emerged.

Keywords: Capacity building, Customs, LMOs, Plant quarantine, Transboundary movement.

1519 (P-391)

RT-PCR Method for Detection of *Peanut Stunt Virus* in Soybean Germplasm

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Seed-transmitted viruses pose an important threat to agrobiodiversity, besides being easily introduced into new areas when infected seed is planted. Reliable and sensitive detection methodology is an important tool to identify and intercept such introductions. At ICAR- National Bureau of Plant Genetic Resources, most of the legumes are subjected to mandatory testing for seed-transmitted viruses in quarantine of germplasm. These tests generally include a combination of more than one technique viz., grow-out test followed by electron microscopy, enzyme-linked immunosorbent assay (ELISA) and reverse transcription-polymerase chain reaction (RT-PCR). Twenty one soybean leaf samples from symptomatic and asymptomatic plants were collected and analysed for the presence of 12 seed-transmitted viruses by ELISA using polyclonal antisera corresponding to each virus and *Peanut stunt virus* (PSV), a seed-transmitted virus, not yet reported from India was detected in two accessions of soybean imported from Costa Rica. Using RT-PCR, the ability of specific primer pairs to amplify PSV from soybean leaf samples was evaluated. The RT–PCR specifically amplified the 282 bp size of DNA fragment in two accessions of soybean. The amplified product was sequenced and it was found that it has 94% similarity with the other sequences of PSV available in the NCBI Genbank. The results indicate that the designed primer set is specific for the PSV and is useful for detection of PSV in soybean and other legume crops. The standardized RT-PCR assay will be useful for PSV-free germplasm exchange, trade and certification programmes.

Keywords: Detection, *Peanut stunt virus*, Soybean, RT-PCR, Quarantine

1631 (P-392)

Virus-infected Strawberry Seedlings from Himachal Pradesh Grown in Jeolikote (Nainital), Uttarakhand: A Need for Domestic Quarantine

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A survey was conducted in April 2013 in strawberry (*Fragaria vesca* L.) growing areas in Jeolikote (District Nainital) Uttarakhand. Strawberry plants (18) of cultivar Chandler showing yellowing viral symptoms on leaves were collected from farmer's field for testing. Commercially available strawberry antiserum kits against *Arabis mosaic virus* (ArMV), *Raspberry bushy dwarf virus* (RBDV), *Raspberry ring spot virus* (RpRSV), *Strawberry latent ring spot virus* (SLRSV), *Strawberry mild yellow edge virus* (SMYEV) and *Tobacco necrosis virus* (TNV) were used by DAS-ELISA and electron microscopy (EM) techniques to detect viruse(s). The results revealed presence of RBDV in 7 plants and SLRSV in 2 plants. Two plants were found infected with both the viruses. However, no virus particles could be detected by EM when leaf-dip method was used. Since the virus infected seedlings (suckers) were procured by farmer from Himachal Pradesh, there is need for strict interstate monitoring of movement of strawberry planting material and establishment of domestic quarantine. There is also a need for availability of diagnostic kits and production of virus-free strawberry seedlings for commercial use by farmers in strawberry growing states in India.

Keywords: Quarantine, Strawberry, Viruses

1653 (P-393)

Scyphozoan Jelly Fish Diversity in the Gulf of Mannar and Palk Bay with an Account on the Invasive Jelly Fish *Phyllorhiza punctata*

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Gulf of Mannar and Palk bay are the two unique ecosystems situated on the southeast coast of India bordering the state of Tamil Nadu. These two ecosystems boast a variety of marine fauna from all the phyla of the animal kingdom. The fringing coral reef ecosystem supports a thriving faunal community and the Gulf of Mannar, has been designated as the marine biosphere reserve, first of its kinds in India. However, increasing fishing pressure, provided opportunity for the invasive and nuisance species to establish in the ecosystem due to the absence of predators, which are regularly harvested by the fishing operation. The seasonal swarming of the scyphozoan jellyfishes in these two ecosystems is a regular occurrence in the summer months especially April, May and June months. The continuous monitoring of jelly fish swarm in the Gulf of Mannar and Palk bay since 2013 revealed that there are nearly nine species have been found to occur in these waters viz., *Mastigias cf. papua*, *Netrostoma coerulescens*, *Cassiopea cf. andromeda*, *Chrysaora caliparea*, *Rhopilema cf. hispidum*, *Crambionella stuhlmanni, Cyanea sp., Aurelia aurita* and *Phyllorhiza punctata*. The species *Phyllorhiza punctata* which is commonly called Australian white spotted jelly fish, native of Australia and Philippines has spread through various tropical countries through ships ballast. The routine swarming of this invasive jelly fish; especially in Palk bay is a cause of concern.

Keywords: Gulf of Mannar, Jellyfish, Palk bay, Scyphozoan

1752 (P-394)

Koi Sleepy Disease (KSD) in Koi Carps: A Wake up Call for Implementing Biosecurity Measures in India

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The ornamental fish trade encompasses more than 90% of the freshwater species and Koi carp (Cyprinus carpio koi) is one of the most extensively traded fish species in the ornamental fish industry. The global ornamental fish trade relocates large quantities of live species between countries, and could spread exotic pathogens. Intensification of fish production provides an ideal environment in which disease causing organisms can cause serious damage to productivity. Some of the viral diseases affecting koi carp are infection with koi herpes virus, spring viraemia of carp virus, infection with ranavirus and carp edema virus (CEV), which causes 'koi sleepy disease' (KSD). The disease is spreading worldwide and causing huge losses in koi trade. KSD first reported from juvenile koi in Japan during 1970s and later, the disease has been reported from several countries, including USA, Germany, France, Austria, England, Czech Republic, Brazil and Netherlands. In India, KSD was detected recently in December 2015 in a ornamental fish farm in West Bengal. Sixty two out of 320 samples collected from 10 different locations found positive for KSD in PCR testing. The trade in koi might have lead to the spread of KSD in koi worldwide. Therefore, biosecurity measures in aquaculture need to be followed to minimize the risk of introducing exotic pathogens and its spreading. Biosecurity elements viz., reliable source of stock, diagnostic techniques, disinfection methods, quarantine and best management practices can help in minimizing spread of diseases and reducing the economic loss.

Keywords: Koi sleepy disease, Carp edema virus, Koi carp

1758 (P-395)

Red Bellied Pacu, *Piaractus Brachypomus*: An Exotic Fish Species of Concern in Indian Aquaculture

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Total fish production in India is 9.65 million t (2015), out of which more than 6.0 m t comes from aquaculture alone. Though legally many exotic species were introduced for improving fish production, of late farmers and aquarium traders are introducing many more exotic species illegally. Red bellied pacu, *Piaractus brachypomus*, an exotic fish species belong to family characidae is of Latin American origin, which was introduced in India illegally. The culture of pacu spread to almost all the state of India and recent survey shows 30% of the famers culturing pacu, either mono or polyculture with Indian major carps. Though, in its natural habitats, this fish is omnivorous in nature, the strong dentition of this fish resembles of carnivorous fish. There are reports of pacu caught from rivers of Kerala and Andhra Pradesh. If it get established in rivers, it may pose threat to our native fish diversity, as it is a voracious feeder. Pacu is also difficult to identify morphologically from its related species, red bellied piranha, *Pygocentrus nattereri*, also native of South America. We collected pacu from Periyar River, Kerala and identified using molecular markers, COI & 16s rRNA genes. Also confirmed the species by observing its dentition. It possess one row of human molar like teeth, which they probably use for breaking nuts etc. We found mostly vegetable matter, aquatic weeds in the gut and some digested fish parts also. This shows, pacu may consume fishes also. As more reports are coming up of availability of this fish in nature, more effort is required to content this species in natural waters and spread awareness among farmers for controlled culture of this species.

Keywords: Pacu, *Piaractus brachypomus*, Molecular identification, Exotic fish, India

Technical Session 6 :

IPRs, ABS and Farmers’ Rights

33 (O-54)

Alternative Options for Benefit Sharing under International Treaty on Plant Genetic Resources for Food and Agriculture

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Multilateral System (MLS) established under in the Treaty envisaged facilitated access to Plant Genetic Resources for Food and Agriculture (PGRFA) among contracting parties, through Standard Material Transfer Agreement (SMTA). To ensure benefit sharing accrued from utilization of the PGRFA the Benefit Sharing Fund (BSF) of the Treaty was established to receive financial resources for achieving the objectives of the Treaty. There is an accumulation of shortfall of funding in relation to targets established under the Treaty which was discussed at its Fifth Session of the Governing Body of the Treaty. It was felt to give highest priority to support BSF for continued resource mobilization to sustain funding. Ad Hoc Open-ended Working Group (WG) to enhance the Functioning of the MLS of Access and Benefit-sharing was thus established with the objective to increase user-based payments to the BSF in a sustainable and predictable long-term manner. This WG submitted its recommendations highlighting that the functioning of the MLS could be enhanced by increasing the availability of PGRFA, strengthening non-monetary benefit-sharing mechanisms, developing a Subscription Model/System for users of PGRFA and revisiting SMTA to increase user-based payments. All Regions expressed substantial support for Subscription Model/System. There is a need for a debate involving all stakeholders to suggest a possible revision of the SMTA specifically the Article 6.11. India needs to support the possibility of differential treatment for inclusion of types of users and crop groups for payment obligations such as non-profit institutes, small enterprises, and public organisations.

Keywords: Benefit Sharing, MLS, PGRFA, SMTA, Treaty

732 (O-55)

The Global Conservation Status of Indian Germplasm and its Implications

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Every nation has a unique cropping system that involves both ethnic and exotic food crops, with the latter forming a significant part of the staple diet, in many countries. These exotic crops have been introduced in those regions over a period of time through political and cultural interventions and their crop production has been sustained by an unrestricted global flow of plant genetic resources (PGR). This global flow of germplasm has always been channelized under an umbrella of policy networks that have been framed through international consensus. Though India has ratified all major global policies/treaties pertaining to germplasm access, repeated concerns have been raised globally, about the restrictions placed on flow and access of Indian germplasm from within the country. Using Genesys Global Portal on Plant Genetic Resources, we analysed the global conservation status of Indian-origin PGR accessions. According to Genesys, there are a total of 2,802,770 accessions in the global germplasm pool, accounted by 446 organizations. Amongst these, 100,607 are Indian-origin accessions, with 62,920 being conserved by CG genebanks. Similarly, out of 824,625 accessions of PGR conserved by 60 genebanks in Svalbard Global Seed Vault (SGSV), 66,339 accessions are of Indian-origin. The national import and export data has also been analysed for assessing the temporal pattern of germplasm flow, as influenced by the regulatory PGR policies, with special reference to the International Treaty on Plant Genetic Resources for Food and Agriculture as well as the newly enforced Nagoya Protocol under the Convention on Biological Diversity.

Keywords: Indian germplasm, Global gene banks, PGR policie

756 (O-56)

Mainstreaming Biodiversity into the Agricultural Sector

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Biodiversity mainstreaming is the process of embedding biodiversity consideration into policies, strategies and practices of key public and private actors that impact or rely on biodiversity, so that biodiversity is conserved, and sustainably used, both locally and globally. In Nagoya, Japan, in 2010, countries made a commitment to future generations and adopted the strategic plan for Biodiversity 2011-2020 and 20 Aichi biodiversity targets. The CoP-10 to the CBD has urged parties to develop national regional targets, using the Strategic Plan and its targets. Accordingly, India had revised its National Biodiversity Action Plan (NBAP) prepared during 2008 by developing National Biodiversity Targets (NBTs), keeping in view of the Aichi Biodiversity targets as a frame work. The NBT 5 says that, by 2020 measures are adopted for sustainable management of agriculture and NBT 7 advocates that genetic diversity of cultivated plants, farm livestock and their wild relatives including other socio-economically as well as culturally valuable species is maintained, and strategies have been developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity. The concept of “mainstreaming” biodiversity also includes the integration of biodiversity considerations into “cross-sectoral plans, programmes and policies. The suggested approaches adopted in the on-going study includes: a) Ecological intensification of production; b) Improved diversity in agricultural systems and landscapes and c) Sustainable consumption. Presently, the author has carried out substantial analysis and reviewed the existing policies mission’s/programmes/ projects implemented by the agricultural ministry and come out with a policy analysis on how efficiently the biodiversity can be mainstreamed into the agricultural sector. The outcome of this policy analysis will recommend some of the good agricultural practices that can be integrated into the agricultural sector towards conserving and sustainable utilization of agro-biodiversity, which will help us to achieve the mandate of the Biological Diversity Act, 2002.

Keywords: Mainstreaming, Agro-biodiversity, Biological Diversity Act

1580 (O-57)

Germplasm Exchange from India under the Multilateral System *vis-a-vis* the Biological Diversity Act, 2002: A Critical Appraisal

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The Multilateral System of access to plant germplasm is implemented in India through the Guidelines for Implementation of the International Treaty on Plant Genetic Resources for Food and Agriculture notified by the Department of Agriculture and Cooperation on 16th February 2015. This notification came into being through an exception provided under section 40 of the Biological Diversity Act, providing for non-applicability of sections 3 and 4 of the said Act. This paper explores the scope of germplasm exchange in India through this facilitated access and examines how far the two legal instruments are mutually supportive. The paper throws light into the issues of interpretation of the different provisions under the two systems and recommends a few options for their better convergence.

Keywords: Multilateral system, Access, Annex I crops, Biodiversity

12 (P-396)

Identification of Tomato (*Lycopersicon esculentum* Mill.) Cultivars using DUS, Electrophoresis and Chemo Taxonomical Methods

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Tomato genotypes consisting of six varieties (PKM 1, Arka Abha, Arka Ananya, Arka Meghali, Arka Saurabh and Arka Vikas), one hybrid (CoTH 3) and its parental lines (HN 2 and CLN 2123) where identified and characterized using morphological (DUS) markers, chemical test, dry seed protein profiles and SSR markers. Using 41 morphological DUS descriptors of PPV & FRA Authority, New Delhi and two new seed morphological descriptors based on the intensity of seed coat trichomes and embryo cotyledon curvature, the plant, fruit and seeds were discriminated for their morphological features. Among the 41 descriptors, 12 were monomorphic, 20 dimorphic and nine polymorphic. Seed chemo taxonomy was attempted by seeds of nine tomato genotypes were exposed to different chemicals *viz.,* phenol, NaOH, KOH and $FeSO_4$ and classified based on colour development for varietal characterization. Pantone colour matching system (PMS™) was used to assess the intensity of colour development. Both total soluble and water soluble proteins were extracted from dry seeds by 0.2 M Tris HCl and Millipore water respectively, then separated by SDS-PAGE. Between these two methods, water soluble seed protein profile had polymorphic bands, that could differentiate seven out of nine genotypes. Tomato genotypes were characterized based on five SSR markers and LESSRPSPGa amplified allele at 400bp only in HN2 genotype and this would be a useful reference for identification of HN 2. All the four different methods of grouping tomato cultivars varied in Mantel t-test. The lack of significant correlation among the four methods may due to SSRs measure genetic variation mainly in non-coding sequences and chemo taxonomical test is being specific to seed coat (only maternal character). Significant effects of SSRs, chemo taxonomical test and water extracted dry seed protein profiles might be useful for genetic purity assessment of tomato seed lot in a short period.

Keywords: Chemo taxonomical test, DUS, SSR markers, Tomato.

562 (P-397)

Do's and Don'ts F\for Farmers and Breeders under Present Indian Legislations

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India has been quite sensitive to the issues like conservation and sustainable use of biodiversity and illegal appropriation of biological resources by biopiracy and related activities. The need to protect the interests of local communities and indigenous people, who have been developing and conserving the biological diversity, from being ruthlessly exploited by multinational companies, has been long felt. Therefore, amendments have been made in the Indian Patents Act, 1970, in the year 1999 and in the year 2002. Also, the PPV & FR Act, 2001 and Biological Diversity Act, 2002 has been brought into effect. These acts were made to uphold the spirit of CBD, which provides a comprehensive and an internationally binding framework for the protection of biodiversity and for the recognition of sovereign rights of the Third World countries (rich in biodiversity) over biodiversity and its components. Incomplete knowledge among the stakeholders is a major constraint in effective implementation of these legislations. The major challenge to defend the nation's biological resources against biopiracy and related activities is the implementation a system of governance and conservation that efficiently protects against all unethical, unsustainable, unfair and inequitable exploitations of biodiversity. Without such efforts, such activities would continue to aid destruction of biodiversity and threaten the livelihoods of the communities that possess priceless knowledge about the secrets and conservation of the natural/biological resources. This article jots down the major do's and don'ts for farmers (both individually and as community) and breeders for efficient protection of their rights.

Keywords: Farmer's right, Biodiversity, Breeder's right, PPVFRA 2001, Biological Diversity Act 2002

25 (P-398)

Redefined National Action Plan for Effective Management of Plant Genetic Resources for Food and Agriculture (PGRFA)

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An internationally accepted framework for effective management of Plant Genetic Resources (PGR) was formulated as the first Global Plan of Action (GPA) for the conservation and sustainable utilization of Plant Genetic Resources for Food and Agriculture (PGRFA). It was formally adopted during the 4th International Technical Conference on PGR held in Leipzig Germany in 1996. The GPA was prepared with the active participation of 155 countries including public and private sectors and is considered to be a major contribution to the implementation of the CBD and also the supporting component of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA). The GPA has assisted national governments to reset their priorities and strategies for PGRFA. A National Plan of Action drafted on the basis of GPA is instrumental in reorienting and prioritizing the research and development agendas with regard to management of PGRFA. In the first GPA, there were 20 priority activities which have been revised to 18 in the Second GPA in four key areas. The priorities are inter-linked and may overlap for collective gains. The Second GPA has addressed the new challenges and opportunities. In India a National Action Plan (NAP) on agrobiodiversity was developed in 1999 from series of dialogues and in association with NAAS, ICAR and ISPGR. The priority areas identified served as the baseline for the development of redefined NAP which is drafted based on priority areas identified in the Second GPA. GIS based survey, inventorization and mapping of PGR, public-private-farmer participatory PGR

Keywords: Global Plan of Action, National Action Plan, PGR

280 (P-399)

Cashew Germplasm Exchange: Problems and Prospects

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Cashew (*Anacardium occidentale*) is an economically important crop cultivated in India. It was introduced from Brazil by Portuguese during 16th century. ICAR- Directorate of Cashew Research, Puttur, Karnataka established in 1986 is the nodal agency for cashew research in India. The Directorate has the largest cashew germplasm collection (539) in the country. In addition to these, three wild species namely, *Anacardium pumilum, A. othonianum* and *A. microcarpum* are also conserved. Of the 29 cashew varieties and 13 hybrids released in the country so far, the varieties are *per se* selections made from the germplasm and about 155 germplasm accessions have been effectively utilized for developing hybrids. Over the years, there has been an interest to grow cashew under high density planting systems akin to mango and guava to harness early benefits of higher productivity per unit area and efficient use of land, water and other resources. Since dwarf, high yielding genotypes/dwarfing root stocks are not available in cashew, periodic and intensive canopy management is necessary which escalates the cost of cultivation. Breeding efforts to change the architecture of cashew plant from tall to dwarf are not successful due to the kind of genetic material available in India. This warrants exchange of high yielding and dwarf varieties/germplasm from the native of cashew i.e. Brazil or adjoining countries. Unfortunately however, the attempts of germplasm exchange in this direction have not been successful so far and hence the present paper discusses the attempts, failures and future prospects of cashew germplasm exchange in India.

Keywords: Brazil, Cashew, Germplasm Exchange

423 (P-400)

Policies and on-going initiatives for enhancing access and benefit sharing and ensuring rights of farmers in conservation and sustainable use of Agrobiodiversity in Nepal

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Conservation and sustainable use of agricultural biodiversity is important for ensuring food and nutrition security and improving livelihood of smallholder rural farm families. Nepal has become party to major international Conventions and Treaties, formulated some relevant policies and strategies and drafted some legislations that are in the process for revision and approval. Since last two decades, the country has initiated and accomplished some novel programs and projects in conservation of agricultural biodiversity, enhancing access and benefit sharing (ABS) mechanisms and efforts to ensure rights of farmers and local community. These include few innovative Bioversity International supported projects such as in situ agrobiodiversity conservation, home gardens, Genetic Resource Policy Initiative, Neglected and Underutilized Species and most recently Local Crop Project for mountain food security and Diversifying seed sources for smallholder farmers. These projects have developed and piloted some good practices, approaches and tools for enhancing ABS mechanisms at the local level and ensuring rights of farmers in genetic resources. These include community based biodiversity management approaches including Community Seed banks, Participatory Plant Breeding, Diversity Field School and Diversity Fairs that are being promoted in agrobiodiversity conservation, community empowerment and livelihood improvement. This paper aims to document some of these novel approaches and good practices as well as recent initiatives in developing policy and legal framework. In addition, the paper also highlights current gaps and issues in policy and legal framework and field implementation of ABS mechanisms and farmers' rights provisions that support long term conservation of agrobiodiversity in Nepal.

Keywords: Access and benefit sharing, Farmersâ€™ rights, Policy and legal framework, Livelihood

599 (P-401)

Morphological and Molecular Variability in Mulberry (*Morus* Spp.) for the Development of Distinctness, Uniformity and Stability (DUS) Descriptors

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Mulberry (*Morus* spp.) is a crop of economic importance in sericulture industry and its leaf is the sole source of nutrition for the production of silk by the domesticated silkworm (*Bombyx mori* L.). The plant is predominantly out breeding and heterozygous therefore, genetic variability and diversity in the crop species is significantly high. An assessment of morpho-genetic variability in the mulberry germplasm was undertaken for the development of DUS descriptors. Based on the UPOV guidelines, 48 characteristics with unambiguous states of expressions were selected. Among the characteristics, 20 were categorized as asterisked (essential) and the rest 28 as non-asterisked. The characteristics were also categorised based on the type of expression as qualitative (13), quantitative (22) and pseudo-qualitative (13). Besides, 43 germplasm were selected as example varieties for representing states of expressions of all the descriptors. Further, the identified descriptors were validated using 16 extant varieties by recording the data across 3 different seasons. The cluster analysis of data by DARwin program depicted the distinctness, uniformity and stability of varieties indicating the utility of characteristics in development of DUS test guidelines of the crop. In addition, utility of the molecular markers in distinction was demonstrated with 36 important mulberry genotypes using 50 SSRs. The DUS test guidelines was prepared which will pave way for the test or examination required for registration of new or extant variety under Protection of Plant Varieties and Farmers' Rights (PPV & FR) Act, 2001 and also scientific basis for the protection of Plant Breeders' Rights.

Keywords: DUS Descriptors, Genetic Variability, Mulberry, SSRs, Test Guidelines

670 (P-402)

Recognition and Protection of Intellectual Contribution of Farmers and Plant Breeders in Development of New Plant Varieties in India- A Legal Perspective

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In India plant variety protection law is one of the nascent branches of intellectual property that has several facets. Till not for long and even for majority of farmers in India agriculture is not a business activity but a matter of culture. However, notion of property is based upon the psyche of commerce. Therefore before our farmers could start asserting their intellectual property in their contribution to the development of new plant varieties either directly or indirectly much time will pass as this realization is going to take longer some intermediate mechanism which could act like trustee of the Indian farmers interest is imperative. However, the present legislation suffers from a serious drawback in failing to create such mechanism. As the theory of dualism governs the relationship between Public International Law and Municipal Law in India. The present paper is a descriptive note on the relevant provisions of the International and National legal instruments.

Keywords: Recognition, Protection, Intellectual contribution, Farmer, Mechanisum

902 (P-403)

An Interactive Web Application and Data Management System for Hosting and Managing PGR and Associated Intellectual Property Records

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ICAR-National Bureau of Plant Genetic Resources besides being a conservator and curator of the germplasm, is a nodal organization for registering unique germplasm and facilitating registration of plant varietiesvarieties inlcuding farmers varieties with the Protection for Plant Variety and Farmers Rights Authority, India . Documentation and maintenance of the information related to Intellectual Property associated with PGR including plant varieties and germplasm registrations is a prerequisite for facilitating benefit sharing procedure. A web application has been developed for structured documentation and maintenance of the data being generated at ICAR-NBPGR. This application is developed in three tier architecture using Asp.net with C# and database has been designed in SQL Server. It has a user friendly interface through which basic information related to registered germplasm, plant variety applications, technologies developed and associated IPs viz, patents, trademarks, copyrights and designs can be accessed by all. It has six modules designed for management of user authentications and records of above mentioned IP domains. This web application links two very discrete yet cognate spheres of PGR and IP. Besides being a hosting and management tool, it may also serve as a reference portal for hosting important IP ownership information which will reduce risks of misrepresentation. The application is available at http://pgrinformatics.nbpgr.ernet.in/ipr/.

Keywords: Data Management, Intellectual Property Rights, Misrepresentataion, Plant Genetic Resources, Web application

1452 (P-404)

Management of Reference Collection in Wheat (*T. aestivum*) for DUS testing

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Conservation of Agro-biodiversity for the development of new plant varieties is duly recognized in Protection of Plant Varieties and Farmers' Rights Act, 2001 by conferring breeders' rights to the breeder of the variety based on the novelty, distinctness, uniformity and stability (DUS) testing. Thus, DUS test involves growing candidate variety and varieties of common knowledge (including released and notified varieties under section 5 of the Seed Act, 1966) under similar growing conditions and DUS characters are recorded for assessment of distinctness in the candidate varieties. So far about 340 bread wheat (*T. aestivum*) varieties have been released and notified in India. Every year, growing 340 varieties of bread wheat along with candidate varieties and recording DUS characters is a huge task in itself. ICAR-IIWBR, Karnal being the nodal centre for DUS testing in wheat has developed a data base on DUS characters of over 340 released and notified varieties of wheat in MS excel sheet, wherein each variety is described by a set of 38 DUS characters. This database can be used in limiting the number of varieties from reference collection by selecting the most similar varieties on the basis of information provided in the technical questionnaire by the breeder of the candidate variety. The grouping characters followed by essential characters in the candidate variety are used in a sequential manner in order to select the most similar varieties for DUS testing. This has helped in reducing the workload and cost of testing and also increased the efficiency of DUS testing.

Keywords: Reference collection, DUS testing, Wheat, Database

1563 (P-405)

Breeder - Farmer Benefit Sharing: New Way Forward

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The effective system of Benefit sharing for the Breeders is in operation in many countries. However ,the benefit sharing is only for the original and for the sponsor breeder. In India, on other side the farmers communities are also sharing the benefits of the releasing the farmers variety. However, the Breeders are interested in knowing the performance of the newly released varieties on farmers fields and on the other hand the farmers are interested in testing the new farmers variety by the qualified breeder at his farm. This will increase the performance of both the Breeders variety as well as the farmers variety on the commercial farmers fields .Hence a "sui genesis" system of benefit sharing amongst the farmers and scientist can be designed. The group of farmers who are keen to test the promising material of the crop breeder can be assigned the yields trials .The actual yield levels on the farmers field will boost the confidence of the original breeder if it is upto the mark. Hence he can share some of the benefit of his share to the farmers as the variety will be fulfilling the VCU in total. On the other hand the farmers who want to release a farmers variety often come across certain problems regarding the identification of the DUS characters of the variety and also for testing the variety for certain quality parameters. The group of the Breeders can be assigned this technical job who are entitled to get some benefit share of the farmers variety.

Keywords: benefit sharing, Breeders variety, Farmers variety

1646 (P-406)

Access and Benefit Sharing of Marine Genetic Resources in Areas beyond National Jurisdiction for Sustainable Conservation

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The International legal body that defines rules and regulations for trade through World Trade Organisation has Trade Related Intellectual Property Rights annexed, that defines territorial nature of a country with respect to jurisdiction. The adoption of Convention on Biological Diversity (CBD), ensures sovereign right of a nation on genetic resources. Though territorial flora and fauna have legally evolved from being common heritage of mankind to sovereign right of a nation, the marine environment comprising aquaflora and aquafauna of the seas need clarity of regulation from mare librium to global regulation of high seas for ecological sustenance and conservation as the principal of sovereign right of a state for Marine Genetic Resources (MGR) does not apply to Areas Beyond National Jurisdiction (ABNJ) through United Nationals Convention on the Law of the Sea (UNCLOS) declared seabed area for 90% patent claims related to MGR opening a Pandora's box of access and benefit sharing issues. An analysis of nucleotide patents in GenBank related to MGR was done for ABS. With deep sea mining activities under contract of International seabed Authority, regulation through policy governance structure is needed before the unknown/unexplored/undocumented flora and fauna is lost in golden chase of poly metallic Sulphides/ Hydrothermal Vents, Cobalt rich Ferromanganese Crusts and polymetallic nodules. The paper discusses MGR ABS issues related to ABNJ and policy intervention needed to regulate impact of deep sea mining on Marine Genetic Resources.

Keywords: Access and Benefit Sharing, Biodiversity, Marine Genetic Resources

1662 (P-407)

Implications for Access and Benefit Sharing of pre-CBD and post-CBD Sharing of Zebra Fish (Danio rerio) Germplasm from India

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Zebra fish has been used as a model experimental animal since 1960's (Pre-CBD era) when biological material was considered common heritage of mankind. Its introduction to the western world was fuelled as an aquarium tradable commodity, later on becoming an instrument in the hands of biologist. The model experimental fish, Danio rerio, Zebra fish procured from Asian freshwater streams ranks second with most patented nucleotides among bony fish was studied for its implication in access and benefit sharing from C12N, C07K, C12P, A61K, C07H, G01N, C12Q, A01H, A61P and H04B International Patent Classification Codes . Of the strains widely used in experiments, Wild Indian Karyotype (WIK) source of origin was screened. After enactment of Biological Diversity Act and Rules, for accessing any germplasm from Indian territory for research , permission from NBA is mandatory. Further on, for any Patent grant related to the germplasm, NBA approval is needed where access and benefit sharing course is decided. CBD through Nagoya protocol allows for present day sharing, with governance rules in place. According to GenBank Release 92 to Release 211, a total of patented 12103 nucleotide sequences belonged to181 species of fish genetic resources from a total of 32,100,979 nucleotide sequences from all biological organisms were seen. Zebrafish alone had 25,8713 sequences submitted of which 2684 were patented sequences. An examination of patent claims and description reveals that the origin of wild type strain is not mentioned. Hence, having governace implications on access and benefit sharing of Indian Germplasm

Keywords: Access and benefit sharing, Patent, Zebra fish

1795 (P-408)

Registration of Onion and Garlic Varieties for Protection through PPV&FRA

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Distinctness, uniformity and stability test (DUS) are essential for registration of varieties under “Protection of Plant Variety and Farmers' Rights Act 2001 (PPV&FRA) and 114 crops/ species have been notified for registration including onion and garlic in India. DUS test guidelines for onion and garlic have been notified by PPV&FRA in 2009 in India with 34 DUS test characters for onion varieties and 32 characters for garlic varieties. ICAR-DOGR, Rajgurunagar, Pune is working as a Nodal Centre for conducting DUS test for onion and garlic. All the available short day varieties of onion and garlic are being maintained at ICAR-DOGR, Rajgurunagar and ICAR-IARI, New Delhi whereas, long day varieties are maintained at ICAR-CITH, Srinagar. Multiplier onion is being maintained at TNAU, Coimbatore. Thirty-eight *rabi* onion varieties including land races are being maintained during *rabi* season whereas 10 onion varieties during *kharif*. All the 19 garlic varieties including land races being maintained during *rabi* season. DUS test has been initiated in onion and garlic since *rabi* 2012-13. One dark red onion variety ‘Bhima Raj’ has been registered with PPV&FRA, New Delhi for its protection as extant variety of ICAR-DOGR with Registration No. 262 of 2015 dated 19th October, 2015. However, proposals for seven onion varieties *viz;* Bhima Dark Red, Bhima Shakti, Bhima Shweta, Bhima Shubhra, Bhima Kiran, Bhima Red and Bhima Super have been already submitted and are under registration/ DUS Testing by PPV&FRA.

Keywords: Onion and Garlic, DUS Testing, Registration, PPV&FRA, Breeder Rights

1940 (P-409)

Access and Benefit Sharing in Participatory Plant Breeding in Southwest China

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This contribution discusses access and benefit sharing within the context of participatory plant breeding. It presents how Chinese farmers and breeders interact in relation to crop improvement and on-farm maintenance of plant genetic resources. Based on more than a decade of action research, a number of institutional changes were accomplished as a result of the interactions between national and provincial breeding institutes, rural development researchers and local maize farmers. Although the respective legislation in China is not yet adequately formulated, access and benefit sharing can still be addressed in contracts and by labeling products of a particular geographic origin.

Keywords: Access and benefit share, Participatory breeding, Plant genetic resources

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Partnership, Networks and Capacity Building

27 (P-410)

Redefined National Action Plan for Effective Management of Plant Genetic Resources for Food and Agriculture (PGRFA)

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An internationally accepted framework for effective management of Plant Genetic Resources (PGR) was formulated as the first Global Plan of Action (GPA) for the conservation and sustainable utilization of Plant Genetic Resources for Food and Agriculture (PGRFA). It was formally adopted during the 4th International Technical Conference on PGR held in Leipzig Germany in 1996. The GPA was prepared with the active participation of 155 countries including public and private sectors and is considered to be a major contribution to the implementation of the CBD and also the supporting component of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA). The GPA has assisted national governments to reset their priorities and strategies for PGRFA. A National Plan of Action drafted on the basis of GPA is instrumental in reorienting and prioritizing the research and development agendas with regard to management of PGRFA. In the first GPA, there were 20 priority activities which have been revised to 18 in the Second GPA in four key areas. The priorities are inter-linked and may overlap for collective gains. The Second GPA has addressed the new challenges and opportunities. In India a National Action Plan (NAP) on agrobiodiversity was developed in 1999 from series of dialogues and in association with NAAS, ICAR and ISPGR. The priority areas identified served as the baseline for the development of redefined NAP which is drafted based on priority areas identified in the Second GPA. GIS based survey, inventorization and mapping of PGR, public-private-farmer participatory PGR management models,Inter-ministerial and multi-institutional framework for survey, collecting, mapping and conservation of wild and weedy species of economic importance; long term funding policy support for pre-breeding and genetic enhancement projects are few among the listed priorities in the redefined NAP.

Keywords: Global Plan of Action, National Action Plan, PGR

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159 (P-411)

Ecotourism through Agroforestry: Implication for Sustainable Development

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Agroforestry potential to secure the growing food insecurity is well highlighted and accepted one. Diversified nature of agroforestry could provide multiple alternatives to enhance farm production and income at one side and conservation of natural resources on other side. Here, we emphasized *Ecotourism* as paradigm shifts of Agroforestry, where ecotourism creates awareness among tourists regarding crop diversity, fruits trees, flowering plants, livestock diversity, pisiculture and apiculture, organic farming and others. Since, *ecotourism* concept not only confined to environment and natural resources, but also in the view of society welfare, development and livelihood security, this concept is ideal. In this context, we are addressing use of existing agroforestry systems for *ecotourism* in the new era in view of agrobiodiversity, farm diversification, farm income and society development through awareness. Likely, it will help to generate employment to the local people. Besides this, farmers can even tap for maintenance of site, landscaping orientation, soil erosion control, wildlife habitat management and other ecosystem restoration activities which are highly pre-requisite element for establishment of ecotourism in their farm landscape. Moreover, some recreational activities can also be included such as seed museum, bullock riding, tree climbing, fruit harvesting, traditional games and serving traditional food. Hitherto, a suitable and long adaptive system of model does not exist. There is a call for well diagnosed and systematic suitable models to develop *ecotourism* through agroforestry approach, so that we could make more meaningful and aim for wider application in near future.

Keywords: Agroforestry, Ecotourism, Paradigm shifts

253 (P-412)

Agrobiodiversity Led Innovations for Start-ups in Remote Areas

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Startup companies can come in all forms and sizes but it is important to build a Founder team to secure key skills and resources, which enables them to conduct research and build a first minimum viable product (MVP) to validate, assess and develop the ideas or business concepts. Now that a large number of Farmers' varieties with unique characters and target usages are being Registered under the provisions of Protection of Plant Varieties & Farmers' Rights Act, 2001, it prompts for building of Business Models around them. The Registered Farmers' varieties have intrinsic market value in the emerging markets which are based on the consumers' demand for traditional products. The Start-ups based on the cultivation, grading, processing and packaging of products from these traditional Farmers' varieties can open new vistas for the educated rural youth. To promote these Start-ups there will be a need of assured and secured funding from different agencies along with the specialized support for capacity buiding of the rural youth to orient them for such professional activities. Such Start-ups will make Agro-biodiversity conservation self sustaining and commercially vaible as well.

Keywords: Start-ups, Farmers' Varieties

308 (P-413)

National Herbarium of Cultivated Plants: A Resource for Study of Crop Genepools

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National Herbarium of Cultivated Plants (code 'NHCP') at ICAR-National Bureau of Plant Genetic Resources, New Delhi occupies a place among 25 major Indian herbaria. NHCP presently holds collection of 21,878 herbarium specimens (representing 265 families, 1484 genera and 4,061 species) taxa mainly of cultivated and wild/ weedy relatives, potentially important species, native or introduced species for use in breeding. Besides, seed and carpological samples are represented as complementary collections. It differs in its mandate from other herbaria across the country in having emphasis on collection of variability in crops depicted as cultivars, primitive landraces, wild forms and their wild relatives from different agro-ecological conditions. It is intended to serve as a reference collection for identification, taxonomic study of plant genetic resources and a resource for teaching on plant taxonomy, ethnobotany and economic botany with Post Graduate School, Indian Agricultural Research Institute, New Delhi. Significant holdings include ~500 crop wild relatives (species number in parenthesis) under genera: *Oryza* (21), *Sorghum* (6), *Vigna* (25), *Cajanus/Atylosia* (10), *Allium* (29), *Abelmoschus* (14), *Solanum* (30), *Cucumis* (11), *Trichosanthes* (7), *Piper* (21), *Curcuma* (24), *Rosa* (19), *Prunus* (16), etc. Over 3,500 species of crop genepools (~6,000 images) are maintained as Virtual Herbarium. The NHCP provides technical input on identification, validation and taxonomic know-how on taxa of PGR relevance. The NHCP accepts unique and unrepresented genetic resources (as herbarium specimens and seed) and encourages depositing vouchers for future reference.

Keywords: Crop Genepools, National Herbarium of Cultivated Plants, Virtual Herbarium

324 (P-414)

Joint Forest Management: Evolvement of Self-help Groups and a Source of Livelihood

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Joint forest management (JFM) is people oriented system of forest management where approaches are engaged in such a way that state forest departments support local forest dwelling and forest fringe communities to protect and manage forests and share the cost and benefits from the forests with them. This is a kind of programme which was initiated in accordance with the National Forest Policy of 1988. Self help group (SHG) is a small voluntary association of poor people come together for the purpose of solving their common problems through self-help and mutual help. A study was conducted to assess the impact of JFM through SHGs. It was carried out in four villages viz. Khamaral village, Lamdeng Awang Leikai, Lamdeng Mayai Leikai and Lamdeng Makha Leikai of Imphal West District under Central Forest Division of Manipur during 2014. Questionnaire survey was conducted and observations on regeneration, plantations were taken by visiting the forest sites under JFM. The participation of women was appreciated in different JFM activities and SHGs were formed with women members. Monetary help provided by forest department acted as initial investment for the SHGs. The SHGs mainly involved in weaving, embroidery, mora-making (bamboo stools) as the source of income. With the help of SHGs, different activities of Forest department under JFM like weeding, cleaning, added natural **(**artificial**)** regeneration, plantation, nursery establishment were carried out by providing them wages. Forest area under JFM was found to be regenerating, improving productivity, diversity of forest composition and increased income to the villagers.

Keywords: Forest Department, JFM, SHGs

365 (P-415)

Building Partnership with Farming Communities for Community Management Mechanisms in Crop Diversity

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Capacity building and partnership with farming communities for Community based conservation and management mechanism and policy processes of crop diversity to bring about improved food sovereignty/ livelihood in different agro climatic zones of Maharashtra. Partnerships and Capacity building of farming communities especially with women farmers has gave us enormous experiences to share that communities traditional knowledge and integrated with new technique knowledge from database of crop diversity in cultivation and value addition. Community based conservation and management process helped us to improved livelihood through value addition and market linkages. Consultative mechanisms have helped us to established behavior changes and practice *in situ* conservation of crop diversity. Partnership and capacity building procedures helped generate morphological and nutritional and also knowledge data. Participation of communities has shown interest to develop protocol for value addition and to develop seed banks. More number of community members has shown interest to form network of traditional seed keepers. This network of seed keepers not only document the processes besides crop diversities they are documenting wild vegetables. Regenerating traditional knowledge of food will help to generate food security and nutrition of farming community. Many of experiences of related activities and more importantly will facilitate a coordinated and coherent approach to capacity building, sharing of resources and knowledge will strengthen farming and backward communities to improve livelihood and food sovereignty.

Keywords: Partnership, Capacity building, Food sovereignty livelihood, Community Consultation

869 (P-416)

Community Based Management of Fish Germplasm Resources: A Case Study of Gangrel Reservoir on River Mahanadi, Chhattisgarh State, India

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Need for sustainability of natural resources have led the researchers and managers to pay attention to newer approaches towards resource management. This paper describes a case study of the management of fisheries resources in the Gangrel reservoir in upper basin of river Mahanadi in the Chhattisgarh State of India, by tribal people and fishing communities through cooperative societies. Mahanadi, a major river in East-Central India, flows through the states of Chhattisgarh and Odisha. It drains an area of around 141,600 square km. with a total course of 858 km. Gangrel reservoir with an area of 6935 ha. is surrounded by several villages of three districts namely, Dhamtari, Balod and Kanker, in the foothills mainly comprised of dam displaced people of tribal and fishing community. Most of these people who either did not have land or it has submerged in the reservoir, mainly depend on fisheries resources from reservoir. They organised themselves into eleven fishing cooperative societies and undertook responsibility of managing fisheries resources of the reservoir by taking it on lease from the government on prescribed lease rent. These people's institutions, however, are faced with continuously emerging socio-economic and institutional challenges to maintain their successful track record in resource stewardship and generating livelihood for their members. Based on field work and interactions with office-bearers, members and state fisheries officials, this paper attempts to present people's experience of resource management and lessons learnt from it for conservation and management of germplasm resources.

Keywords: Community based management, Fishing cooperative societies, Mahanadi

1312 (P-417)

Informing the Debate on GM Food in India: Policy Interventions for Resolving the Conflicting Stance

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Recent Policy articulations by Government of India point to the strong pro-active stance towards introduction of genetically modified (GM) food crops in India (for example Economic Survey 2016-17). The economic and social stakes are high as evident from debates that have happened after the introduction of GM cotton in 2002. Strong positivistic approach has underscored the potentiality of GM to address food security, agricultural productivity and sustainable production approach, etc. On the other-hand the opposition has ranged from extreme stance (a strong precautionary approach) of disallowing GM technology in India to calling for long gestation period before scientific evidence emerges to strengthen the regulatory process. Issues of high royalty of GM cotton, seed unavailability for non-GM cotton growers, field trials being too confined to properly assess the impact of this technology on environment, health and food has further informed this debate. The debate on Bt brinjal points to regulatory failure which is visible again in the indigenously developed GM Mustard. Keeping above issues in context, the study has revisited the debate supplemented by a limited field study. Study underscores that policy articulations should be in parallel to strong institutional changes in the regulatory process, and proposes a coordinated framework involving multiple stakeholders. It argues that this can bring more clarity and improve decision making and help to address the information asymmetry in the regulatory process. Further, the paper shows how this framework can be a useful platform for resolving conflicting stance among the different stakeholders including bench level scientists.

Keywords: GM food crops, GMO, Policy, India

1406 (P-418)

Hand-Holding for Effective Conservation and Use of Genetic Resources – A Case Study with *Musa* spp.

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Musa spp. (bananas and plantains) is one of the most important food-fruit crop, both for myriad uses and the enormous inter- and intra-specific genetic diversity. The Indian Council of Agricultural Research (ICAR, an autonomous Society under Ministry of Agriculture, Government of India) has established several institutes for crop improvement and genetic resource management. For *Musa*, ICAR-NRCB, Tiruchirapalli and ICAR-NBPGR, New Delhi are the nodal institutes, besides many other national institutes and State Agricultural Universities. Complementarity in different aspects of genetic resource management between these institutes has resulted in very rich indigenous and exotic *ex situ* collections of cultivated and wild germplasm. Currently, more than 1,200 collections in Field Gene Banks, 420 accessions in *In Vitro* Gene Bank and about 70 accessions in Cryobank are conserved in the National Agricultural Research System (NARS), and 60 accessions are safety duplicated in the global collection at *Musa* International Transit Centre (ITC), Belgium. More than 100 accessions have been thoroughly characterized/ evaluated, and some of these used in breeding programmes in the All India Co-ordinated Research Network. Some 26 collecting missions undertaken in the last 20 years have resulted in a varied assembly of germplasm. Research in crop breeding, *in vitro* conservation, cryopreservation, DNA fingerprinting and genomics has led to effective utilization. Selections from important exotic introductions (e.g. FHIA hybrids, Saba, Popoulu, Yangambi Km5 and Big Ebanga) have led to adoption by farmers. Collaboration amongst national partners and linkages with international organizations has been the key for successful conservation and use of banana germplasm.

Keywords: Banana and plantains, Networking, Exchange, *Ex situ* conservation, Utilization

1629 (P-419)

Empowering Farming Community to Conserve Traditional Varieties

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India has rich crop diversity and has been reported to be habitat of 167 important cultivated plant species.. It is one of the top 17 mega biodiversity countries because of its varied physiographic, diverse climatic conditions and variety of habitats. Krishi Vigyan Kendras of northern states namely Punjab, Haryana, Delhi, Himachal Pradesh and Jammu & Kashmir come under the supervision of ICAR-ATARI, Zone-I. Among 22 agro-biodiversity hot-spots in India this zone comprises of two agro-biodiversity hot-spots i.e cold desert and western himalayan region. The cold desert includes districts Leh and Kargil of Jammu & Kashmir and Lahual & Spiti of Himachal Pradesh. Similarly, Western Himalayas covers 16 KVKs of Srinagar and remaining 11 districts of Himachal Pradesh. Since 2013-14, ICAR in collaboration with PPV&FR Authority have been making various efforts to generate awareness among masses about the PPV&FR Act and its provisions through Krishi Vigyan Kendras for encouraging them to conserve traditional varieties. ICAR-ATARI organized three training programmes from 2014-15 to 2015-16 in which 150 Subject matter Specialists and Programme Coordinators of KVKs of Zone-I were trained. During the last three years from 2013-14 to 2015-16, KVKs of Zone-I organized 87 training cum awareness programmes in which 7851 farmers participated. Farmers from the region have sent 107 varieties of crops for registration from 2014 to 2016; out of which six (6) varieties were registered. So through these programme the farmers have come forward in preserving our traditional heritage.

Keywords: Krishi Vigyan Kendras, Stakeholders, Awareness, Biodiversity

1780 (P-420)

Information Sources and Utilization Behaviour of Vegetable Growers at Ladpura block of Kota district in Rajasthan

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The importance of agriculture in the economy of India is profound. The Food and Agriculture Organization, suggested that in order to enhance agricultural development, new commodities and technologies for production must be developed. The development of agricultural technologies requires among other inputs, a timely and systematic transmission of useful and relevant agricultural information (message) through relatively well educated technology dissemination (extension) from formal technology generation system (research) via various communication media (channels) to the intended audience " farmers (Oladele). According to Reddy, the quantum of agricultural technology information available in the Indian systems developed by research institutes, and faculties of agriculture in universities is quite enormous. The problem therefore, lies with effective dissemination of information about these innovations by the dissemination agencies. The purpose of the study is to determine the agricultural information sources utilized by vegetable growers. The study was undertaken purposively at Ladpura block of Kota district in Rajasthan between 120 respondents. The analyses revealed that most (51.38%) of vegetable growers preferred extension agents as their source of information, while the least (5.81%) source was libraries. The major constraint indicated by vegetable growers in sourcing information was financial problem. It was recommended that credit facilities and subsidies or incentives be provided to farmers to purchase radio receivers to enhance information sourcing. Also more extension agents be recruited and properly trained as they are main information source used by vegetable growers.

Keywords: Agricultural information source, Sourcing constraints and utilization.

Satellite Session 1 :

Harnessing Biodiversity for Food Security and Sustainable Development

1936 (O-58)

Evaluation of Wheat Pre Breeding Germplasm in North Western Plain Zone

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The demand of wheat in developing countries is anticipated to increase by 60% by 2050 despite current rate of yield increase is about half of the required. Climate change effects and the decreasing availability and high cost of land, water, energy resources and fertilizers present further challenges to overcome. In view of this FAO has launched 'Climate Smart Agriculture' initiative which encourages the enhanced use of GeneBank germplasm resources in to crop breeding programs. A total of 1423 exotic wheat accessions from CIMYT's wheat GeneBank were analyzed through genotyping-by-sequencing and 244 lines were selected from different genetic spaces to use in pre breeding. These selected exotics were then crossed with CIMMYT's best elite genotypes to produce pre breeding populations which underwent multiple rounds of selections under heat, drought and disease prone conditions. Finally, a set of 1000 advanced pre breeding lines were selected and evaluated in Borlaug Institute of South Asia, India for yield performance. The grain yield and yield components were measured including biomass, heading, maturity, grain yield and thousand kernel weight. Based on preliminary observation superior genotypes have been identified. Second year evaluation of these genotypes will be carried out in coming crop season. Sequence characterization is also performed at CIMMYT. Efforts are being made to mobilize the better performing lines to varietal pipeline of Punjab state.

Keywords: Pre-breeding, Wheat, Grain yield

1937 (O-59)

Linking and Leveraging SeeD Resources in Indian Wheat Breeding Program-Prospects and Future

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At Punjab Agricultural University, Ludhiana we are working with landrace as well as linked top cross populations (LTPs) from SeeD project. While the immediately apparent traits constitute the first wrung of germplasm evaluation and use, a greater value may lie in diversity available for more cryptic traits. While the exploitation of functional Gpc-B1 allele from Triticum dicoccoides, for increased grain protein content, now qualifies as a classical example, studies in wheat as well as model plant species are identifying a large number of genes with vital roles in crop productivity, resistance and quality. Huge sets of germplasm have come alive as potential donors of useful alleles for these genes of interest. Availability of DNA sequence data for the donor germplasm, including the entire landrace set mentioned above can serve as a gateway for in silico allele mining, followed by functional validation and marker assisted mobilization. One of the experiments formulated, which is illustrative of this strategy, is the allele profiling of genes, such as Asparagine Synthetase 2 (Ta ASN 2), responsible for free asparagine in the wheat grain. On baking this free amine is responsible for polyacrylamide formation, a powerful neurotoxin and a potential carcinogen, which now attracts food regulatory restrictions in case of cereals in some countries. Similarly, allelic diversity for genes involved in nutrient use efficiency (particularly nitrogen and phosphorus) is another area of interest. The landraces are a uniquely desirable resource as the first port of call for allele mining as these combine high genetic diversity, simple conditions for maintenance and ease of characterization.

Keywords: SeeD, Wheat breeding, *Triticum dicurles*

1938 (O-60)

The Seeds of Discovery Initiative A Learning Model Towards Effective and Equitable use of Genetic Resources

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“Seeds of Discovery” (http://seedsofdiscovery.org, SeeD) is a pioneering initiative that is funded largely by the Mexican Government under the name “MasAgro Biodiversidad”. SeeD aims to characterize and mobilize the genetic diversity of maize and wheat, two of mankind's three major cereal crops, to contribute to the nutrition of a growing population in the face of challenges from major drivers such as changing climate, emerging biotic stresses, and shifting diets due to urbanization and economic development. The germplasm bank at CIMMYT houses more than 175,000 accessions - the world's largest collections of maize and wheat – and these seeds, and all information about them, are international public goods. Every year, several tons of these materials are distributed to researchers worldwide. SeeD has genotyped more than 80,000 wheat and 28,000 maize accessions, has phenotyped sets of wheat and maize for various key traits, and has applied informatics tools to identify novel sources of genetic diversity for use in breeding programs. SeeD’s pre-breeding projects are developing bridging germplasm that is already being evaluated by breeders in Mexico and India, and will soon also be grown in various African countries. Ensuring equitable access to the benefits of the SeeD project, however, requires a diverse portfolio of capacity development products, including user friendly software tools, and a range of workshops, on-line training modules, graduate student mentorship and visiting scientist research projects. The SeeD project is an evolving model that will be widely useful across crop species for enhancing the equitable use of genetic resources. We analyze the costs of maintaining the genebank and the pre-breeding platform and the benefits of the global public goods it produces using a Real Options approach, showing that the investments in this research are well worth it.

Keywords: SeeDs, CIMMYT, Germplasm

Satellite Session 2 :

Agrobiodiversity for Nutrition and Health

1930 (O-61)

Utilizing Agro-biodiversity to Scale Up Nutrition The Kenyan Experience

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Malnutrition greatly affects Kenya's socio-economic development and potential to reduce poverty. Nearly 2 million children or 26% of all children in Kenya are undernourished, and micronutrient deficiencies are widespread. These children will never achieve their cognitive potential.. In addition to hunger and malnutrition, evidence from the 2014 KDHS points at the growing prevalence of an overweight and obese population in Kenya. The emergence of diet related non-communicable diseases (NCDs) such as cancers, hypertension and diabetes and cardio vascular diseases in Kenya is worrying. This nutrition scenario is against a background of an overabundance of wild and cultivated highly nutritious edible agro-biodiversity in terms of African indigenous vegetables, fruits, legumes, roots and tubers. These crops have the potential to provide ready access to affordable macro and micro nutrients for health balanced diets. Kenya is working with partners to scale up nutrition by employing a multiplicity of approaches including promotion of breastfeeding and appropriate complementary feeding, supplementation of vitamin A, iron and folic acid as well as raising awareness among communities on the available options such as using agro-biodiversity as part of a basket of options to scale up nutrition in the country. Other options include working with schools to incorporate agro biodiversity in school feeding programs including early child hood development and community health units. This paper will discuss how Kenya has mobilized stakeholders to scale up nutrition to address key nutrition related sustainable development goals.

Keywords: Malnutrition, NCDs, Agrobiodiversity

551 (O-62)

Curative Agro-biodiversity and Indigenous Knowledge – Case Studies on Conservation through Farming Communities

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Curative agro-biodiversity includes all components of the diversity (plants, animals and microbes) at all levels (genetic, specific and ecosystem) along with local knowledge and cultural practices which leads to sustainable health security of the agro-ecosystems. India with two hot-spots of diversity and tremendous traditional knowledge embedded in her age-old Indian System of Medicine (ISM) needs intensive efforts for its conservation through cultivation and utilization. Under National Agricultural Innovation Project (NAIP) on "Harmonizing biodiversity conservation and agricultural intensification through integration of plant, animal and fish genetic resources for livelihood security in fragile ecosystems", survey of villages in Rajasthan and Himachal Pradesh revealed that local farming communities are still dependent on herbal plants for primary health care and curing veterinary ailments. As per the collected information, multiple home remedies using 112 species are employed for the treatment of stomach diseases, skin infections, eye infection, fever, refreshing mind, hair loss, general weakness, diabetic, lose motions and impotency, prepared in the form of paste, powder, decoction, extract and smoke from the freshly collected or dry herbs. Of these 72 species are collected from the wild and 40 are being grown either in home gardens/kitchen gardens or around the cultivated fields on bund areas.

Keywords: Medicinal plants, Indigenous knowledge, On-farm conservation

221 (O-63)

Triticum dicoccum A Low G.I. Food for the Diabetics

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Cultivated emmer wheat(*Triticum dicoccum*), a tetraploid species with hulled grain has been cultivated during seven millennia. It has been largely replaced by hulless species and is a minor crop with exception of some countries like India, Ethiopia and Yemen where its grain is used for preparing traditional food.. In India, known as Khapli is gaining importance as functional/therapeutic food because of the low glycemic index (GI)(<55), slow digestibility, high satiety value, high antioxidant compound concentrations coupled with resistant starch, high protein(16%) and fibre(>16%). These quality attributes are considered vital for the dietary management of diabetes and cardiovascular risks. In recent years, India has become the 'Diabetic Capital of the world". Rigid architecture in the starch granules of dicoccum wheat provides resistant nature to starch. Incorporation of dicoccum wheat in the diet of diabetic patients resulted in reduction in total lipids, triglycerides and LDL-cholesterol concentration, Thus the current view of dietary carbohydrates as simply providing us with energy should be reconsidered. Traditional varieties of emmer are tall, low yielding with high quality, but modern semi dwarf cultivars are high yielding with low quality. Most of semi dwarf dicoccum cultivars derived their dwarfing genes from *Triticum durum* and has strong linkage drag in altering the quality traits. So, gamma irradiation of traditional variety(NP201), provided a semi dwarf, high yielding and comparable quality line(HW1098), released for cultivation for the farmers of India. Emmer wheat, a minor and underutilised cereal today should know a new development due to the nutritional value of its grain.

Keywords: Diabetes, Emmer wheat, Functional food, Resistant starch, *Triticum dicoccum*

944 (O-64)

Nutritional Composition and Antioxidant Capacity of Peels, Pulp and Arils of Spiny Gourd (Momordica Cochinchinensis Spreng) Fruits Grown in Malaysia

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The study was to examine nutritional properties and antioxidant capacity of peels, pulp and arils of spiny gourd (Momordica cochinchinensis Spreng) fruits grown in Malaysia. The proximate composition of peels, pulp and arils were performed according to AOAC in triplicates. Antioxidant capacity of the samples was determined by DPPH free radical scavenging activity and ferric reducing antioxidant power (FRAP) assay. Pulp had significantly highest the moisture content (94.9g/100g), compared to arils (90.7g/100g) and peels (88.1g/100g), on wet weight basis. Pulp also found to have high ash content at the range of 17.3g/100g to 23.5g/100g followed by peels (14.0g to 16.0g/100g) and arils (6.3g to 13.1g/100g). High available carbohydrate content was determined with 55.6g/100g, 30.9g/100g and 19.3g/100g in arils, pulp and peels respectively. Meanwhile, the peels contained the highest protein content (6.2g/100g) followed by arils (5.8g/100g) and pulp (4.6g/100g). Nevertheless, arils found to contain significant amount of fat content at 22.3g/100g and low percentage for both peels and pulp (1.6g/100g). The peel and pulp of the fruits were categorized as low energy dense foods with the energy content 107.4kcal/100g and 147.4kcal/100g dry weight, respectively. Meanwhile, arils were categorized as high energy dense foods with the energy content 446.3kcal/100g that mostly contributed by fat content. According to student t-test, the proximate and FRAP assay showed significantly different between the peels, pulp and arils ($p<0.05$), except for the DPPH assay. Several factors such as geographical and climate differences and stage of maturity might influence the nutritional contents of the Momordica cochinchinensis Spreng fruit.

Keywords: Nutritional composition, Spiny gourd, Momordica cochinchinensis spreng

1186 (O-65)

Participatory Approach to Improve Dietary Diversity in Vihiga County, Western Kenya

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This research examines the suitability of a community-based participatory approach for diversifying diets through improved use of local agrobiodiversity. The study is part of the Humidtropics and Agriculture for Nutrition and Health CGIAR Research Programs. It consists of a diagnostic phase documenting agricultural biodiversity and nutrition (phase I), participatory development of activities to improve nutrition (phase II) and participatory implementation of the activities (phase III). This paper describes phase I and II. Phase I applied cross-sectional and longitudinal study designs. Data on agrobiodiversity, nutrition practices, anthropometry and dietary intakes was collected in ten randomly selected sub-locations in Vihiga County. In each sub-location, 40 households with a child aged 12-23 months were sampled. After pair-matching, five of the ten sub-locations participated in phase II. Participatory workshops were carried out aiming to develop community activities to improve nutrition. Vihiga County is rich in local food biodiversity (67 cultivated and 38 wild edible plant species). However, only 74.8% of children and 45.1% of women meet Minimum Dietary Diversity. Stunting affects 28% of children. To diversify diets, all sub-locations decided to plant traditional vegetables and legumes and to raise poultry. Community action plans were developed specifying how these activities are going to be realized. The results of phase I point to the need of developing innovative ways of putting the rich agrobiodiversity into use for improved nutrition. A community-based approach in form of participatory workshops is well suited for developing agricultural activities in order to diversify diets in Western Kenya.

Keywords: Dietary diversity, Agrobiodiversity, Nutrition, Community-based participatory approach

1287 (O-66)

Micro Level Politics of Land Use Impacts Agro-Biodiversity and Rural Food and Nutritional Security A Case Study from Wayanad, Kerala

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The discourse of food security has changed over time from security to self sufficiency and then to sovereignty. This paper examines the changing food baskets of three different tribal communities of south India in the frame work of food severity debate. The paper argues that right to good food is more linked with macro and micro politics of land ownership and access to agro-biodiversity than the distributive welfare measures of the state. This paper is the result of one year research among Kurichya, Mullukuruma and Paniya communities in 6 different villages of Wayanad district. The research focused on the changes in food baskets of these communities and the corresponding agro ecosystems in a historical perspective using ethnographic field research and tools of participatory research. These communities have a tradition of rich food baskets with 56 species of fish, 92 species of leafy green, 89 verities of cultivated vegetables, 22 species of birds, 6 verities of cereals, 72 verities of rice, 25 verities of cultivated and collected fruits and milk and milk products. This research reveals the status of alarmingly shrinking food baskets of these communities due to changes in agro-ecosystems caused by land use policies. Land use policies and trends define agro biodiversity richness and the rate of genetic erosion in each locality. It explains how land ownership, power to take decision on land use and participation in larger development decisions defines degrees of sovereignty of each community over their food basket.

Keywords: Agro-biodiversity, Community access, Land use, Right to food

1457 (O-67)

Linkage Between Child Nutrition and Agrobiodiversity Gender Role in Home Gardening in North West of Vietnam

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The promotion of agrobiodiversity and gender equality in home-gardening is an essential strategy to ensure nutrition security for children in Highland ecosystems that experience a reduction of nutrient-rich species and changing gender roles in agriculture. A cross-sectional study from 177 households of the Thai minority group in North West Vietnam showed that children 12-24 months who did not reach Minimum Child Dietary Diversity Score (CDDS) were twice as likely to be underweight than those who reached it ($p<0.05$). Linear multivariable regression indicated that increased species diversity from home-gardens led to increased CDDS ($p<0.01$). Decision making by both mother and father in home gardening was positively correlated to child nutrition status and dietary diversity. Child wasting and underweight was 3.6 and 4.4 times respectively lower when both parents acted as joint primary decision makers regarding the selection of species to cultivate and consume compared to when those decisions were made alone ($p<0.05$). When the father alone decided on the use of income from home-garden harvest, children were 4 times more likely to be underweight than when the primary decision maker was the mother alone ($p<0.001$). Equivalently if this decision wasn't by both parents, children were 3.6 times less likely to meet the minimum CDDS ($p<0.05$). To ensure dietary diversity and improve nutrition status for children, we recommend increasing production and consumption of diverse foods from the home-garden and promoting gender equality and shared decision making in home-gardening.

Keywords: Agrobiodiversity, Diet diversity, Gender role, Home gardening, Vietnam

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1925 (P-421)

Agrobiodiversity and Wild Foods for Improving Nutrition, Health and Well Being

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Lack of dietary diversity is the main cause of unacceptably high rate of undernutrition prevalent in children in the developing world where diet consist mainly of starchy staples with very little animal source foods, fruits and vegetables. Agrobiodiversity can provide dietary and nutrient diversity, act as a safety net against hunger and strengthen local food systems. Also next to on farm biodiversity, the variety of foods collected from the wild plays an important role in dietary diversity and contributing to the important nutrient requirements. This paper examines how agrobiodiversity and wild foods affects nutritional quality, consumption patternas well as nutrition and health status of the Chakhesang people, an indigenous tribe of Nagaland in Northeast India. The variety of foods including insects and game animals collected from the forest still constitute the bedrock of Chakhesang traditional food systems. The activities involved in food acquisition and distribution not only allow the practice of cultural value but also confer benefit through increased physical activity. Data are presented to highlight the diversity of these food resources, their nutritional attributes and the impact of their use on food and nutrition security. Traditional foods remain important from both cultural and nutritional perspectives, and are associated with much lower rate of stunting, wasting and underweight among children as compared to the rest of India. Efforts should be made to capitalize the positive effects of traditional food systems and integrate it into contemporary food systems to be able to fully support the health and nutrition of the population.

65 (P-422)

Evaluation of Indian Potato Germplasm for Iron and Zinc Content

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Micronutrient deficiency affects more than half of the world's population especially in developing countries. Iron and zinc are the two major micronutrient elements for human nutrition. Biofortification of food crops is an emerging area of research to overcome the mineral deficiencies. Potato has a priority claim for biofortification as it yields more nutritious food per unit area and time and may contribute significantly in meeting nutritional requirements of the population. Keeping this in view a breeding programme is initiated for which germplasm characterization was done. Forty-six potato germplasm with varying degree of flesh colour from white to yellow were evaluated for iron and zinc content in raw and peeled tubers. The iron content ranged between14.90-67.13mg/ kg dry weight and zinc between2.78-35.40 mg/kg dry weight basis in tuber flesh. A significant and positive correlation (r=0.6865) between these two nutrients suggests that breeding varieties with high content of both these nutrients is feasible. Carotenoids content enhances the bioavailability of the micro nutrients but lack of correlation between tuber flesh colour index and nutrient concentration in the present study indicated that these traits are independent. The genotypes CP Nos. 3443, 1978, 2067, 3772, 1239 and 1435are promising as parental material for developing zinc and iron rich potato varieties.

Keywords: Micronutrient content, Potato germplasm, Tuber flesh

186 (P-423)

Diversity of Nutrimental and Ethno Veterinary Therapeutic Potential Plants of Bahraich (UP) India

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Bahraich district of Eastern Uttar Pradesh is situated in Upper Gangetic Plane. It lies between 27Â°43Ê¹ and 28Â°51Ê¹ North Latitude and 81Â°8Ê¹, and 82Â°10Ê¹, East longitude with a total area of about 6944 sq km. Due to vast area of natural forests Bahraich is also known as City of Forests. The present ethno medicinal investigation was under taken for the documentation of information regarding the uses and conservation of ethno medicinal plants being used in various veterinary ailments. Out of one hundred thirty four families found in Bahraich the plants of fifty seven families represented by one hundred and six genera of one hundred thirty two species are found to be used in various veterinary ailments. Papilionaceae is represented by ten species; Asteraceae is being represented by nine species whereas Cucurbitaceae and Poaceae by seven species; Solanaceae by six species; Caesalpinaceae and Moraceae by five species, Apiaceae, Brassicaceae and Amaranthaceae by four species; Acanthaceae, Lamiaceae, Menispermaceae and Liliaceae three species; Meliaceae, Sapindaceae, Anacardiaceae, Mimosaceae, Rosaceae, Rubiaceae, Combritaceae, Lytharaceae, Apocyanaceae, Asclepiadaceae, Piperaceae, Euphorbiaceae, Zingiberaceae, Dioscoraceae and Cyperaceae by two species each; Annonaceae, Fumariaceae, Cappariadeace, Carryophyllaceae, Malvaceae, Linaceae, Oxalidaceae, Rutaceae, Mitaceae, Leaceae, Myrtaceae, Punicaceae, Cactaceae, Plumbagenaceae, Oleaceae, Buddlejaceae, Cuscucataceae, Bignoniaceae, Verbenaceae, Plantagenaceae, Nyctagenaceae, Chenopodiaceae, Polygonaceae, Louraceae, Loranthaceae, Cannaceae, Agavaceae and Araceae are found to be represented with single species each.

Keywords: Bahraich, Ethno veterinary plants

688 (P-424)

Nutritional Quality Traits in Rice Landraces from Different Climatic Zones of India

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Rice (*Oryza sativa L.*) is the oldest domesticated crop grown in most of the Indian states as staple food. The ancestral landraces adapted to specific human needs and environment niches are still grown by small and marginal farmers, tribal people in remote villages of India. These landraces are valued for both nutritional and medicinal properties which require special attention for collection, conservation and evaluation for exploiting quality traits from them for utilization. Present investigation has been undertaken in 25 landraces of rice from 11 different states of India for seed morphology and nutritional trait analysis. The seeds varied in hull and grain colour, hull percentage, size and 100-seed weight. Wide variations in nutritional qualities of seeds were observed. Seed protein, amino acids and starch content varied from 7-15%, 4-21% and 36-69%, respectively, while amylose and amylopectin varied from 18-36% and 3-45%. Amylose content has a positive correlation with the starch and negative correlation with amylopectin content. Highest protein content was observed in landrace (NE-7) from Assam, while highest starch content was observed in Kalafultash landrace from Himachal Pradesh. All these landraces are either rich in one or the combination of several promising traits. This study demonstrates the benefits of using these local landraces in our diet as high protein, amino-acids and amylase content are preferred traits. These landraces can be utilized in ongoing nutritional crop improvement programme and can be conserved for posterity in genebank.

Keywords: Landrace, Nutritional quality, Rice

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723 (P-425)

Chemoprofiling of *Andrographis paniculata* Germplasm for Andrographolide Content

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Andrographis paniculata (Burm.f.) Wall. Ex Nees. (Acanthaceae), commonly known as Kalmegh is an important medicinal plant of India which is used both in Ayurevda and Unani system of medicine. The dried herb is a remedy for a number of ailments related to digestion, hepatoprotection, vermicide, analgesic, anti-inflammatory, antibacterial, antityphoid, antibiotic activities, hypoglycemic, besides immune enhancement. The present study was undertaken to study phytochemical diversity among *A. paniculata* germplasm collected from diverse geographical regions across fourteen states of India. Forty-three accessions of *A. paniculata* grown at Issapur Experimental Farm of NBPGR, New Delhi were evaluated for medicinally active compound andrographolide by High Performance Thin Layer Chromatography (HPTLC) method. Results revealed a wide range of phytochemical variation among these accessions in andrographolide content varying from 1.15% -2.44% with standard deviation of 0.26. Superior accessions having high andrographolide content (>2%) were IC342134, IC111291and IC421436. DIVA-GIS analysis of *A. paniculata* germplasm for andrographolide content indicated that diverse accessions can be collected from Assam, Uttar Pradesh, Chhattisgarh and Madhya Pradesh states of India. The studies suggested that superior germplasm of *A. paniculata* can be utilized for commercial cultivation for meeting growing demand of this plant for pharmaceutical industries.

Keywords: *Andrographis paniculata,* Kalmegh, Andrographolide, Germplasm, HPTLC

751 (P-426)

Nutritional Profiling of Germplasm using NIRS Chemometrics

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Present study was aimed to develop the NIRS based prediction model for multiple quality traits in chickpea amaranth and buckwheat. 225 accessions in chickpea, 200 accessions in amaranth and 150 accessions in buckwheat were evaluated for proximate components, fatty acids, amino acids and phytochemicals after recording their reflectance spectra from 400 to 2500 nm on Foss NIRS 6500. Outliers were identified and removed based on Mahalanobis distance (H distance) > 2.5. Mathematical treatment from first order derivative to fourth order derivative were applied to the raw optical spectrum (log 1/R), with the aim of identifying calibration equation with best prediction accuracy in external cross validation. R2 and standard error of prediction (SEP) was used for comparison to select the equation with wider prediction capability. In chickpea 2nd derivative for starch (r2-0.9406), protein (r2-0.9338), oil (r2-0.9235), saponin (r2-0.9315) and phytate (r2-0.9024); 3rd for moisture (r2-0.9436) and dietary fiber (r2-0.9681); 4th derivative for total soluble sugar gave best prediction accuracy. In Amaranth and buckwheat 2nd derivative for protein, oil and fatty acids were found suitable. In amaranth r2 values were 0.9718, 0.9515, 0.9944, 0.9212, 0.9043 for protein, oil, oleiate, linoleate, linolenate respectively, while in buckwheat r2 values were 0.9294, 0.9157, 0.8780, 0.9084, 0.8953, 0.8935 for oil, palmitate, stearate, oleate, linoleate, linolenate respectively. Based on these prediction models germplasm are screened to identify trait specific germplasm. In chickpea 733 accessions were screened and 50 accessions for each trait were evaluated by wet chemistry methods to validate and further strengthen the prediction model.

Keywords: Amaranth, Buckwheat, Chickpea, Prediction model

1013 (P-427)

Underutilized Fruit Crops of Sikkim for Health and Nutrition

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Some of the major fruit crops grown in Sikkim are mandarin orange, peaches and other temperate fruit crops. However, it is also seen that people of Sikkim also utilizes some of the traditional wild edible plants as an important part of their diet. Due to the altitude that varies from sea level to summits that touch the skies, the flora and fauna naturally covers a wide spectrum. Nowhere in the world in such a small area can one find flora and fauna of all varieties - Tropical to the Alpines. Naturally there are number of wild (underutilized) edible plants having good nutritive value as well as medicinal properties. Some of those plants are Kusum (*Baccaurea sapida* Mull), Lupsi (*Spondias axillaris* Roxb), Muslerhi/maldhero (*Elaeagnus latifolia* Linn), lapche kawlo/phumsi (*Machilus edulis* King), Mael (*Eriolobus indica),* Pummelo (*Citrus grandis*), Fig (*Ficus roxburghii)*. These fruits are consumed either raw or processed into value added products such as pickles. So, use of such wild yet nutritious fruits have a promising influence in supplementing the people with better nutrition and also holds a good prospect to set up processing factories which not only favors domestication of such fruits in commercial level but also avoids over exploitation of such fruits in their natural habitats.

Keywords: Fruit, Sikkim, Underutilized

1000 (P-428)

Diversity Analysis of *Physalis Peruviana* Collected from Different Locations in India

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Domestication of wild/weedy species which are nutritionally sound, environmentally well adapted and locally available may go a long way in alleviating malnutrition and ensuring food security with dietary diversity. *Physalis peruviana* L. is common weed found mostly in non-framing lands. *Physalis peruviana* is mainly known for its medicinal and nutritional values of fruits. The main aim of the study was to assess the nutritional potential of *P. peruviana* which can be utilized against malnutrition in India or elsewhere. Extensive surveys across the agro-climatic zones of India were conducted to collect the different accessions. Out of these, twenty accessions were used to analyse the morhpo-physiological, nutritional and molecular diversity. Vast variation in morphological and physiological traits as well as yield attributes was noticed. Considerable variation was evident in gas exchange parameters, shape, colour and size of fruits. Molecular diversity analysis using 42 RAPD primers revealed divergence among tested entries. Fruits are rich source of minerals, vitamins and β-carotene. In yield trial, selected accessions of *P. peruviana* yielded upto 10 t/ha fresh fruits which at a prevailing market price may prove very remunerative to the growers. An innovation has been made by double planting to shorten the duration of cultivation of *P. peruviana* by 40 days enabling the plants to complete their life cycle by the end of March. Cultivation of *P. peruviana* may prove a boon in providing good economic returns to growers, and at the same time, may also help in fighting against malnutrition especially against the deficiency of β-carotene.

Keywords: β-carotene, Malnutrition, Molecular diversity

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780 (P-429)

Harnessing Benefits of Finger Millet in Combating Micronutrient Malnutrition through Genetics and Genomic Approaches

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In developing countries, 80% deaths are attributed to continuous persistence micronutrient deficiency and associated infections and chronic diseases. Traditional crops harbouring health benefitting characteristics and micronutritional richness can deliver a low cost sustainable food-based solution for nutrition and health in such countries. Finger millet, one such traditional crop grown in most marginal areas of Africa and Asia, is a rich source of health benefitting micronutrients, phytochemicals, vitamins and several essential amino acids. The objective of this work is to use advances in genetics and genomics approaches for better understanding the genetic control of these health benefitting traits and to breed them effectively into other staple crops consumed on daily basis. A set of 190 genotypes incorporating a minicore collection of finger millet together with a number of elite breeding lines has been assembled to capture and characterise entire genetic variation associated with such traits in the crop germplasm. These genotypes have been extensively characterised for diversity in micronutrients (such as iron, zinc, calcium, magnesium, sodium, and potassium), protein and anti-nutrients (phytate and oxalate). Large-scale GBS performed on this association panel has generated 156,157 SNPs which are being used in genome-wide association studies. Our work has identified a number of genomic regions in finger millet associated with both the health benefitting traits as well as with other factors that affect their bioavailability. This work will significantly contribute in developing means of assessing how such genetic variations are distributed in other staple crops.

Keywords: Finger millet, Micronutrients, Health benefitting traits, Genotyping-by sequencing, Genome-wide association study

1014 (P-430)

Underutilized Medicinal Plants of Sikkim for Health

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More than 80% of the population of Asian and African countries depends on traditional medicine for primary health care. So, local knowledge is becoming increasingly importance in Primary health care system. Sikkim is a small state of India that falls in the Eastern Himalaya and is rich in cultural and biological diversity. There are about 420 plants used by the tribal people for curing various diseases in Sikkim Himalayas region, out of which few are in utilized on commercial basis. Some of the major medicinal plants found in Sikkim are *Acorus calamus, Artimesia indica, Curcuma longa, Dioscorea deltoida*. However there are many more plants which are being used by the locals for its medicinal properties and it has not been commercialized unlike the major plants found. Some of those plants are *Aconitum bisma (Hamilton) Rapaics*, *Aeschynanthus sikkimensis* (Clarke) *Stapf*., *Alnus nepalensis*, *Astilbe rivularis*, *Betula alnoides*, *Bridelia retusa* L., *Clematis buchananiana, Commelina benghalensis* L., *Entada rheedei Sprengel*, *Equisetum diffusum*, *Heracleum wallichii*, *Kaempferia rotunda* L., *Podophyllum hexandrum* Royle., *Rhododendron arboretum* Smith *etc*. This paper deals with the use of these underutilized medicinal plants in primary health care as it has found to cure diseases like arthritis, fracture, jaundice, diarrhea and respiratory diseases of children with other persistence, long lasting chronic health conditions. It is also important to bring these plants under commercial cultivation as it is being constantly exploited from their natural habitats thereby making it endangered.

Keywords: Medicinal Plants, Sikkim, Underutilized

1086 (P-431)

Can Agrobiodiversity Support Healthy Foods and Healthy Eating in India's School Feeding Programme

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The Indian Mid-Day Meal Scheme (MDMS) being the world's largest school feeding programme, covering 120 million children and 950 thousand schools, gives an opportunity to policy-makers to ensure better health and nutrition for children by providing healthier food, healthy eating education, and the setting of appropriate food standards and regulations. The scheme aggregates grains from across the country and supplies them to each district however the percentage of severely malnourished/under-weight children of ages 10-13 remains stubbornly high at around 30%. To date MDMS has had very limited focus on local underutilized crops and their comparative nutritional advantages. Research shows the positive impact agrobiodiversity can have on nutrition yet in few states has there been inclusion of micronutrient-rich neglected and underutilized species of crops (like minor millets) in MDMS. Globally there is growing interest in diversifying foods and diets in school feeding and countries like Brazil have made considerable progress in this area. Further, when food procurement linked to such programmes provides incentives for local underutilized crops it can also result benefiting small farmers financially. The successes and lessons learned from these programmes, including the many barriers and challenges facing the integration of agrobiodiversity into school feeding, will be highlighted. We also argue that such approaches to better mainstream agrobiodiversity into school feeding could be highly beneficial to India, contributing on the one side to leveraging the untapped potential of local underutilized crops, while also benefiting small farmers, and simultaneously improving nutrition in children through healthier food systems and eating environments.

Keywords: Agro-biodiversity, Neglected and underutilized species, School feeding

1156 (P-432)

Do Home Gardens Promote Agrobiodiversity, Homestead Food Production and Household Consumption of Diverse and Quality Foods Evidence from Rural Nepal

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Home gardens are considered as a time-tested good practice for smallholder livelihoods and sustainable diets, which contributes to conservation of unique and rare biodiversity. This study aims to assess the role of home gardens practices in on-farm biodiversity, homestead food production and household consumption of nutritious foods using a random sample survey of 164 households from home garden project districts of Gulmi and Rupandehi in rural Nepal. Survey data are analysed to compare the changes in management of on-farm biodiversity, homestead food production and household consumption for the project villages with those found in a set of comparable non-project villages. Regression models were employed to analyze factor determining adoption, cultivation of diverse plant species and assessing the net gain in household consumption of fruits and vegetables. The findings showed that adopters of home garden practices maintain significantly higher number of plant species and crop varieties, produce and sell more food as compared to those households that are not adopting home gardens. The quantity, frequency and diversity of nutrient rich quality foods produced and consumed from home gardens have also increased significantly among participant households. Regression analyses and their results indicated that some household, farm-specific and institutional factors are influencing home garden adoption, homestead biodiversity maintenance and consumption gains. In the context of smallholder and land poor community integrated home gardens could be strategic development intervention that enhance on-farm biodiversity, increase homestead food production and promote household consumption of quality and diverse foods resulting in better dietary diversity and household nutrition.

Keywords: Adoption, Biodiversity, Consumption, Home garden, Nutrition

1270 (P-433)

Nutritional and Sensory Quality of Quinoa Based Extrudates

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Quinoa is an ancient grain which was observed to have high nutritive value and good tolerance for extreme climates and was promoted by FAO as possible grain to contribute in food security, hunger and poverty. It is recommended to incorporate quinoa in the diet which can be done in many forms. The present study focused on extrusion cooking of quinoa based formulation and studying the effect of four temperatures on its nutritional and sensory properties. It was observed that temperature didn't have significant effect on the nutritional properties except for the dietary fiber content. However, sensory attributes of the extrudates was affected significantly by temperature. Highest temperature was observed to have highest sensory scores in all attributes evaluated. The extrudates were found to contain good amount of nutrients. Moreover extrudates observed to meet 6 out of 10 essential amino acid requirements for adults namely lysine, methionine, cystine, threonine and phenylalanine + tyrosine which met 111%, 187%, 550%, 125% and 222% of the requirements respectively. The fatty acids composition of extrudates was interesting because of presence of good proportion of omega 3 fatty acids (4.47 g/100g fat) and also presence of Trans-11 vaccenic acid (1g/100g fat) which was reported to have substantial hypo-triglyceridemic effects that can play a role in reducing obesity. Present study proved that it was possible to get acceptable snack product from quinoa based formulation which was observed to have good nutritional value.

Keywords: Quinoa, Extrusion, Fatty acids, Essential amino acids

1298 (P-434)

Nutrition Sensitive Landscapes A Case Study from Vietnam

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Nutrition-sensitive landscapes aims to simultaneously improve human nutrition, landscape health and ecosystem-services within a landscape. A sample of 416 households was randomly selected from Mai Son, Vietnam. Quantitative questionnaires were administered on agricultural production (including wild foods) and on nutrition (including a 24 hour diet recall). A market survey was also conducted. In total, 398 species were produced on-farm or collected from the wild (292 plants, 106 animals). Whilst there was wide production diversity at the landscape level, foods were not evenly distributed across food groups. The diet recall showed food groups with low consumption (<26% of women or children consumed) were legumes, nuts and seeds, dairy, dark green leafy vegetables and vitamin A-rich vegetables and fruit. These food groups also represented a low percent of production (13%) and market (8%) diversity. Food groups with high consumption (>40% of women or children consumed) were flesh foods and other fruits and vegetables, and represented higher production (67%) and market (45%) diversity. The percentage of women Minimum Dietary Diversity (MDD) was 59 and only 18% of reported that diet diversity was important to prevent undernutrition. Increased rate of consumption of these food groups was seen by those who reached MDD compared to those who did not reach it (up to 44%). Targeting fruits, dark green leafy vegetables, legumes, nuts and seeds for increased consumption through direct nutrition counselling as well as promoting increased diversification of species from these food groups for production in the homegarden, could increase both landscape agrobiodiversity and MDD.

Keywords: Agrobiodiversity, Diet diversity, Landscape, Vietnam

1380 (P-435)

The Use of a Rapid Participatory Method to Map the Role of Agricultural Biodiversity in Local Production Systems of Different Ethnic Groups

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There is little documented evidence of the role that different minority ethnic groups play in utilizing and maintaining the availability of local agrobiodiversity in Northwestern Vietnam. The adapted Four-Cell Approach (FCA) (a rapid participatory appraisal method), was used to identify trends in the availability of agrobiodiversity in local production systems (including the collection of wild species) of 5 different ethnic groups in Son La province: Hmong, Khomu, Kinh, Thai and Sinhmun. A total of 256 species were reported produced (including wild species) across all 5 ethnic groups. Of which 149 were cultivated or reared, 96 were wild species, and 11 that were both cultivated and collected in the wild. Plant species accounted for 63% and animal species account for 37% of the 256 available species. The Hmong reported the lowest number of species produced (n=94), representing 102% less species richness than the Thai, who reported the highest number of species produced (n=190). Nearly 20% (n=46) of species were uniquely produced by one ethnic group only, nearly half (n=22) of these species were exclusively produced by the Khomu. The presence of species exclusively produced by one ethnic group and the different species richness produced seen across the different ethnic groups highlights the significant role that different populations have in ensuring the continued use of certain species in local production systems, and why it is important to consider ethnic and cultural diversity within a landscape when conducting agrobiodiversity assessments.

Keywords: Food and Nutrition security, Participatory methods, Food-based approach, Vietnam

1538 (P-436)

Analysis of Chemical Composition and Anti-Oxidative Effect of *Coriandrum Sativum* L. Foliage

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This study was conceptualized and implemented to investigate the possibility of greater functional material between *Vulgare alef* and *Microcarpum DC* varieties of coriander foliage through analyzing their nutritional & nutraceutical components and antioxidant activity. Both varieties were analysed for crude protein, crude fat, ash, dietary fibre, flavonoids, polyphenol content, fatty acid profile, and antioxidant activity. The carotenoid composition was analysed using HPLC. The foliage of *Vulgare alef* and *Microcarpum DC* contained protein (3.17±0.16and 3.58±0.13 g/100g), crude fat (0.43±0.09 and 0.73±0.12 g/100g), ash (1.47±0.07 and 2.57±0.09 g/100g), insoluble dietary fiber (3.3±0.18 and 5.44±0.21 g/100g), and soluble dietary fiber (0.29±0.01 and 0.63±0.03 g/100 g), respectively. *Microcarpum DC* contained higher extract yield (5.64±0.17%), flavonoids (5.79±0.31 g/100g), and polyphenol content (44.93±0.64 g/100g) as compared to *Vulgare alef*. Major fatty acids as identified by GC-MS in *Vulgare alef* and *Microcarpum DC* were Palmitic acid (7.68±0.13 and 8.70±0.16 %), Linoleic acid (16.85±0.23 % and 19.79±0.31 %) and Linolenic acid (20.49±0.16 % and 20.46±0.24 %), respectively. The major carotenoids identified (DWB) in *Vulgare alef* and *Microcarpum DC* were lutein (77.15 and 64.71 mg/100 g), chlorophyll b (2.95 and 2.95 mg/100 g), chlorophyll a (2.99 and 3.59 mg/100 g) and β-carotene (11.04 and 15.79 mg/100 g). Ethanol (50%) extracts (200 ppm) of *alef* and *Microcarpum DC* showed higher radical scavenging activity of 77.85±1.42% and 89.68±1.6%, respectively. Our finding reveals the high content of nutritional, nutraceutical and antioxidant activity present in *Microcarpum DC* forge it greater functional material as compared to *Vulgare alef*.

Keywords: Antioxidant potential, Carotenoids, Coriander foliage, Nutraceutical composition, Nutritional composition

1539 (P-437)

Moringa Olifera A Potential Source of Antioxidant for Ready to Eat Food Product

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Study was undertaken to find a natural cheap source of antioxidant that could be used in ready to eat (RTE) foods. A budding source of antioxidants in the diet, *Moringa oleifera*, which possess balsamaceous properties, but consumed by only a small section, while a major section of the society is still unaware of its potential. The bioactive components present in leaves may extend the shelf life of foods, as synthetic antioxidants have been reported to be toxic and carcinogenic. For the study, the leaves were plucked, cleaned, washed, dried and powdered to a particle size of 841microns (Drumstick Leaves Powder, DLP). Antioxidant activity was determined using DPPH. DLP was then incorporated in the most widely accepted RTE product *namely*, biscuits. Proximate composition, acceptability, antioxidant activity and storage studies was done for a period of 3 months. Results revealed that the free radical scavenging activity of DLP was 89.10 ± 0.22 %. Addition of DLP enhanced the nutritive composition significantly making it a good source of protein (7.89 ± 0.01), fibre (3.07 ± 0.47), and ash (2.92 ± 0.04). DLP incorporated biscuits were found to be highly acceptable, with an overall acceptability of 8.88 ± 0.02 for control and 8.70±0.27 for DLP added biscuits (5%). Difference of 6.86 % was noticed in the free radical scavenging activity of the control and DLP added biscuits by the end of storage. Products where well accepted even by the end of storage period and the powder was highly effective as an antioxidant reducing the peroxidative changes and production of free fatty acids.

Keywords: *Moringa oleifera*, Antioxidant, Ready to eat food

1577 (P-438)

Exploitation of Rice Germplasm for Grain Zinc Content and Characterization using Microsatellite Markers

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Micronutrient deficiencies or “hidden hunger” affect two billion people across the world. Rice bio-fortification programme addresses mineral deficiency in the rice eating community by enhancing zinc and iron content in grains of rice. There is wide genetic variability among the rice germplasm with diverse grain zinc content. Understanding the polymorphism of microsatellite markers between genotypes with high and low zinc content of rice grains can be helpful for the development of rice cultivars with high mineral content using marker assisted selection. Five hundred and twenty eight diverse rice accessions *viz.,* Landraces from India and Africa, improved lines and high yielding varieties were cultivated at IIRR with standard agronomic practices. After harvesting paddy, de-husking was done with non-ferrous millers (Krishi International) and mineral content was estimated with ED-XRF in brown rice. Genomic DNA of 24 gentoypes was extracted from young leaves and subjected to rice micro satellite analyses. The iron content in brown rice was ranged from 7.8 ppm to 24.1 ppm with a mean of 12.1 ppm. The mean value of zinc content was 25.2 ppm and ranged from 8.9 to 50 ppm in brown rice. The polymorphic study was conducted for set of 24 rice genotypes using 40 SSR markers covering all chromosomes. Distinct polymorphism was shown by 20 primers among the genotypes studied, and eight markers have shown above 0.9 polymorphic information content. These polymorphic markers are being used for characterization of mapping populations and identification of lines with high zinc content.

Keywords: Biofortification, Rice, Germplasm, Microsatellites, Iron and Zinc

1604 (P-439)

High Grain Iron and Zinc in Rice Introgression Lines using Progenitor Wild Species

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Wild rice species are a good source of high Fe and Zn in seed which is required to alleviate deficiency. Disorders in rice eating population. As part of a program on mapping genetic loci for yield in introgression lines (IL) derived from elite x wild crosses, the seed iron and zinc concentration was also measured using ED-XRF. Two populations were used Swarna x O. nivara ILs (BC2F8) and BPT5204 x O. rufipogon ILs (BC4F10). Two Swarna ILs 233K (Fe-13 ppm Zn-20 ppm) and 24K (Fe-9ppm and Zn-22ppm) with high grain yield were crossed and unpolished F3 seed analysed from 445 lines. Fe ranged from 6to 26ppm and Zn from 6 to 23ppm. 233K (RPBio 4918-233K, IET25459) also showed 10% protein in grains. It showed 3ppm Fe and 15ppm Zn in polished rice as mean value when grown at 7 locations in Biofortification multilocation trials of All India Coordinated Rice Improvement Project (AICRIP) and is now in Advanced Varietal Trial-1. Likewise in 126 BPT5204 ILs the Fe ranged from 7.6ppm to 13ppm and Zn from 10ppm to 28ppm. One elite line 51 B (RPBio 4920-51B, IET24775) showed 10ppm Fe and 17ppm Fe in unpolished rice. It had 4.6ppm Fe and 19ppm Zn in polished rice as mean values from seed grown at 9 locations during 2014-15 in AICRIP and 4.2ppm Fe and 17ppm Zn in polished rice at 16 locations in 2013-14 trials. These high iron and zinc rice lines with high grain yield can be used in biofortification programs.

ICAR-NPTC-FG project 3019 (NPTC/FG/05/2672/33) to NS is acknowledged.

Keywords: Introgression lines, Biofortification, Iron and Zinc

1654 (P-440)

Harnessing of the Power of Some Traditional Plants for Nutrition and Health

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Due to eating out of whack, industrialized foods and due to change in lifestyle a society of sickly individual is produced. Traditional plants are the most ideal for the improvement of nutrition and health. To equip the society with the knowledge of traditional plants and to cease the disease or to improve nutrition by it, two very important parts are there i.e., their knowledge and application. This abstract is based on some traditional plants i.e. Moringa oleifera, Achyranthes aspera, and Cissus quadrangularis which can be used to improve nutrition and health in safe manner. Moringa oleifera is one of those plants that is being investigated for its good nutritional attributes. Its leaves are outstanding source of Protein which suggests that the plant leaves, can serve as a boon for curing 'P.E.M. (Proteins Energy Malnutrition)' in lactating women and weakened children. Its flowers are very good source of flavonoids, so that floral extract can be used as an effective antimicrobial agent. The active principles present in A. aspera and C. quadrangularis have been reported to possess anti-obesity effect. The special property of the seeds of A. aspera, as an anorexient, bestows valuable effect, to cure the excessive hunger in obesity, study have examined role of C. quadrangularis in fighting obesity and symptoms of metabolic syndrome. These Traditional plants can be used effectively to increase nutrition security and improve health. For this, people can be made well aware of their remarkable benefits in counter acting various ailment and to improve health.

Keywords: Moringa, Achyranthes, Cissus, Traditional plants

1671 (P-441)

Backyard Nutrition Gardens A Remedy for Malnutrition

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Backyard nutrition gardens were promoted in 2014-15, covering 200 households across five villages in Wardha district, Maharashtra, as part of an ongoing study to demonstrate Farming System approach to address undernutrition. The criteria were availability of land, water source and fencing to prevent domestic animals from entering. A season-based calendar of vegetables including green leafy vegetables, roots and tubers and other vegetables was developed in discussion with the community. Seeds of nutritious vegetables that are locally available were provided. The importance of including vegetables in the daily diet was stressed. The backyard nutrition gardens are found to provide fresh harvest of seasonal vegetables and necessary micronutrients on a regular basis to the households. Water scarcity is however a recurrent problem, hampering production in some months. An analysis of data collected over the three month period Dec 2015 to Feb 2016 showed that 27 different vegetables were cultivated. By way of illustration, 0.9 kg of spinach and 1 kg of fenugreek leaves was the quantity of average monthly production and consumption by 115 households during this period. Converting the quantities into nutrition equivalence, it was found that on an average, the additional micronutrients available to each household from monthly consumption of just these two vegetables was: iron 29.44 mg, Vitamin A 9121.72 µg, Vitamin C 769.16 mg, calcium 4602.2 mg and zinc 6.27 mg. The experience shows that properly designed nutrition gardens can help address the malady of malnutrition through greater access to vegetables for inclusion in the daily diet.

Keywords: Backyard nutrition garden, Malnutrition

1696 (P-442)

Evaluation of Millet Recipes for Dietary Polyphenols, Antioxidant Activity and Anti-Diabetic Effect in the Management of Diabetes

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Minor millets are nutritionally superior to conventional food grains and exhibit hypoglycaemic effect due to presence of higher proportion of unavailable complex carbohydrates, resistant starch, nutraceutical components and slow rising sugar. Moreover, the most important thing is that millets have the ability to delay the onset of secondary complications of diabetes. Millets like little millet (*Panicum sumantrense*), foxtail millet (*Setaria italica*), ragi (*Eleucine coracana*), pearl millet (*Pennisetum typhoideum*) and sorghum [*Sorghum bicolor* (L.) *Moench*] were taken for preparation of *upma*, *khichdi*, *bisibelebhat*, *roti* and *thalipattu* and compared with the staple cereals like rice and wheat. Recipes were evaluated for their polyphenol content and antioxidant activity using Folin - Ciocalteau method and DPPH radical-scavenging method respectively. Selected recipes were evaluated for anti-diabetic effect using α-amylase and α-glucosidase inhibition activities. The polyphenol content of the millet recipes ranged from 27.66 to 202.81mg GAE /100g and that of rice and wheat recipes ranged from 16.78 to 148.05mg GAE /100g. The antioxidant activity of millet recipes ranged from 27.36 to 95.47 and that of rice and wheat recipes ranged from 15.72 to 61.45 % DPPH radical scavenging activity. The α-amylase and α-glucosidase inhibitory activities were found highest in little millet upma (71.95%) and little millet dosa (17.89%) and lowest in rice dosa (9.54%) and wheat chapatti (2.76%) respectively. A positive correlation was found between polyphenol content and antioxidant activity (r= 0.736**) and for α-glucosidase inhibition activity (0.396*). These recipes along with recommendation for diabetics can also be introduced in the regular diet of healthy people.

Keywords: Antioxidant activity, Anti diabetic effect, Diabetes, Millets, Polyphenols

1768 (P-443)

Technology Development for the Production and Storage of Gluten Free Cracker

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In the world, around 0.2–1.0% people suffer from celiac disease, an autoimmune disorder, also known as celiac spruce or gluten-sensitive enteropathy. Thus, the present investigation was aimed at formulating a new product i.e. gluten free cracker. Roasted brown rice flour (RBRF) was used for the preparation of the product in combination with amaranth flour (AF), flaxseed flour (FF) and whey protein concentrate (WPC-70) by employing CCRD of RSM. The optimized levels of the ingredients i.e. Amaranth flour (20%), Flaxseed flour (10%) and WPC-70 (3%) were selected on the basis of highest desirability for the preparation of product. The prepared product was analysed for sensory attributes (colour, uniformity, shape, surface, aroma, taste, firmness, flakiness, crunchiness and overall acceptability), physical parameters (L*, a*, b* and aw), chemical composition (protein) and shelf life of the developed product. Non-significant difference was obtained on comparing the predicted values with experimental values by employing t-test. The optimized product had 10.35% protein, 10.02% fat, 2.15% ash, 22.5% total dietary fibre and 2.44 mg/100g iron. Crackers were packed in LDPE pouches, stored at 37±1°C in a B.O.D. incubator and analysed for sensory and physico-chemical analysis during its storage for 28 days (May- June, 2016). Non-significant effect on uniformity, surface, aroma, taste, flakiness, crunchiness, overall acceptability, aw, color (L*, a*, b*) value and protein were noted, while significant ($p<0.05$) effect was observed on remaining sensorial attributes, phenolic content and peroxide value of product during its storage period. Gluten free crackers made from BRF, AF, FF and WPC-70 showed excellent nutritive value besides being a potent product for people suffering from celiac disease.

Keywords: Gluten Free Cracker, Amaranth Flour, Flaxseed Flour, WPC 70, RSM

1815 (P-444)

Antioxidant Potential of Diverse Lines of Lentil

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Antioxidants are known to have beneficial effects to prevent/reduce risk of many diseases related to oxidative stresses caused because of reactive oxygen species (ROS). Besides nutritional value, lentil cultivars possess high levels of natural antioxidants, which could significantly contribute to the management and/or prevention of degenerative diseases associated with free radical damage. Fifty five lentil genotypes comprising Indian released varieties/ advanced breeding lines and germplasm lines, Mediterranean landraces and ICARDA germplasm were evaluated for antioxidant activity. 2,2-diphenyl- 1 picrylhydrazyl (DPPH) method was used to determine antioxidant activity. Free radical scavenging capacities of lentil genotypes ranged from 0.41 (IG73920) to 21.08 (P13138) µmol TE/g. Based on the observations, this study is helpful for lentil breeders as well as neutraceutical industries.

Keywords: Antioxidant Potential, Degenerative diseases, Lentil, Reactive oxygen species

1821 (P-445)

The Potential of Genetic Diversity of Glutinous Rice for Conservation and using in Laos

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Rice is life in Laos. Rice is the key crop for securing national food and livelihood security. Lao people consume on average 165.5 kg of milled rice per annum. Seventy three percent of the population is employed in the rice sector that accounts of 25% of the national GDP (total agricultural GDP is 30.8%). Rice is culturally important for all ethnic groups and is used in many traditions and rituals. Laos is a center of biodiversity for glutinous rice varieties and the primary center of origin and domestication of the Asian rice (*Oryza sativa* L.). The objective of the project had to conservation and using genetic diversity for improving rice yield and quality. The project had started for survey and collecting rice sample before 1995 but very small amount then in 1995 had developed the national gene bank (Under Lao-IRRI project). Recently, it has been conserved more than 14,000 accessions of rice with 80% as glutinous rice. Among the glutinous rice accessions 55% are upland rice accessions and 45% are lowland rice accessions. Traditional glutinous rice varieties have good aroma, eating quality, resistance to GM disease, drought tolerant, flood tolerance, pest and diseases resistance and other traits. This paper reports on the characterization of the glutinous accessions which were used in breeding programmes and since 1991 the Ministry of Agriculture and Forestry had released over 20 improve varieties for improving rice production, among that 18 varieties were glutinous rice. Rice germplasm are very importance genetic resource for rice breeding programmes in Laos.

Keywords: Genetic diversity, Germplasm, Glutinous rice

1891 (P-446)

Colored Wheat as a Novelty Crop Understanding Potential Health Benefits

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Colored wheat carry anthocyanins in pericarp and/or aleurone layer. Anthocyanins are water soluble flavonoids. This study was aimed at generating colored wheat germplasm adapted to local climatic conditions and understanding the nutritional benefits associated with these lines. These lines exhibited high anthocyanin content and the anthocyanin content between the different lines was in the order black>blue>purple>white. Our selected advanced lines showed insignificant yield difference from high yielding cultivars. DPPH, ABTS, PCL and NO assays suggested a very good anti-oxidant potential of these lines. Further, animal cell culture based assays of the anthocyanin enriched fractions from these lines suggested that they could attenuate lipopolysaccharide induced nitric oxide, IL-β and TNF-α production by the murine macrophage cell lines (RAW264.7). In vivo studies using high fat diet induced obesity models suggested that black wheat line could effectively prevented fat deposition, improved glucose homeostasis, insulin tolerance and lowered the serum cholesterol and free fatty acids levels. Elemental analysis indicated significantly higher iron and zinc content in colored wheat lines. Nutrition parameters including major constituents (carbohydrates, sugar, protein, ash, dietary fibers), minor constituents (vitamins, metals and minerals) and processing quality parameters (SDS sedimentation, gluten content, alveograph) of advanced colored lines were similar to high yielding white wheat. Selected purple wheat line was more suitable for biscuit making and black wheat for raised bread making. Our results are suggestive of future utilization of these advanced colored wheat lines for nutraceutical product development and commercial utilization.

Keywords: Anthocyanin, Antioxidant, Colored wheat, Nutraceutical, Nutritional profiling

Satellite Session 3 :

Climate Change as an Opportunity for Agrobiodiversity Management

1934 (O-68)

Will Climate Change have only Adverse Effects on Species, Communities, and Ecosystems in North-eastern India Evidences from Predictive Modeling and Field Studies

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Positive and negative impacts of climate change on different ecosystems, communities and species of north-eastern India have been analyzed. The evidences are based on predictive models using Regional Climate models and the distribution models at appropriate scale for different levels of biological organization. The model predictions were validated through extensive field survey. The predictions were also discussed in light of temporal changes in land use and land cover (LULC) *vis-a-vis* temperature and precipitation. Case studies describing positive and negative effects on agriculture (including shifting cultivation), forest and wetland ecosystems, species as well as agro-biodiversity in north-eastern India have been described. Possible out-break of various vector-borne diseases has also been predicted.

Keywords: Climate change, Community, Ecosystem

1933 (O-69)

Work of GIZ in the Field of Agrobiodiversity

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In many Asian countries people depend on what nature can provide: Food, medicine, fodder for their animals as well as construction and biofuel materials. At the same time there is an increasing pressure on natural resources by a growing population and changing consumption patterns. Agrobiodiversity is the outcome of the interactions between genetic resources, the environment and the management systems and practices used by farmers and pastoralists. Agrobiodiversity has developed over millennia, as a result of both natural selection and human interventions. The conservation and sustainable use of agrobiodiversity is essential for the survival of humankind. Besides its supporting role in risk-management for smallholder farmers in developing countries by assuring their survival and livelihood, agrobiodiversity holds important keys for the future adaptation of agriculture to a changing climate and environment. Greater genetic diversity contributes to reducing climatic and disease-related risks and increases resilience. However, in the past few decades agrobiodiversity has decreased at an alarming rate and these losses are still increasing rapidly, especially in developing countries where agricultural biological diversity is often very rich. The extinction of traditionally cultivated crop species and varieties as well as local animal breeds has many causes. The main challenge for the agricultural sector is to simultaneously secure enough high-quality agricultural production for food and nutrition security, conserve biodiversity and manage natural resources, as well as improve human health and well-being. Essential approaches in slowing down the present rate of loss of agrobiodiversity are the active involvement of the rural population in *in-situ* (on farm) conservation, considering the vital role of women and smallholders in the conservation process, traditional knowledge and local innovation. Therefore GIZ with its partners is working with integrated, mulit-sectoral and multi-level approaches, ranging from village interventions and capacity-building to providing policy advice and mainstreaming agrobiodiversity at local, national and international levels. In this session a 10-20 min presentation of the work of GIZ in the field of agrobiodiversity in Asia will be presented, including project examples from different countries.

Keywords: Agrobiodiversity, GIZ, *In-situ* on-farm

1931 (O-70)

Traditional Knowledge of Tribal People of Meghalaya in Adaptation to Climate Change Integrating Traditional Knowledge of The Indigenous People with the Computer Model Output in Vulnerability Assessment and Adaptation Actions

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People of Khasi, Jaintia and Garo communities in Meghalaya have lived in symbiotic relationship with the natural ecosystems since hundreds of years. Their livelihood including agriculture and allied activities are closely linked to the natural resources. Their closeness to nature has taught them ways and means to cope with the adversities of nature and ill impacts on their livelihoods due to other reasons, over the years. Agriculture practiced by the tribal people in the State still remains largely organic. They are rich in traditional knowledge accumulated through the generations in natural resource management. The impact of climate change on natural resources, agriculture and other livelihoods has already been perceived by them. The climate change is impacting natural resources and their livelihood adversely in significant way. They are using their traditional knowledge in fighting climate change in their own ways. Meghalaya Climate Change Centre has undertaken a State-wide study to document and analyse perceptions of indigenous people of the State on the impacts of climate change and their traditional knowledge in adaptation to it. The State has also initiated a study in mapping hot spots of vulnerability to climate change using latest computer models on high resolution with the help of premier institutions in the country. A bottom-up and top-down knowledge integration approach is being followed in assessment of vulnerability to climate change for the climate sensitive sectors such as agriculture, water resources, forest, livestock & animal husbandry. Socio-economic data and natural features of the State are used in developing appropriate adaptation strategies for the crucial sectors of the State. The paper presents findings of the above study and an integrated approach in assessment of vulnerability to climate change for the sectors impacting livelihood of the rural people in the State.

Keywords: Traditional Knowledge, Tribal, Meghalaya, Climate change

1932 (O-71)

Importance and New Utilization Opportunities for Bamboo in Northeast India under the Angle of Climate Change and Inclusive Agro-economic Development

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As an essential part of forest ecosystems and traditional agriculture, Bamboos strengthen resilience, contribute to maintain biodiversity, and secure the livelihoods of millions of people in the northeastern region of India.The multitude of products that can be made and environmental services in e.g. watershed conservation and soil amelioration make Bamboos ideal for sustainable income generation and its ability to sequester large amounts of CO_2 can contribute to India's INDC for the reduction of greenhouse gas emissions. Despite this, potential of Bamboo in regard to its management and application in the northeast has not been adequately realized, leading to stagnant growth of the sector even though the land is endowed with plentiful resources.In Mizoram state, the value chains of Bamboo charcoal and shoots have been identified for overcoming existing constraints by providing new utilization and marketing opportunities and initiate an integrated and inclusive development of the sector, which could serve as a model for other states in the northeast. Key for success is seen in niche products that are well investigated but not well established in the market yet, are easy to transport, provide a good ROI, are carbon neutral or negative, and can be manufactured from readily available resources in best quality and large scale by MSMEs to unlock the potential of households, small farmers and enterprises for economic development. Derivatives of the charcoaling process (Pyroligneous acid, biochar, activated charcoal) and newly developed nutritious food products fulfill those criteria supplying the market sectors health, environment, and bioenergy that will gain even more importance in future.

Keywords: Bamboo, Northeast India, New utilization opportunities, Climate change

1935 (O-72)

Advocating for Shifting Cultivation in the Context for Climate Change in the Eastern Himalayas - Lessons and Issues

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Shifting Cultivation is amongst one of the most traditional and widely practiced land use amongst the tribal communities of north east India. Shifting cultivation is more than just a production system, as it integrates land-use and resource management systems at the landscape level and is very closely linked to the culture, tradition, institutions and knowledge systems. It also houses rich and diverse cropping and forest systems. Unfortunately, shifting cultivation has always been in the limelight for all the wrong reasons both at the scientific and policy levels. It has been termed as "unproductive, unsustainable and destructive" and for years, governments have rather than trying to improve the system, advocated for abandoning or weaning away farmers from such practices. Such policies have not only failed over the years but have negatively impacted traditional resource management systems, its institutions and even the sustainability of traditional seeds. This paper stems from the experiences and lessons in advocating for a change in policy with regard to shifting cultivation, especially, in the context of climate change. The paper illustrates not just the policy processes but also highlights field evidences of the benefits and opportunities of shifting cultivation in the context of climate change.

Keywords: Climate change, Shifting cultivation, Eastern Himalayas

Satellite Session 4 :

Crop Wild Relatives: Back to the Wild to Save the Future

645 (O-73)

Conservation Planning for Crop Wild Relative Diversity in the SADC Region

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The Southern African Development Community (SADC) includes 15 countries and is an important region for its diversity of wild relatives of a number of crops, including coffee, cucurbits, eggplant, lettuce, millets, okra, pulses, rice, sorghum and watermelon. Crop wild relatives (CWR) are wild plant taxa closely related to crops that are potential sources of traits for crop improvement, and therefore an important socio-economic resource for food and economic security. As part of an EU-ACP funded project, conservation planning for CWR diversity of the SADC region is currently being undertaken. Among the more than 1900 CWR species found, 102 have been prioritized for immediate conservation action based on the regional and global food security and economic value of the crops to which they are related; and their potential for utilization in crop improvement programmes. CWR of regionally and/or globally important crops, such as coffee (*Coffea*), cottonseed (*Gossypium*), cowpea (*Vigna*), eggplant (*Solanum*), millets (*Echinochloa*, *Eleusine*, *Eragrostis*, *Panicum*, and *Pennisetum*), rice (*Oryza*), sorghum (*Sorghum*), watermelon (*Citrullus*) and yam (*Dioscorea*) are amongst those prioritized. The results of diversity and conservation gap analyses for these regional priority CWR, as well as the main conservation recommendations will be presented. In parallel to this regional analysis, National Strategic Action Plans for the conservation and sustainable use of CWR in Mauritius, South Africa and Zambia have been developed within the project. Considerations on how to integrate both regional and national conservation priorities in order to address the conservation of CWR in a holistic manner will also be made.

Keywords: Crop wild relatives, *Ex situ*, Genetic conservation, *In situ*

286 (O-74)

A Strategic Approach to Crop Wild Relative Conservation in Mega-Diverse Mexico

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The effects of climate change, habitat degradation, increasing human population, among other factors, are threatening the diversity of Crop Wild Relatives (CWR) globally and specifically in Mexico, an important center of agrobiodiversity, including globally important crops such as maize, common bean and tomato, and their CWR. Thus, the objective of this research is to analyze the diversity and conservation status of the CWR related to the most important crops in Mexico, as a basis for the development of a national CWR conservation strategy. Three main procedures are employed: a) creation of a national CWR inventory, b) *in situ* and *ex situ* gap analyses and c) enhancing the utilization of priority CWR through predictive characterization. CWR were prioritized for conservation action based on their geographical distribution, threat status, socio-economic values of the related crops and the level of relationship to the crop and resulted in 313 taxa that integrate the national CWR inventory. Priority sites were identified throughout the country for complementary *in situ* and *ex situ* conservation of these taxa. In addition, CWR accessions of maize wild relatives were selected for their potential utilization in crop breeding. Finally, the CWR conservation strategy will help establish the foundations of CWR conservation in Mexico, by making recommendations for immediate conservation action thus helping mitigate the threats to Mexican agrobiodiversity and global food security.

Keywords: Crop Wild Relatives, Mexico, National CWR conservation strategy

1002 (O-75)

Identification and Collection of Priority Crop Wild Relatives in Three Provinces of South Africa

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Crop Wild Relatives (CWR) are wild species closely related to landraces and commercial crops. CWR can be a source of genes for food crops, however, researchers have neglected these species and they are becoming more threatened in the wild. The objective of this study was to identify and collect priority CWR occurring in three provinces of South Africa. Prioritization of CWR process was conducted using criteria such as potential use in crop improvement, socio-economic value, threat and relative distribution with 292 species recorded. Field survey was planned and conducted in three provinces (Mpumalanga, Limpopo and KwaZulu-Natal). A feasible number of 31 species were identified in terms of conservation status, using the field survey criteria on selected species that occurs and does not occur in protected areas, including species on oldest records (above 30 years). Parameters such as collection date, collector, species name, genus, family, land use, associated species, plant height, locality, co-ordinates, population size and specimen for herbarium were collected using collection form. Out of these collected species, families with the higher number of species in all provinces were Solanaceae (7 taxa) andon Poaceae (2 taxa). Species were found in both unprotected and protected areas and recorded. Although most of these species occurred in all three provinces across the ountry, Oryzalongistaminata only occurred in one province (Limpopo) in a wetland in Nylsvley Nature Reserve. KwaZulu-Natal had significantly high number of 34 localities with Miscanthusjunceus found in 5 of these localities on private land (plantations), compared to Mpumalanga with 18 and Limpopo with 12 localities. Among the 31 species, 20 were collected along roadsides, especially in disturbed areas, whereby they are exposed to threats that need sufficient attention for conservation.

Keywords: Identification, Collection, Prioritized CWR

988 (O-76)

Re-collection to Assess Temporal Variation in Wild Barley Diversity in Jordan

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Many crop wild relative (CWR) species are threatened by habitat loss and climate change and are not adequately conserved. Genetic erosion may impact their resilience to changes in environmental conditions. Data about the extent and distribution of diversity, and knowledge about temporal changes in diversity are frequently limited, but are important to assess vulnerability of CWR populations and to inform conservation actions. Assessing temporal changes requires time series data. Past germplasm collecting missions are considered useful resources to establish a diversity baseline for temporal comparisons. Through re-collecting samples from old collecting sites a contemporary snapshot of genetic diversity can be established for comparison with the diversity in earlier samples. We applied this methodology to wild barley populations, *Hordeum vulgare* subsp. *spontaneum*, in Jordan to generate a data set that would allow assessing changes in genotypic and phenotypic diversity, using seed samples collected in 1981 and 2012 from the same sites across Jordan. Sufficient information records from the past collecting and seed material were available, the historical sites could be located and re-collected, and a useful second time point (31 years later) was established for comparison. Collected samples were planted in a common garden to generate microsatellite and phenotypic data. Based on the genetic and morphological data, changes in genetic diversity could be assessed and inferences on pressures driving the observed changes be made. This approach allowed to study possible responses to environmental pressures exhibited by CWR.

Keywords: Genetic diversity, Genetic erosion, Re-collection, Wild barley

921 (O-77)

Spatial Analyses of Occurrence Data of CWR taxa as Tools for Selection of Sites for Conservation of Priority CWR in Zambia

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Crop wild relatives (CWR) are valuable gene pools for crop improvement and adaptation to climate change. Current national actions towards conservation of plant genetic resources do not adequately cover ex situ CWR occurring in the country and there is no active in situ conservation of CWR. Through the three years EU-ACP supported SADC project, Zambia prioritized a total of 30 CWR taxa from the generated partial checklist consisting of 459 taxa. Occurrence data of priority CWR taxa were compiled from several sources including national herbaria, the national plant genetic resources collections database and other online sources. The populated occurrence data of priority CWR taxa were subjected to spatial analyses employing DIVA-GIS version 7.5 and CAPFITOGEN tools to establish species distribution, species richness, gaps in *in situ* and gene bank collections to objectively identify priority sites for *in situ* conservation and *ex situ* collecting. The results generated from these analyses have provided information on priority CWR species richness indicating the spatial differences in richness of the priority CWR in the country, distribution of priority CWR of rice (*Oryza* spp.), cowpea (*Vigna* spp.), finger millet (*Eleusine* spp.), sorghum (*Sorghum* spp.), *Dioscorea* spp. and *Solanum* spp. Gap analysis has indicated priority CWR taxa not actively conserved through both *in situ* and *ex situ* strategies. Consistent with the national developmental agenda, results of the spatial analyses of occurrence data of priority CWR taxa objectively provide the basis for decision making on targeted sites for the conservation of CWR taxa in Zambia.

Keywords: Crop wild relatives, *In situ* and *ex situ* conservation, Spatial analyses

1096 (O-78)

Exploring the Wilds Harnessing Genetic Potential for Crop Improvement

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The wild relatives of the crop are being gradually recognized and sincerely taking into breeding efforts in making climate-resilient agriculture. The genetic diversity of most of the crop plants has been significantly reduced during the process of domestication and rigorous breeding. The reduction in diversity specifically in Indian mustard has placed a major constraint over the brassica breeder's ability in expanding its cultivation into varying climate and stress conditions. Although, the wild relatives of brassica possess wide genetic diversity that bears more numbers of adaptive traits of agricultural significance, including seed oil quality and resistance to numerous abiotic and biotic stresses. However, focused efforts have been made for a specific trait to use them to introgressed into a growing cultivar and dealt with wild species in a meager way. While expedient, this approaches has omitted the prospect to test various traits and explore the full potential of wild relatives to counter the imminent challenges appeared in oilseed crop. Finding resistance to stem rot (SR), orobanchae, white rust, alternaria blight etc. are the major challenges ahead of brassica researchers to curb the yield losses. As the resistance source for SR and orobanchae has not been yet found in the existing cultivars, we are exploring the wild relatives of brassica including those earlier reported to be resistant to alternaria and other diseases. We assume the present study will yield a germplasm resistant to SR and that would be used as donor parents for introgression into high yielding mustard varieties.

Keywords: Sclerotinia, Stem rot, Brassica, Wild-relatives, Alternaria

1059 (O-79)

Genetic Variability for Nutritional Traits among Wild Relatives of Pearl Millet Conserved at ICRISAT Genebank

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Pearl millet is an important food and feed crop across the semi-arid tropics of Asia and Africa. Efforts are being made at global level to enhance the pearl millet nutrition including micronutrients to overcome malnutrition. Although enough diversity is noticed for nutritional traits in pearl millet germplasm, the content among open pollinated varieties and hybrids has been moderate. The wild relatives of pearl millet in primary genepool (*Pennisetum violaceum*, *P. mollissimum*) are useful sources for various stresses and for broadening the genetic base of pearl millet. The present study assessed the genetic variability for Fe, Zn, and protein content among 335 accessions of *P. violaceum* conserved at ICRISAT Genebank, Patancheru in an augmented design along with controls during post-rainy 2014-15. The open pollinated seeds were assessed for Fe, Zn (ICP method), and protein contents. Enormous genetic variability was observed among the 318 accessions of *P. violaceum* for nutritional traits like Fe (20-325 ppm), Zn (20-86 ppm), and protein (11-23%) content. Large numbers of accessions had higher levels of Fe (164 accessions), Zn (105 accessions), and protein content (319 accessions) compared to the best controls (Fe 53 ppm; Zn 52 ppm, protein 12%). One hundred and one accessions had combination of all three nutrients higher than the best controls. The present study has identified several accessions with high to very high levels of Fe, Zn, and protein compared to pearl millet. The research is in progress to identify stable sources to develop nutrient dense broad based open pollinated and hybrid cultivars.

Keywords: Genetic Variability, Nutritional Traits, Pearl Millet Wild Relatives

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154 (P-447)

Prioritisation *vis-à-vis* Germplasm Collection Status of Crop Wild Relatives in India

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Crop wild relatives (CWR) are wild taxa closely related to crop plants, including wild progenitors and/ or wild forms of crops, which are the important source of useful traits in crop improvement. Though ICAR-National Bureau of Plant Genetic Resources has reasonably explored the vast area of country and collected diversity in wild species of plant genetic resource importance, systematic CWR collection and conservation efforts have gained momentum only in current decade in the wake of increasing threats to environment. In this regard, major criteria followed for prioritisation includes economic importance of crops *per se*, level of closeness to crops, possessing traits of breeders' interest/ need, extent of distribution/threat and seed storage behaviour. Accordingly, a total of 588 species have been shortlisted as CWR of 168 crops belonging to 14 crop-groups. Collection Database indicates that out of 588 species, only 243 amounting to 10,529 accessions were collected so far; accounting to about 30% of total wild germplasm collected. However, this excludes those accessions involving wild/weedy/semi-wild populations of 142 crop taxa as well as those identified only up to genus level. Significant collections were made in some CWR under crop genera of *Oryza*, *Vigna*, *Sesamum*, *Citrus*, *Abelmoschus*, *Cucumis*, *Momordica*, *Solanum* and *Saccharum*. Analysis revealed the existence of huge gaps in CWR collection in terms of number as well as representative collection, even in crucial crop-groups such as cereals and pulses; in protected areas and fragile ecosystems such as coastal and cold-arid ecosystem.

Keywords: Crop wild relatives, Germplasm collection, Prioritisation, India

209 (P-448)

Enhancement of Maize Allelic Diversity Using Wild Relative Teosinte (*Zea Mays Ssp. Parviglumis*)

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Racial diversity has been the basis for maize improvement worldwide that has enhanced productivity along with increased genetic erosion globally as well as locally. Wild relatives have always been a source for novel gene (s) for both biotic and abiotic stress tolerance and therefore seem to be an integral part in breeding programme for germplasm development. In the present investigation, teosinte, a probable progenitor of maize was crossed with maize inbred line with objective to increase allelic diversity for different characters in maize. Evaluation of teosinte derived 92 maize lines in replicated trials revealed significant variation for different morphological characters. Days 50% anthesis, siliking and anthesis silking interval (ASI) were varied from 59 days to 81 days, 0 days to 13 days respectively. Plant height, ear height and flag leaf length were varied from 55 cm to 205 cm, 20 cm to 100 cm, 13 cm to 39 cm respectively. All the lines exhibited 75% leaf senescence between 108 days to 121days. Grain yield/plot (2.25 m^2) was noted to vary from 50g to 1000g. Teosinte derived lines also exhibited enhanced tolerance to banded leaf and sheath blight (BLSB). The present investigation therefore indicates wide range of variability for different characters. Therefore, the use of wild relatives may be a potential option for enhancing allelic diversity in maize.

Keywords: Teosinte, Maize, Allelic diversity, Wild relative

235 (P-449)

Survey, Collection and Utilization of *Grewia* and *Cordia* Species for Human and Animal Nutrition in Arid Kachchh, Gujarat

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Underutilized plants like Grewia and Cordia species have great potential for contribution to food and fodder security for rural families and their animals; these plants have medicinal properties. In Kachchh, great diversity of these species viz. G. tenax, G. villosa, G. flavescences, C. myxa and C. gharaf is available in arid lands. However, these species are under severe neglect from research and extension despite their potential to grow over large areas. Hence, this study conducted comprehensive botanical surveys in spring and winter 2015 to collect 97 diverse and valuable germplasms of these species for their characterization and utilization from 55 sites of 5 blocks of Kachchh by adapting selective sampling strategy. Each collected germplasms was allotted individual accession number. It was found that G. tenax (72.71%) was distributed widely followed by G. villosa (49.09%), C. gharaf (29.09%) and C. myxa (21.81%). Whereas, G. flevescence (3.63%) was minimally distributed. Distribution of 69 Grewia germplasm was maximum in Nakhatrana (44%) followed by Bhuj (27.53%), Mandvi (15.94%), Rapar (8.69%) and Bhachau (2.89%). However, 28 sites of Cordia germplasm collection were mostly distributed in Bhuj (53.57%) followed by Mandvi (28.57%), Rapar (10.71%) and Bhachau (7.42%). Finally, it is concluded that there is fair diversity of G. tenax and G. villosa in Nakhatarana, while, C. myxa and C. gharaf were mainly found in Bhuj and Mandvi. It was found that Kotda Chakar (Bhuj), Dahisara and Koday (Mandvi) are the diversity regions for all selected species except G. flevescence which is only found in Dhinodhar (Nakhatrana).

Keywords: Collection, Grewia, Cordia, Diversity

461 (P-450)

Conserving an Extremely Rare Wild *Momordica* Species of Economic Importance from Nagaland, India

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Momordica subangulata Blume subsp. *subangulata* is a rare Indo-Chinese taxon, collected for the first time in India from a 10 km stretch in Tuensang district of Nagaland. Six samples were collected. Excavated dormant tubers broke their dormancy within two weeks when brought to Thrissur and have profuse vegetative growth, but shy flowering in the hot and humid summer months. *In vitro* micropropagation was standardized using shoot tips and nodes. Shoot differentiation was obtained on MS medium supplemented with BAP. Rooting of 3-node vine cuttings as well as regeneration of new plants from tuber cuttings was obtained. October is the best time for seed collection and late October - early November is the best time for collection of senescent tubers. A ten kilometer stretch in Tuensang district of Nagaland from Kuttur to Tuensang on Tuensang-Kifri route, by the sides of NH 202 was found to have more than 200 plants comprising male and female of all age cohorts. Restricted to a small stretch of secondary forests in Ngangpong, Chingmelon and Kuttur villages in a 10 km radius of Tuensang, it is a critically endangered taxon demanding both *ex situ*, *in situ* and on-farm conservation. Situated at 1920 ft. MSL in the heart of its narrow distribution range, KVK Tuensang will be an ideal place for its simulated *in situ* conservation. Tender fruits, young leaves and clippings are cooked and eaten and is a valuable genetic resource for improving bitter gourd, spine gourd and teasel gourd.

Keywords: Agro-biodiversity of Nagaland, *Momordica* gourds, Wild edible vegetable

668 (P-451)

Collection and Conservation of Wild Mango (*Mangifera* spp.) in Bay Islands

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In Andaman and Nicobar Islands, six species of mango are distributed, of which five are wild species and *Mangifera indica* is the commonly cultivated species in the Island. Exploratory surveys were carried out to locate the genetic diversity and distribution of wild and indigenous mango species within the Islands. The indigenous mango species like *Mangifera griffithi*, *M. camptosperma*, *M. andamanica, M. nicobarica* and *M. sylvatica* were distributed in specific locations of the Island. Except *Mangiferra nicobarica*, other wild species are identified and their distributions are documented. The wild mango species of the Island are characterized based on the NBPGR minimal descriptors. The conservation of these wild species are important because they are useful for widening the genetic base of mango and for improvement of commercial mango through breeding programmes to address biotic and abiotic stresses. These wild species are less represented in the Island gene banks. For clonal multiplication of these wild species, modified *in-situ* approach grafting proved to be the successful propagation method by using *Mangifera indica* as rootstocks. The successful grafts are conserved in the experimental farm of ICAR-CIARI for further establishment of field gene banks of the wild mango species of the Andaman and Nicobar Islands.

Keywords: Andaman and Nicobar Islands, Conservation, *In-Situ* Approach Grafting, Wild Mango

754 (P-452)

Genetic Diversity in Wild *Hevea* Germplasm and Identification of Cold Tolerant Ecotypes from the International Rubber Research and Development Board Expedition in Brazil

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Hevea brasiliensis is a commercially cultivated species for its natural rubber (NR) latex in South East Asian countries and its genetic base is very narrow. India has received a share of the wild *Hevea* germplasm from the 1981 IRRDB collection of Brazil, which are under evaluation. To meet the ever-increasing demand, NR cultivation has been extended to non-traditional regions in India, and these areas often confronted with various abiotic stresses, especially low and high temperatures which affect its growth and productivity. Eighteen wild *Hevea* accessions along with two modern clones RRII 203 and PB 235 and two check clones RRIM 600 and Haiken 1 were evaluated at Nagrakata, West Bengal, the sub-Himalayan cold-prone region of India. The genotypes exhibited highly significant clonal differences (P=0.05) for all the growth traits viz. plant height, bark thickness, girth of plant in the 14th year after planting, annual and winter girth increment (cm/year) over seven years. Wide differences between the phenotypic coefficient of variation (20.13) and genotypic coefficient of variation (13.76) were observed for bark thickness. The 22 genotypes were grouped into 5 clusters based on six growth traits, reflected the presence of considerable genetic diversity in the population. The top 30% of the potential accessions showing high growth vigour under cold stress were identified which could be used in reducing immaturity period in this crop. These ecotypes/selections have high potential value for the development of cold-tolerant clones to mitigate climate change for these regions and also in broadening the genetic base of the present-day cultivated rubber.

Keywords: Cold tolerance, Genetic diversity, Growth vigour, *Hevea brasiliensis*

1222 (P-453)

The Impacts of a Changing Climate on Conservation Priorities for Crop Wild Relatives at a National Level

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Crop wild relatives (CWR) are a key resource in preparing our agriculture for climate change. Their broad genetic diversity can enable adaptation to the environmental stresses associated with the changing climate. However unless effectively conserved, both *in situ* and *ex situ*, we will not be able to harness this genetic diversity to improve our crops. Few, if any, studies have been done at a national level regarding the effects of climate change on CWR. In order to determine such changes, we have used species distributions modelling to examine the threat of climate change upon CWR. Here we used the most recent IPCC climate change scenarios from the present to the year 2080 to assess how CWR distributions may change. We used the change in population area as a proxy for change in population size and related this to the IUCN threat categories. Our results suggest that there will be a shift in CWR distribution from the south to the north, with areas of high species turnover in northern parts of Norway. Furthermore our study suggests there may be an increase in the severity of threat to CWR under the IUCN categories. Both *in situ* and *ex situ* conservation recommendations are made with this in mind. It is only with national level recommendations for conservation of CWR that global food security issues can begin to be tackled.

Keywords: Climate change, *Ex situ*, *In situ*, National strategy, Species distribution modelling

1237 (P-454)

The Use of Crop Wild Relatives in Environmental Sustainability and Food Security

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CWR are wild species that are found in natural and semi-natural ecosystems. They tend to contain greater genetic variation than crops because they have not passed through the genetic bottleneck of domestication; therefore, they provide a reservoir of genetic variation for improving crops and are the obvious choice for meeting contemporary food security demands. CWR were first routinely used by agricultural scientists to improve major crops in the 1940s and 1950s, and by the 1960s and 1970s. As a result, this practice was leading to some major breeding improvements. Almost all modern varieties of crops contain some genes derived from a CWR and they are now recognized as a critical resource with a vital role in food security and economic stability for the 21st century, as well as contributing to environmental sustainability.

Keywords: Crop wild relatives, Food security, Conservation

1409 (P-455)

Regeneration Studies *In Vitro* in Orchid Wild Species of Karnataka

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Karnataka is one of the hot spots for wild and endangered orchid species of India. Propagation and conservation of orchid diversity through conventional method is tedious. An investigation was conducted to study the *in vitro* regeneration of medicinally important wild orchids, *Cymbedium bicolor*, *Aerides maculosa* and *Rhynchostylis retusa*, sourced from the forest of Kodagu district. Four nutrient media, namely full strength Murashige and Skoog (MS), ½ MS, ¼ MS and Lindemann orchid medium in both semi solid and liquid were used for regeneration. Embryos were used as explant. Initiation of protocorms like bodies (PLBs) was found best on half strength semi solid MS media. PLBs were remarkably best in *C. bicolor* with 91.9 per cent and it was 29.03 per cent in *R. retusa* and 22.85 per cent in *A. maculosa* (¼ MS semi solid) as on 90 days after culture. In aqueous media, apart from PLBs there was remarkably a great number of different stages of embryo formations were also observed. This could serve a great deal for studying the stages towards plantlet formation as well as for producing plants on a large scale. PLBs produced on ½ MS semi solid media were cultured on ½ MS media supplemented with varying levels of NAA from 0.25 to 1.5 mg l-1 and plantlets were obtained from PLBs successfully. However the best media to obtain plantlets with enhanced rate of growth and proliferation was found to be on media containing 1.5 mg/ l of NAA. *In vitro* regeneration serves as an easy method for regeneration and conserving the valuable orchid diversity.

Keywords: Conservation, *In vitro,* Orchid

1433 (P-456)

Genetic Diversity Analysis of Wild Yams in India

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Wild Yams belonging to the family Dioscoreaceae makes significant contribution in the diets of the tribal community in India. They also have immense medicinal properties due to the presence of secondary metabolites especially diosgenin and hence is of great interest to the pharmaceutical industry. It serves as a precursor for the production of corticosteroids, sexual hormones, oral contraceptives and possesses cancer chemotherapeutic activity. Morphological, biochemical and molecular variation among the major wild yams were studied to establish their genetic relationship. Morphological characterization of 27 accessions belonging to 18 species of wild yams (*Dioscorea* spp.) was done based on 21 IPGRI descriptors. Tuber weight/plant ranged from 40g (*D. belophylla*) to 2.860kg (*D. hispida*) while tuber flesh color of the accessions varied from white to red purple. The biochemical studies on starch, sugar, crude protein, crude fat and crude fiber was done keeping in mind the nutritive value of the yam tubers. Among the accessions, *D. belophylla* recorded the highest content of starch on D.W basis (98%) while *D. tomentosa* the lowest (25%). *Dioscorea bulbifera* recorded highest protein value (1.82 f. wt. %) while for the fiber and fat content, *D. wallichi* and *D. floribunda* recorded the highest values of 2.2% and 21.75% respectively. The species were also characterized at molecular level using 15 ISSR primers, of which, UBC 810 and $(GA)_9$ AT showed high polymorphism for all the 18 species of wild yams studied. Hence the present study depicted the genetic variability and relationships among the major wild species of yams.

Keywords: *Dioscorea*, Diosgenin, Germplasm

1546 (P-457)

Use of Crop Wild Relatives of Sugarcane in the Development of New Types of Canes in Mauritius

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Sugarcane breeding and selection in Mauritius has been an ongoing process since 1891. The Mauritius Sugarcane Industry Research Institute (MSIRI) has an extensive collection of 2450 sugarcane germplasm which it uses to make new crosses every year. There has been a paradigm shift worldwide from maximizing sugar from cane to use the crop not solely for sugar but also for multipurpose use and for ensuring the sustainability of their sugarcane industries. This will ensure environmental sustainability in the sugar producing countries especially with the objective of reducing the CO2 emission aggravated by the use of fossil fuel for energy generation as well as to generate additional funding for the industry. The use of crop wild relatives (CWR) of sugarcane, namely Saccharum spontaneum, S. robustum, Miscanthus and Erianthus spp., has been intensified over the last decades, in Mauritius, so as to develop more productive varieties, new types of canes for biomass, energy and ethanol production, that can adapt to diverse agro-climatic zones and soil types. A number of S. spontaneum clones and early generation progenies have been highly successful in producing elite parents as well as new commercial varieties. Promising clones are being tested in contrasting marginal environments from very early and very late harvests. Preliminary results demonstrate that some elite clones, derived from CWR of sugarcane, are producing 40 to 50% more biomass compared to commercial varieties. In 2016, one variety was released for commercial cultivation and was derived from a first generation backcross CWR-derived clone. The variety, M 1002/02, is adapted to a wide range of environment, and under rainfed conditions it outyields current commercial varieties by more than 20%, thus confirming the potential of CWR as useful germplasm.

Keywords: Germplasm, Evaluation, Characterization, Breeding and selection

1614 (P-458)

Crop Wild Relatives Conservation in Rodrigues

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Rodrigues Island, located in the south-west part of the Indian Ocean, is an outer territory of the Republic of Mauritius. Rodrigues has initiated in the 1990's a series of integrated management projects aiming at conserving its rich but threatened native vegetation comprising of 142 species. These projects have generated encouraging results and remarkable good conservation practices which are now being replicated. The economic, social and environmental benefits derived from these efforts range from direct job creation, improvement of ecosystem services, better availability of raw materials for a variety of uses, and the establishment of unique natural reserves which are high profile touristic products. Part of the native plants are Crop Wild Relatives (CWR), which are wild plant species more or less closely related to food crops and forage plants as well as other useful plants having other socio-economic uses. A National Strategic Action Plan (NSAP)for the conservation and sustainable use of CWR, using a strong participatory approach, has recently been prepared with the support of the SADC Crop Wild Relatives programme, with a view to enhance the conservation of 10 identified CWR. Having an approach which focuses on CWR increases the leverage of extending the conservation work started through the enhancement of capacity building, institutional strengthening, research and development as well as increasing the number of *in situ* and *ex situ* conservation projects.

Keywords: Crop Wild Relatives, *In situ* conservation, National Strategic Action Plan (NSAP) for the Conservation of CWR,

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1828 (P-459)

Wild is the Future – Story of Indian Alliums

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Genus *Allium* consists of more than 750 spp. out of which more than 35-40 species occur in temperate and alpine regions of Himalayas in India. Out of all the species, onion and garlic are mostly grown throughout the different parts of India and India is the second largest grower in the world. Besides this, other species having minor importance are grown in selected pockets as semi-domesticated types or wild economic species. These wild species are used as vegetable, condiment, spices, ornamental or as medicine to cure various ailments. Wild spp. such as *A. tuberosum*, *A. hookeri*, *A.fasciculatum* are consumed raw, cooked or pickled. Cloves of *A. ampeloprasum* are used as medicine for knee pain, arthritis and ear pain. Several explorations to Lahaul & Spiti (HP); Sikkim, Arunachal Pradesh and parts of Assam (North East) and Ladakh-Kargil regions of J&K were undertaken to collect, identify and maintain the wild *Allium* spp. A range of wild spp. consisting of *A. carolinianum, A. fistulosum, A. hookeri, A. tuberosum, A. macranthum, A. przewalskianum* and other wild spp. were collected and the uses of these wild species as food item or medicinal purpose by local inhabitants were documented. How these wild species can be utilized in the in pre-breeding experiments for resistance to biotic and abiotic stresses will be discussed.

Keywords: *Allium spp*., Prebreeding, India, Medicinal purpose, Food item

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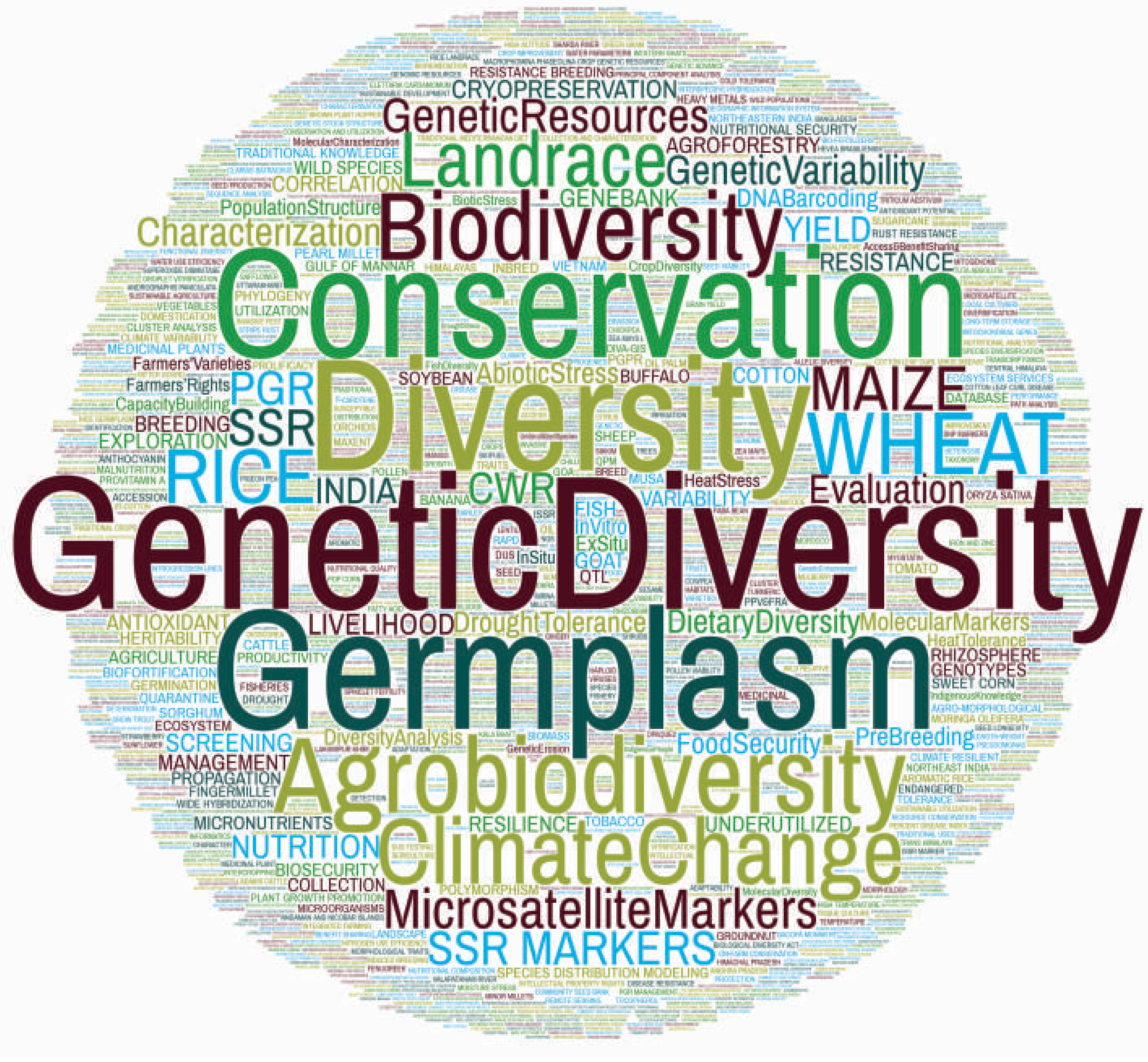
Front-cover : A Warli mural depicting in the simplest form the cobweb of life where human beings are components of biodiversity. Warli painting, where only white color is used on a red ochre background, is an art form of tribal community from North Sahyadri Range (Western Ghats) in India. It is believed that Warlis practice this tradition dating back to 2500 or 3000 BCE. *Copyright rests with unknown artist.*

Back-cover : A word-cloud of keywords of the abstracts presented in this book. Keywords that occur more frequently appear prominently. Higher frequency of terms “Genetic Diversity”, “Germplasm”, “Diversity” and “Conservation” is expected in the abstracts. However, if low prominence of “Climate Change” and microscopic “Drought Tolerance” are surprising, absence of “Utilization” or “Use” is alarming. One cannot miss the large size of big-three crops “Rice”, “Wheat”, “Maize” and invisibility of pulses. Certainly a food for thought for research managers!


RESISTANCE BREEDING
CRYOPRESERVATION
HEAVY METALS
GeneticResources
NORTHEASTERN INDIA
NUTRITIONAL SECURITY
AGROFORESTRY
TRADITIONAL KNOWLEDGE
Landrace
GeneticVariability
WILD SPECIES
CORRELATION
GENEBANK
DNABarcoding
PopulationStructure
Biodiversity
Characterization
YIELD
RUST RESISTANCE
RESISTANCE
PEARL MILLET
GULF OF MANNAR
INBRED
VIETNAM
CropDiversity
HIMALAYAS
Conservation
PHYLOGENY
UTILIZATION
CLUSTER ANALYSIS
CLIMATE VARIABILITY
MEDICINAL PLANTS
Farmers'Varieties
Farmers' Rights
PGR
SOYBEAN
AbioticStress
BUFFALO
COTTON
MAIZE
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GOAT
QTL
ORYZA SATIVA
ACCESSION
GeneticDiversity
TOMATO
ANTIOXIDANT
HERITABILITY
LIVELIHOOD
DroughtTolerance
DietaryDiversity
MolecularMarkers
HeatTolerance
AGRICULTURE
BIOFORTIFICATION
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SCREENING
DiversityAnalysis
FoodSecurity
PreBreeding
MANAGEMENT
PROPAGATION
FINGERMILLET
WIDE HYBRIDIZATION
Agrobiodiversity
CLIMATE RESILIENT
NORTHEAST INDIA
AROMATIC RICE
ENDANGERED
TOLERANCE
MICRONUTRIENTS
RESILIENCE
TOBACCO
UNDERUTILIZED
NUTRITION
ClimateChange
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PLANT GROWTH PROMOTION
POLYMORPHISM
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