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INDIAN SOCIETY OF PLANT GENETIC RESOURCES

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- To disseminate knowledge relating to various aspects on plant genetic resources.
- To provide a forum for organizing symposia/conferences with a view to develop close relationship among the scientists engaged and interested in plant genetic resources activities.

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Synecological Farming for Mainstreaming Biodiversity in Smallholding Farms and Foods: Implication for Agriculture in India

Masatoshi Funabashi
Sony Computer Science Laboratories, Inc., Takanawa muse bldg 3F, 3-14-13, Higashi-Gotanda, Shinagawa-ku, 〒141-0022, Tokyo, Japan

We experimented a novel system of small-scale market gardening, namely synecoculture, in the 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. Through the measurements and analyses of species diversity, vegetation surface distribution, plant-insect interactions, soil environmental variables, yield performance, food and nutrition diversity, spontaneous organization of ecosystem functions in response to the introduced diversity of plant community was revealed to be compatible with productivity and various regulation services even in marginal environment. The results provide promising possibilities for the application to smallholding agriculture in India, which could potentially recover historical loss of biodiversity and multiple regulation services such as pollination and water cycle, and contribute to resolve poverty and malnutrition, if institutional supports on the access to PGRFA and leveraging technologies were properly coordinated.

Key Words: Biodiversity, Climate change, Ecosystem functions and services, ICT, Malnutrition, PGRFA, Pollination, Small holder, Soil environment, Synecological farming

Introduction

India has harboured megadiversity of culture and ecosystems throughout the human and natural history. Surrounded by the world's highest mountains and abundant traverse of large rivers, Indian subcontinent comprises various landscape ranging over vast plain, high plateau, desert, rain forest, long coastal ecosystems, *etc*, including biodiversity hotspots. Indian population is equivalent to 17-18% of the total world population, who cohabit with important concentration of biodiversity accounting for 7-8% of the species of the world (IBP, 2017).

Despite the gifted natural resources, India has been losing the majority of its biodiversity during the modern development. Original species abundance devastatingly decreased by demographic pressure mainly from agricultural land use, and is projected to further exacerbate the extinction rate by 2050 (Alkemade *et al.*, 2009). Global propagation of conventional agriculture with synthetic fertilizer certainly saved the highest number of population from hunger, yet agricultural land conversion is triggering the 6th massive extinction in life's history that is 500-1000 times faster than natural extinction rate in vascular plants (Pereira *et al.*, 2010). The loss of fundamental diversity of species provokes multiple vicious cycles in social-ecological systems. For example, India is vastly covered by the regions with serious loss of pollination service negatively impacting market output (Potts *et al.*, 2016), which highly coincides with global correlates of emerging infectious diseases (Jones *et al.*, 2008). It was one of the evidential phenomena that during the 1st International Agrobiodiversity Congress on November 6-9 2016, New Delhi was shrouded in the historical record of air pollution arising from surrounding slush and burn agriculture fields, which implied cumulative loss of regulation services. Further monoculture intensification based on solely economic incentive may jeopardize fundamental life-support of farmers by multi-trophic homogeneization of already frail ecosystems (Gossner *et al.*, 2016; Soliveres *et al.*, 2016).

Not only the destruction of ecosystems but the loss of crop diversity is crucial to human health. Since the eradication of hunger by the green revolution in 1960s, the adverse effect of culture homogenization prevails as micronutrient deficiency associated with volatility risk of single crop (Pingali, 2012). Undernutrition such as protein, vitamins and minerals deficiency, and contrary overnutrition in affluent population separate the health state between incremental difference of under- and over-

**Author for Correspondence: Email- masa_funabashi@csl.sony.co.jp*

weight, resulting in the overall expansion of risk factors of non-communicable diseases (WHO, 2003; Sachdev, 2012).

Given that India will become the world's most populated country by 2022, and continue to grow through 2050, simple sector-wise mitigation measures are not sufficient to substantially cope with the developmental conflict. The entanglement of governmental regulations, farmers' economic incentives, health and ecological degradation forms multiple burdens that require comprehensive and fundamental reconstruction of agricultural activities from production to distribution.

This should take a thoroughly integrative approach following the causal structure of social-ecological organization. To secure the fundamental life-support, biodiversity mainstreaming involving other sectors than environment is essential for the premise of sustainable development (IIED, 2014). Especially for major primary industry sectors in India (*i.e.* agriculture, animal husbandry, informal forestry), the living of those population substantially depends on ecosystem services whose benefit counts up to 58% economic value compared to their GDP per capita. Ecosystem degradation is estimated to impose the replacement cost of these services that comes at a price of 200% of their GDP (TEEB, 2008).

Under the global principle of mainstreaming biodiversity, reform of social and economic sectors needs to be addressed with top-down effective promotion such as on pricing, technological leveraging and ownership investment (Haque *et al.*, 2012; Dev *et al.*, 2015), as well as bottom-up agricultural interventions beneficial to the amelioration of nutritional status and well-being of smallholders in rural population, especially women (Bhagowalia *et al.*, 2012; Chandrasekhar *et al.*, 2015; Pandey *et al.*, 2015).

The whole process needs interactive support of information sharing and education in a wide range of geographically dispersed and ecologically diverse areas, which is expected to find compatibility with recently popularizing information and communication technologies (ICT) (Haque *et al.*, 2012; Bhagowalia *et al.*, 2012; GRFAS, 2012).

This situation is not unique in India but common in other countries supported by smallholders. Especially sub-Saharan Africa and South-East Asian countries share common problems in terms of population growth, malnutrition and vulnerability to climate change. Agricultural non-CO_2 green-house gas emissions growth will be greatest in Asia and sub-Saharan Africa (EPA, 2012), which will account for 2/3 of the increase in overall food demand in 2050 (ESA, 2012).

Developed countries are also facing the reform of agricultural sector, in face of aging population and increasing burdens of non-communicable diseases. Japan's farming crisis worsened between 1995-2015 marked with a drastic halving of workers from 4 to 2 million in farming and forestry, associated with the average age increase from 59 to 66 years old (MAFF, 2015). Japan's total health expenditure is rising up to 10% of GDP in 2014, which accounts for more than 40% of the entire national budget (WHO, 2015).

These contexts call for an internationally common development of novel food production systems adapted to the problems of today's smallholders, who produce about 80% of world food, cultivate 80% of the arable land, and occupy one third to half of the world population (FIR, 2013; FAO, 2014). Common requirement and achievement need to be shared beyond local stakeholders with strong institutional support.

Based on such global perspective, synecological farming is developed as an extreme concept of mainstreaming biodiversity and *in situ*/on-farm conservation through utilization of plant genetic resources, which has been experimented in Japan and Burkina Faso (Funabashi, 2016a; Funabashi, 2016b; Tindano and Funabashi, 2017). Initial achievement fits well to the requirement of sustainable and conservation farming in Indian context, in terms of cost reduction and profit maximization under weak infrastructure in marginal environment (Bhagowalia *et al.*, 2012; Aryal *et al.*, 2014).

In light of expansion to the largest small-holding country, this article reports the preliminary results of experiments in Japan and Burkina Faso and discuss fundamental requirement necessary for synergistic application in India, with expectation to contribute to the improvement on the international strategy of plant genetic resource conservation through active exchange and utilization with ICT support.

Materials and Methods

Synecological Farming

Synecological farming, or synecoculture in short, 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 (Funabashi, 2016b). Spontaneous organization of ecosystem functions in response to the diversity of plant community was a major hypothesis that was expected to be compatible with productivity and various regulation services. It was developed in Japan based on the integrated theory of physiological and ecological optima (IMPEO) that converged agronomy and ecology under a unified framework of plant science (Funabashi, 2016a). It has also recently been experimented in Burkina Faso in semi-arid tropical condition (Tindano and Funabashi, 2017). 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 edible species in each plot. Measurements of vegetation surface, species diversity, soil environmental variables, products diversity, and record of harvest were performed, as detailed in the following sections:

Measurement of Vegetation Surface

We developed the 2-step visual analog scale method (2-step VAS) for quick and reliable on-site measurement of species-wise covering surface of complex vegetation during initial stage of succession in synecoculture. The visual analog scale method (VAS) is a continuous psychometric response scale used in questionnaires (Grant *et al.*, 1999). The 1st step of 2-step VAS consists of 10 fixed point scaling as a preliminary step of VAS. Each observer evaluates the surface ratio of a plant species in confined area of about 2 m^2 with 10 degrees, from 1 to 10 representing 0-10% to 90-100% of the total surface, respectively. At least 3 persons evaluate independently with 10 discrete scale, and select the final scale by a majority vote.

In the 2nd step, usual VAS method is applied based on the restriction of 10 discrete scale, *i.e.* choose from 0-10% if the 1st step score is 1, from 10-20% if the 1st step is 2,… and from 90-100% if the 1st step is 10. Final VAS score of the 2nd step takes the mean value of all observers and is normalized to percentage with respect to the estimated surface of all species.

Although 2-step VAS method is based on subjective evaluation, it shows sufficient accuracy and reproducibility for the measurement of complex surface patterns following power law. Based on the evaluation with artificially generated sample pictures, the measurement error of 2-step VAS weighted by true surface ratio is confined within linear scale in double-logarithmic plot, which means that the measurement error has a scale-free property that does not affect the fitting with power function. This conforms to the characteristic of human visual perception known as Weber-Fechner law. In fact, after just a few times of practice, all observers came into perfect agreement of the 1st step of 2-step VAS, which strongly implies that the accuracy and reproducibility of the measurement depends on universal faculty of visual perception rather than trained capacity.

We measured the species-wise surface ratio of introduced crops in synecoculture field during the 1st year of succession from January to August 2011 on 300 m^2 in Oiso, Kanagawa, Japan with the use of 2-step VAS method.

For a comparison with natural vegetation, we also analyzed image data of natural vegetation in Nakagawa, Ashigara in the same region of Kanagawa, obtained from Biodiversity Centre of Japan (BCJ, 2017). Surface measurement was digitally performed with the use of Adobe Photoshop CS5, by segmenting 38 vegetation types classified by different colors in the database. Surface ratio was normalized with respect to the total surface.

Estimation of Plant-Insect Interactions

We predicted the primary interaction between plant and insect species. Based on the biodiversity record of 10 synecoculture fields in Japan along with the observation of surrounding environment and conventional plots, typical vegetation was modeled with 25 common plant species ranging over 20 taxonomical families. The list of the species and representative surface ratio is listed in Table 1.

Insect fauna of primary consumers was predicted based on the actual observation and literature in terms of plant-host relationship (Umeya and Okada, 2003). Only insects that live on direct interaction with listed plants were counted, such as eating of roots, stems, leaves, flowers, fruits and seeds. The predicted primary insect fauna is listed in Table 2. The results are depicted in Fig. 3 with the use of software R (R Core Team, 2015) for the histogram and Gephi (Bastian *et al.*, 2009) for the network representation.

Table 1. Typical vegetation of synecoculture field and conventional monoculture market gardening in Japan. Representative common vegetation of 10 synecoculture fields in Japan was extracted with typical surface ratio (50% of introduced vegetables; 20% of introduced fruit trees; 30% of naturally occurring plants; equally divided among species). Monoculture vegetation is based on 90% single *Brassicaceae* crop and 10% common weeds.

Vegetation Type	Family	Species	Typical Surface Ratio in Synecoculture	Typical Surface Ratio in Monoculture
Introduced Vegetable	Malvaceae	*Malva verticillata* var. *crispa*	0.05	
	Chenopodioideae	*Spinacia oleracea*	0.05	
	Brassicaceae	*Brassica rapa* L. var. *rapa*	0.05	0.9
	Cucurbitaceae	*Cucurbita* L.	0.05	
	Asteraceae	*Lactuca sativa* L.	0.05	
	Araceae	*Colocasia esculenta* (L.) Schott	0.05	
	Lamiaceae	*Ocimum basilicum* L.	0.05	
	Apiaceae	*Daucus carota* subsp. *sativus* (Hoffm.) Arcang.	0.05	
	Solanaceae	*Solanum lycopersicum* L., 1753	0.05	
	Fabaceae	*Phaseolus vulgaris* L.	0.05	
Introduced Fruit Tree	Ebenaceae	*Diospyros kaki* Thunb.	0.04	
	Moraceae	*Ficus carica* L. (1753)	0.04	
	Rosaceae	*Malus pumila* Mill.	0.04	
	Vitaceae	*Vitis labrusca* L.	0.04	
	Rutaceae	*Citrus unshiu* (Swingle) Marcow.	0.04	
Spontaneous Species (Common family with introduced species)	Brassicaceae	*Capsella bursa-pastoris* (L.) Medik.	0.03	0.01
	Asteraceae	*Artemisia indica* Willd. var. *maximowiczii* (Nakai) H. Hara	0.03	0.01
	Solanaceae	*Solanum nigrum* L.	0.03	0.01
	Rosaceae	*Rubus hirsutus* Thunb.	0.03	0.01
	Fabaceae	*Pueraria lobata* (Willd.) Ohwi (1947)	0.03	0.01
Other Spontaneous Species	Poaceae	*Eleusine indica* (L.) Gaertn.	0.03	0.01
	Oxalidaceae	*Oxalis corniculata* L.	0.03	0.01
	Polygonaceae	*Rumex acetosa* L.	0.03	0.01
	Equisetaceae	*Equisetum arvense* L.	0.03	0.01
	Convolvulaceae	*Calystegia japonica* (Thunb.) Choisy	0.03	0.01
Total Number	20	25	1	1

Measurement of Species Diversity and Soil Environmental Variables

We experimented biodiversity response of soil environmental variables associated with synecoculture practice with the use of 250 m^2 plot in Tokyo, Japan. After uniform introduction of silty loam soil according to USDA classification (USDA, 1993), more than 173 edible plant species were randomly introduced and vegetation was self-organized during 4 years (April 2011- March 2015) following the rule of synecoculture (Funabashi *et al.*, 2015). We allocated 36 monitoring circles of 2m diameter regularly over the plot during 3 months (April-June 2015), which were divided into 3 different management strategies A, B, and C. In A: Cut off above-ground part of naturally occurring species; B: Leave the vegetation untouched; and C: Actively introduce seeds of edible herbaceous species. Each of A, B, C group contained 12 monitoring circles. The classification was judged with 4 years of management experience that A: Needs to cut off weeds to protect edible species; C: Achieves high survival rate of newly introduced crops without weed control; B: Situation in between A and C.

We measured plant species diversity before and after the experiment, and basic soil variables at the last of experiment from all monitoring spots as listed in Table 3. Plant species diversity was obtained as the mean value of 3 independent observations. At the last stage of experiment (June 27, 2015), 76 plant species could be recognized above the ground level. Plant species were categorized into introduced and spontaneous species by the way of introduction. Herbaceous and woody species were separately counted from monitoring circles of 1m and 2m diameter, respectively.

All soil variables were measured on 3 samples and mean value for each of 36 spots was recorded. Volumetric water content of soil was measured with 3 different conditions of soil moisture during 3 consecutive days, from field capacity (pF 1.8) on the 1st day followed by 14.5 mm precipitation before the measurement of 2nd day, and further 2mm rainfall before the 3rd day.

Table 2. List of insect fauna in primary food chain. Insects that live on direct feeding relationship of plant species in Table 1 are predicted based on the actual observation record. Only insect species that depend essentially on the modeled vegetation is counted, while broader generalist species that can live on other vegetation and secondary consumers are omitted, based on the literature (Umeya and Okada, 2003). Pollination effect (P.E.) is ranked with 0: no or little pollination effect; 1: intermediate and local pollination effect such as *Coleoptera* and *Hemiptera* species (beetles and shield bugs) with infrequent flying activity; 2: High pollination effect such as *Lepidoptera*, *Diptera* and *Hymenoptera* species (butterflies, flies and bees) with high flying ability.

Order		*Acherontia lachesis*	0	Hemiptera		*Toxoptera citricidus*	0
		Acosmeryx castanea	2	*Eurydema rugosa*	1	*Unaspis yanonensis*	0
Species	P.E.	*Marumba gaschkewitschii echephron*	2	*Eurydema dominulus*	1	*Dialeurodes citri*	0
Lepidoptera		*Coleoptera*		*Graphosoma rubrolineatum*	1	*Orthoptera*	
Papilio xuthus	2	*Anomala rufocuprea*	1	*Halyomorpha halys*	1	*Chorthippus biguttulus*	0
Papilio machaon	2	*Popillia japonica*	1	*Dolycoris baccarum*	1	*Oedaleus infernalis*	0
Pieris rapae	2	*Blitopertha orientalis*	1	*Megacopta punctatissima*	1	*Locusta migratoria*	0
Colias erate	2	*Maladera orientalis*	1	*Acanthocoris sordidus*	1	*Acrida cinerea*	0
Eurema mandarina	2	*Anomala cuprea*	1	*Nezara viridula*	1	*Atractomorpha lata*	0
Pseudozizeeria maha	2	*Anomala albopilosa*	1	*Yemma exilis*	1	*Tetrigidae spp.*	0
Lycaena phlaeas	2	*Melolontha japonica*	1	*Aelia fieberi*	1	*Oxya yezoensis*	0
Lampides boeticus	2	*Gametis jucunda*	2	*Eysarcoris ventralis*	1	*Patanga japonica*	0
Vanessa cardui	2	*Epilachna vigintioctopunctata*	1	*Eysarcoris annamita*	1	*Teleogryllus emma*	0
Mycalesis gotama	0	*Anoplophora malasiaca*	1	*Nysius plebeius*	1	*Truljalia hibinonis*	0
Parnara guttata	2	*Oberea japonica*	1	*Leptocorisa chinensis*	1	*Tettigonia orientalis*	0
Bombyx mandarina	0	*Nupserha marginella*	1	*Riptortus pedestris*	1	*Euconocephalus thunbergi*	0
Spilosoma lubricipeda	2	*Phytoecia rufiventris*	1	*Hygia opaca*	1	*Phaneroptera falcata*	0
Amata fortunei	2	*Xylotrechus chinensis*	1	*Homoeocerus unipunctatus*	1	*Conocephalus chinensis*	0
Plutella xylostella	2	*Buprestidae spp.*	1	*Rhopalus maculatus*	1	*Hymenoptera*	
Tebenna micalis	2	*Paederus fuscipes*	1	*Cletus punctiger*	1	*Allantus luctifer*	0
Scythris sinensis	2	*Gastrophysa atrocyanea*	1	*Piocoris varius*	1	*Athalia* spp.	0
Bedellia somnulentella	2	*Aulacophora femoralis*	1	*Paraparomius lateralis*	1	*Dolerus* spp.	0
Ascotis selenaria cretacea	2	*Aulacophora nigripennis*	1	*Paraeucosmetus pallicornis*	1	Diptera	
Orthonama obstipata	2	*Atrachya menetriesi*	1	*Macroscytus japonensis*	1	*Delia platura*	2
Spoladea recurvalis	2	*Monolepta dichroa*	1	*Apolygus lucorum*	1	*Chromatomyia horticola*	2
Hellulla undalis	2	*Pyrrhalta semifulva*	1	*Creontiades coloripes*	1	*Rivellia nigricans*	2
Pyrausta panopealis	2	*Chrysolina aurichalcea*	1	*Adelphocoris reicheli*	1	*Rivellia apicalis*	2
Rivula sericealis	2	*Gallerucella vitticollis*	1	*Corythucha marmorata*	0	*Nephrotoma virgata*	1
Cucullia fraterna	2	*Fleutiauxia armata*	1	*Stephanitis nashi*	0	*Tipula aino*	1
Helicoverpa armigera armigera	2	*Cassida nebulosa*	1	*Graptopsaltria nigrofuscata*	0	Thysanoptera	
Spodoptera litura	2	*Cryptocephalus approximatus*	1	*Platypleura kaempferi*	0	*Thripidae* spp.	1
Agrotis segetum	2	*Basilepta fulvipes*	1	*Geisha distinctissima*	0	Dermaptera	
Mamestra brassicae	2	*Scelodonta lewisii*	1	*Ledra auditura*	0	*Gonolabis marginalis*	0
Xylena fumosa	2	*Phaedon brassicae*	1	*Aphrophora intermedia*	0	Class other than Insecta	
Oraesia excavata	0	*Psylliodes punctifrons*	1	*Cicadella viridis*	0		
Viminia rumicis	2	*Phyllotreta striolata*	1	*Episyrphus balteatus*	0	Isopoda	
Triaena intermedia	2	*Bruchus rufimanus*	1	*Myzus persicae*	0	*Armadillidium vulgare*	0
Spirama helicina	2	*Ceuthorhynchidius albosuturalis*	1	*Aphis gossypii*	0	Pulmonata	
Nokona regalis	2	*Listroderes costirostris*	1	*Aphis craccivora*	0	*Gastropoda* spp.	0
Sphrageidus similis	0	*Hypera postica*	1	*Uroleucon formosanum*	0	Total Number of Species	150
Theretra oldenlandiae	2	*Scepticus* spp.	1	*Rhopalosiphum padi*	0		
Agrius convolvuli	2	*Anthrenus verbasci*	2	*Aphis spiraecola*	0		

Harvest Record

Synecoculture produce was sold in market by Sakura Shizenjuku Co. in Ise, Japan (Funabashi, 2016b) and Agence de Formation du Développement Rural Autogéré (AFIDRA) in Burkina Faso (Tindano and Funabashi, 2017). Products were sold on-farm and *via* home delivery service in Japan, and local market at Mahadaga situated in the province of la Tapoa in Burkina Faso. High

Table 3. Measurement methods of biodiversity and soil environmental variables

Variable	Species diversity of introduced/spontaneous plant species and insect species	Soil hardness	Soil permeability	Volumetric water content of soil	Soil microbial diversity and activity	Decomposition of organic matters
Method/ Instrument	Visual Observation, photographic record	Soil hardness tester No. 351	DIK-4012 Permeameter, 4 fold type	Test method for water content of soils	Soil microbial diversity * vitality value	Tea bag index, k and S values
Reference	(Funabashi, 2013a)	(Fujiwara, 2015)	(Daiki, 2015)	(JIS, 1999)	(Sakuramoto *et al*., 2010)	(Keuskamp *et al*., 2013)

quality of products allowed us to set the price higher than conventional product, about 1.5 times in Japan and 2 times in Burkina Faso.

Results and Discussion

Power-law Surface Distribution in Synecoculture and Natural Vegetation

The surface distribution of crops in synecoculture field showed long-tail distribution that followed power law with upper limit (Fig.1). This characteristic conforms to the statistical property of natural vegetation both in vegetation-wise and niche-wise segmentation (Fig. 2). Power-law of vegetation surface is known as a self-organized property of plant community growing in ecological optimum with inherent positive interactions (Scanlon *et al.*, 2007), which theoretically forms the basis of community yield in synecoculture (Funabashi, 2016a). Since the power-law distribution implies successful occurrence of symbiotic gain in the development of vegetation, the results indicate that over-yielding based on symbiotic gain could be expected from the very first years of synecoculture installation. This conforms to the harvest record from another farm in Ise, Japan and first-year result of experiment in Burkina Faso (See Yield performance section). The results are also integrated in Fig. 4 as the positive link between species diversity and symbiotic effect (power law of niches).

Estimated Plant-Insect Interactions

Plant-insect interactions based on the typical vegetation (Table 1) and estimated primary consumers (Table 2) are depicted in Fig. 3. Of 150 listed insects, 30 species that account for the top 20% of herbivory interactions occupy 57% of the total in synecoculture, and 85% in monoculture field. This constitutes a long-tail distribution of host plant surface rank of insects in synecoculture

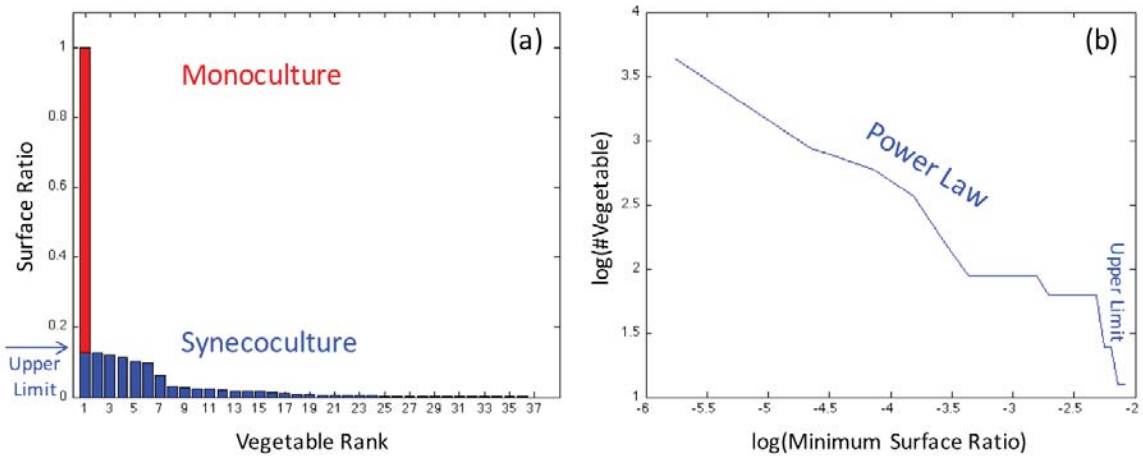

Fig. 1. Surface ratio distribution of synecoculture field in Oiso, Kanagawa, Japan based on 2-step VAS method. (a): Surface distribution of vegetables in synecoculture field (blue bars) and typical monoculture field (red bar). X-axis ranks each vegetable species according to the value of surface ratio in Y-axis. Synecoculture shows long-tail distribution with upper limit, while monoculture is confined to the growth of single crop. (b): Inverse cumulative distribution of vegetable species diversity with respect to minimum surface ratio threshold. X-axis defines the minimum threshold of surface ratio, and Y-axis represents the number of vegetable species that cover the field more than the threshold. The linear relation in double-logarithmic scale indicates a power-law distribution as a self-organized statistical property of the long-tail distribution in synecoculture.

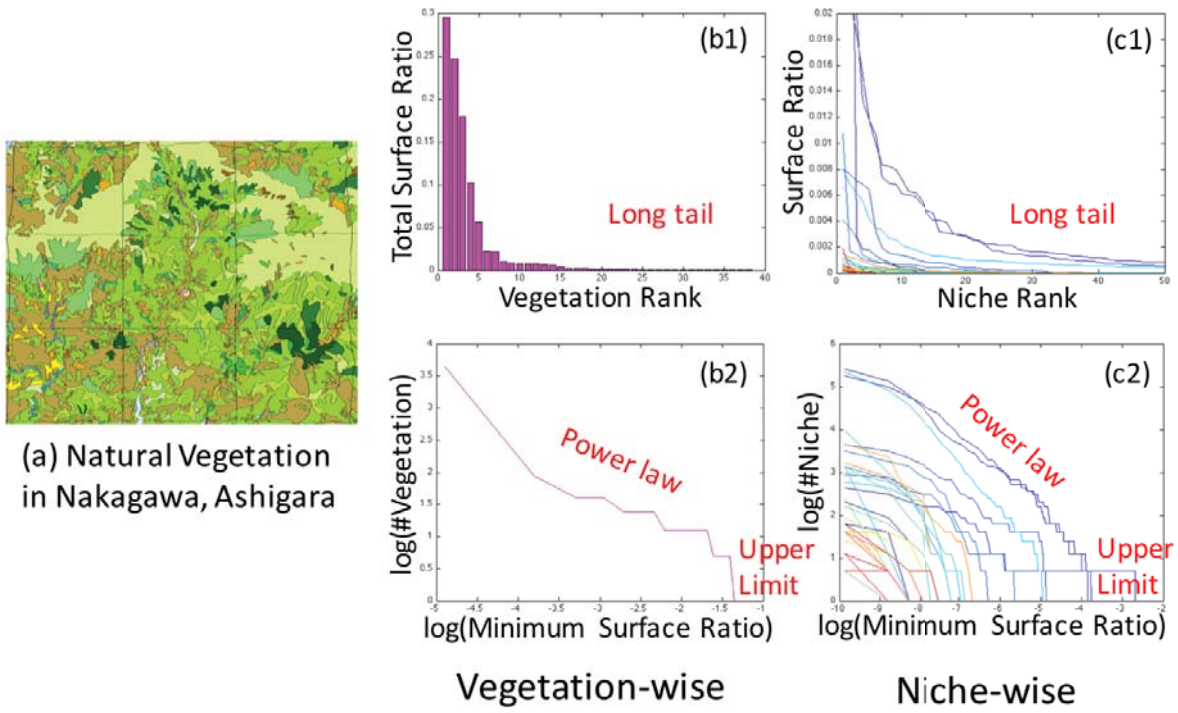

Fig. 2. Example of power-law distribution of natural niche
(a) Image data of Natural Vegetation in Nakagawa, Ashigara in Japan, from (BCJ, 2017). Vegetation types are segmented with different colors. Each segmented patch represents ecological niche of corresponding vegetation.
(b1) Total surface distribution of vegetation types. Surface ratios of segmented niches were aggregated for each vegetation. (c1): Surface distribution of niches in each vegetation. Vegetation types were distinguished with gradient colors.
For (b1) and (c1), X-axis ranks each vegetation and niche, respectively, according to the value of surface ratio in Y-axis.
(b2) Inverse cumulative distribution of vegetation type diversity with respect to minimum surface ratio threshold. (c2): Inverse cumulative distribution of niche diversity with respect to minimum surface ratio threshold. Vegetation type color corresponds to (c1).
For (b2) and (c2), X-axis defines the minimum threshold of surface ratio, and Y-axis represents the number of vegetation type and niches, respectively, that cover the field more than the threshold.
Long-tail distributions are observed in both vegetation-wise (b1) and species niche-wise (c1) surface ratio, which can be interpreted as power-law distributions with upper limit, as depicted respectively in (b2) and (c2).

[(Fig.3 (a1)], while a short-tail and discontinuous uniform distribution in monoculture [Fig.3 (b1)]. Since the host plants surface can be considered as a proxy of insect propagation rate in terms of food resources, this difference of vegetation support can be estimated to substantially affect faunal diversity and consequent ecosystem functions and services in multi-trophic levels (Gossner *et al.*, 2016; Soliveres *et al.*, 2016): Indeed, 28 insect species from the list are lost in monoculture fauna representing 19% of those harbored in synecoculture. At the same time, 96% of herbivory interactions owned by 28% of insect species essentially depend on a monoculture crop, generally considered as a pest.

Since the pest in monoculture system should be eliminated with the application of pesticides, pollination services that are included in the crop herbivory insects [Fig. 3 (b1) black bordered] are compromised in conventional farming methods. Furthermore, other pollination services of weeds owned by 72% of insect species are also subject to the elimination by weed control, which only occupy the marginal 4% of interactions that could be highly vulnerable to perturbation. Such elimination of specialist species specific to farmland is shown to further trigger a regional homogeneization of biodiversity even in case of moderate increase of land-use intensity (Gossner *et al.*, 2016).

On the other hand, synecoculture ecosystems support the community productivity and pollination services at the same time, since it complies with no chemicals practice and controlled coexistence of weeds.

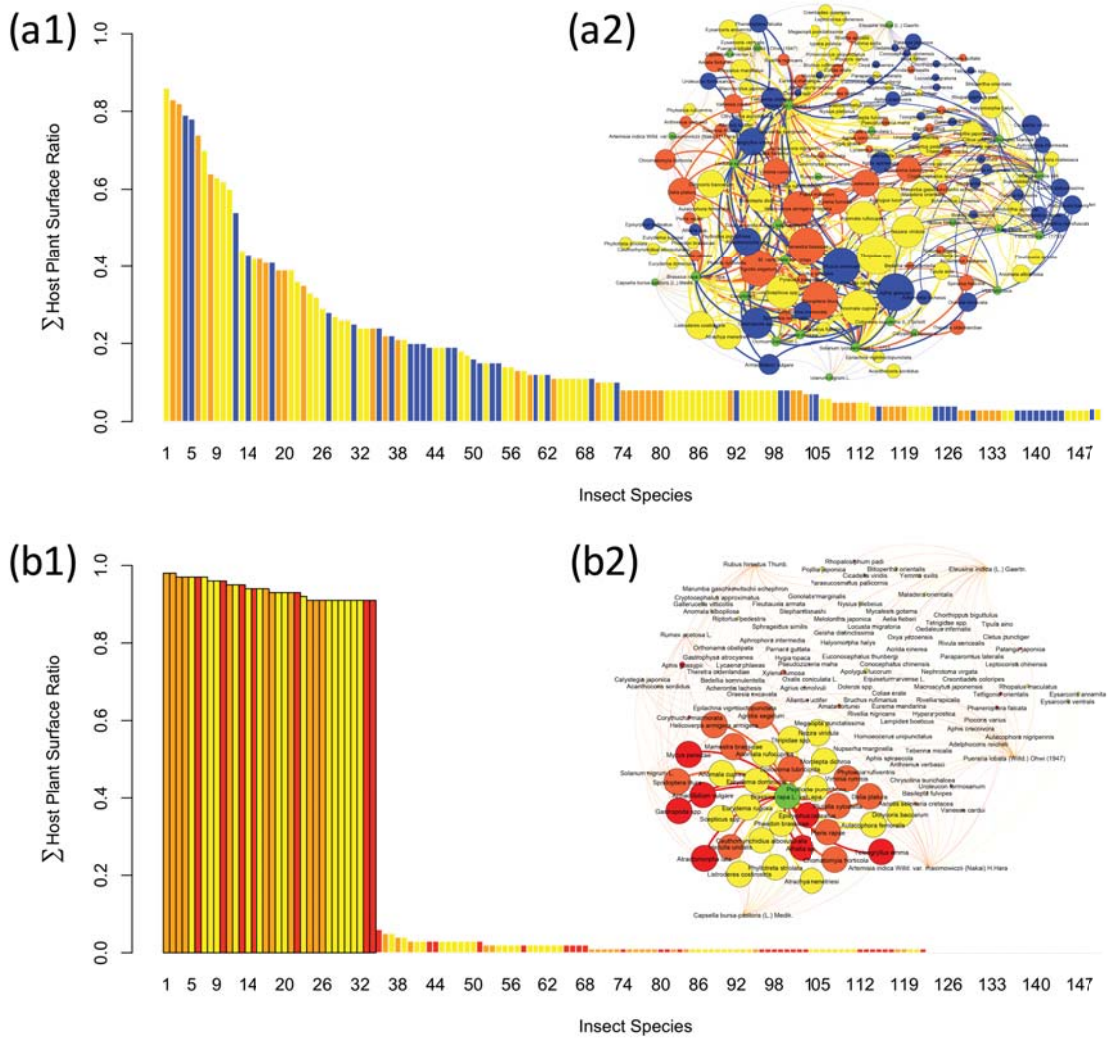

Fig. 3. Estimated plant-insect interactions in typical synecoculture (a1, a2) and monoculture fields (b1, b2).
(a1) Surface rank distribution of insect species with respect to the total surface of host plants in synecoculture.
(a2) Network representation of insect populations, host plants surface and herbivory interactions in synecoculture. The Shannon diversity of links H_2 =2.81 for all interactions, and H_2 =2.67 for pollination network.
(b1) Surface rank distribution of insect species with respect to the total surface of host plants in monoculture. Application targets of pesticide in conventional pest regulation are bordered with black.
(b2) Network representation of insect populations, host plants surface and herbivory interactions in monococulture. The Shannon diversity of links H_2 =1.73 for all interactions, and H_2 =1.62 for pollination network.
Colors represent the degree of pollination effect of insects: Red or blue (conforms to Fig. 1): 0, yellow: 1, orange: 2, and indication of plants: green. The rank of pollination effect is based on Tab. 2. The size of nodes in (a2) and (b2) refers to the surface ratio of the plants (green nodes) and total surface ratio of host plants for the insect species (red or blue, yellow, and orange nodes) that provide a proxy of propagation rate. The network edge width represents the node size of plant species.
The Shannon diversity of links H_2 decreases with higher specialization, which conforms to (Bersier *et al.*, 2002)

Out of 150 specialist species in synecoculture fields, 71% are contributing as pollinators, while 88% of 122 species as potential pollinators in monoculture system are in compromise with chemical treatment and weed suppression. This difference could project serious impact not only on crop productivity but also nutrition profile, especially micronutrients, and may results in the global increase of non-communicable and malnutrition-related diseases (Smith *et al.*, 2015).

In actually observed synecoculture fields, the overall regulation of pest was fairly achieved by the

natural organization of food chain without application of chemicals. Typical realization of "diversity bugs pest" appeared commonly: On the rich diversity of primary consumers, increased diversity of predators such as spiders, wasps, mantises, ants, ladybirds, dragonflies, frogs, lizards and birds were observed (e.g. Funabashi, 2016b, p.12). These empirical evidences are expressed as the positive link between species diversity and disease and pest control in Fig. 4. Furthermore, coexistence with naturally occurring species is shown to enrich biodiversity responses of soil environment (see next section), which contributes to both productivity and pollinator diversity.

In terms of robustness, the vulnerability to perturbation can be intuitively understood with the network representation in Fig. 3 (a2) and (b2). As a general property of ecological network with competing resources, bold connections with thick nodes of multiple host plants augment the robustness and resilience of fauna in the representation of (a2), while scarce and/or thin interactions with reduced number of host plants can be easily disturbed in (b2). Especially, functional resilience of pollination is vital for the resistance of agro-environment to disturbances and can be expressed as the degree of specialization vs. generalization of network connections (Kaiser-Bunbury *et al.*, 2017). With respect to the Shannon diversity of links H_2 (Bersier *et al.*, 2002), the synecoculture network (a2) represents more generalized interactions that imply functional resilience, while monoculture case (b2) corresponds to specialization with nested and fragile structure on a single crop.

These estimations are only based on the primary consumers and do not yet include general pollinators and higher-order predators such as bees, wasps and ants important for regulation services in synecoculture, which appears as a part of the increase in net productivity (see the section Yield performance). Since the estimation is

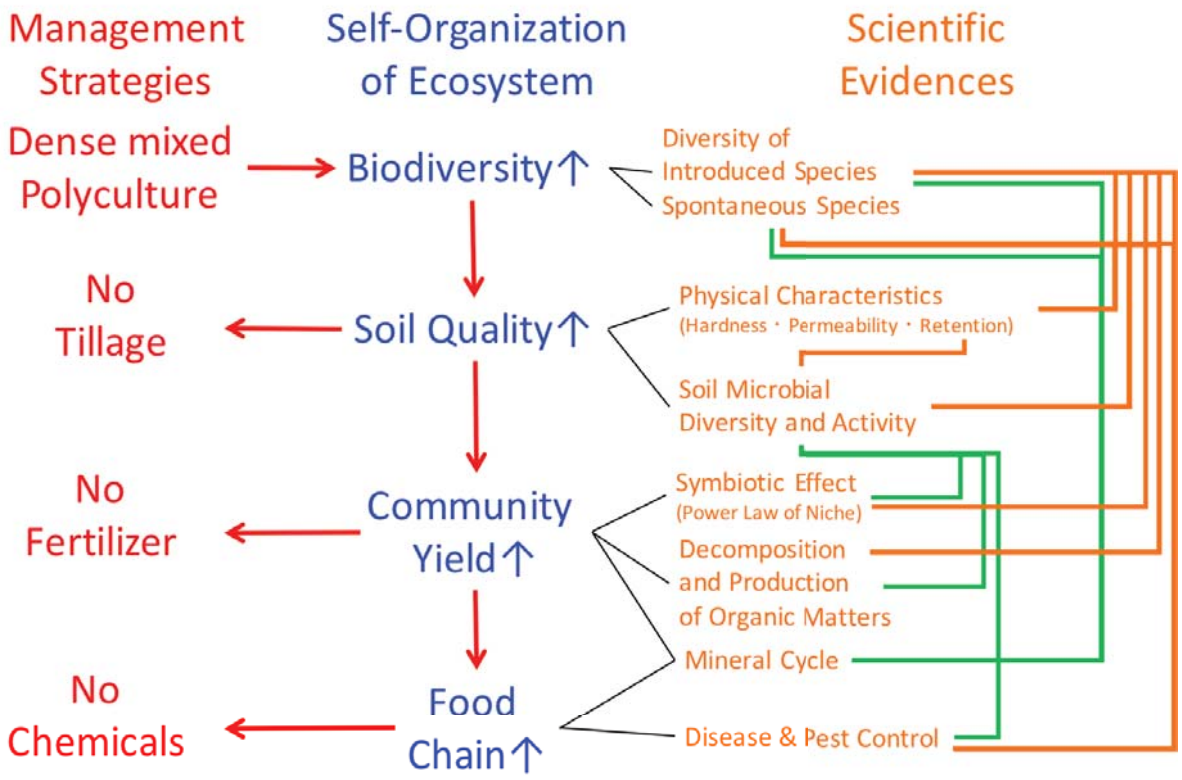

Fig. 4. Relations between management strategies (red words), self-organized properties of ecosystem (blue words), and evidences on the biodiversity responses of species diversity and soil environment (orange words). Red arrows imply consequent causal relationships in a successful development of synecoculture. Orange lines represent statistically significant correlations summarized in Table 4, while green lines show reported evidences and other general relationships associated with the measurement. Evidences in Figs. 1 and 3 are also converged. For simplicity, only direct correspondences are indicated with black lines between the self-organized properties and evidences.

based on the initial succession stage of synecoculture, it will further enrich the composition of arboreal insects that generally forms an important part of above-ground fauna. Shelter provisioning service of complex vegetation that promotes the coexistence of animal species is not considered either. Selection of the plant species is restricted to typical representative species that make up only a small part of the actually introduced diversity of vegetation.

Taking those missing aspects into account, the estimated plant-insect interactions, farming methodologies and field observations clearly indicate that the organization of food chain could be elaborated to rich introduction of natural predators and pollinators in synecoculture, and suppressed to low level in conventional monoculture.

The overall estimations provide important insights on the cause of serious loss of pollination and other regulation services in India as a consequence of conventional monoculture methods (Potts *et al.*, 2016), and how the synecoculture could recover them with the long-tail distributions of vegetation and interactions as a synergistic organization of biodiversity responses.

Biodiversity Responses of Soil Environment

Statistically significant increases and correlation between species diversity and soil environmental variables are summarized in Table 4 and schematized in Fig. 4. In brief, active introduction of edible species with high-density mixed polyculture augmented soil quality, community yield and food chain, which enabled the total replacement of tillage, usage of fertilizer and chemicals with self-organization of ecosystem functions in ecological optimum. Significant relations between evidences are as follows:

Species diversity: Active introduction of edible herbaceous species in group C showed higher establishment of species diversity including the generation of spontaneous species. Removing the above-ground part of spontaneous species (without tillage) did not negatively affect crop diversity in group A.

Soil hardness: Soil hardness after the experiment showed magnitude relation B>A>C between three groups, in which B>A and B>C are significant. Woody species diversity also contributed positively to soil hardness. This implies a trade-off between human intervention (in group A and C) and self-organization (in group B and growth of woody species).

Soil permeability: Magnitude relation A<C<B are observed. Although there exists statistically significant difference between A<B, this relation could not be explained by the difference of species diversity. Therefore, we conjecture that the human interventions affect the soil permeability more than actual species diversity, with operation A working most negatively by removing grass. Active introduction of edible species in group C seemed not to ameliorate soil permeability significantly compared to B.

Water retention ability of soil: All groups significantly increased the water content after 14.5mm of precipitation with the magnitude relation A<B<C, which were released in underground water and significantly decreased on the following day. However, only group C retained significantly higher water content after 48 hours than before the rainfall, which implied increased water retention ability by active introduction of edible species. Interestingly, high soil permeability of group B did not contradict with high water content, which may explain the compatibility of different regulation services in natural vegetation.

Increase of herbaceous and woody species diversity negatively correlated with water content. Nevertheless, since the soil contained in average 45.13% of water that is higher than 40% known as optimal value, this decrease can also be interpreted as the convergence to optimum ratio that maximizes soil function.

Further analysis on the variance of water content with F-test revealed that group A significantly decreased its variance in response to 14.5mm precipitation, indicating rapid loss of buffering capacity. These results conform to empirical facts that the loss of biodiversity negatively affect multiple regulation services of water cycle such as resilience to flood and drought.

Soil microbial diversity and activity: Soil microbial diversity*vitality values were significantly correlated with herbaceous species diversity, and became especially higher with introduced species. Woody species were positively correlated with 7.3% p-value whose edible subgroup reached 5.8% p-value (data not shown). Effects of spontaneous species were not significant and were only collateral.

Standard scores (T score) of the soil microbial diversity*vitality values with respect to 7000 soil samples from other various farming methods, crop types and regions in Japan marked 62.5, 68.9, and 72.4 for group

Table 4. Biodiversity response of soil environment in synecoculture. Results based on the measurement of species diversity and soil environmental variables analyzed with 2-sided t-tests, F-test, and Pearson's product-moment correlation. Only results of p-value lower than 5% significance level are listed. Species diversity "before" refers to the measurement before the division of monitoring sites into 3 groups A, B, and C on 28 Mar 2015, while "after" refers to the measurement after 3 months of experiment on 27 June 2015.

Biodiversity response	Variable 1	Relation	Variable 2	Statistical test	p-value
Species diversity	Group C herbaceous species diversity before	<	Group C herbaceous species diversity after	Paired t-test	0.03852
	Group B herbaceous species diversity after	<	Group C herbaceous species diversity after	t-test	0.0002604
	Group A herbaceous species diversity after	<	Group C herbaceous species diversity after	t-test	0.0002032
	Group B introduced herbaceous species diversity after	<	Group C introduced herbaceous species diversity after	t-test	9.16E-06
	Group A introduced herbaceous species diversity after	<	Group C introduced herbaceous species diversity after	t-test	5.86E-06
Soil hardness	Group A soil hardness after	<	Group B soil hardness after	t-test	0.04301
	Group B soil hardness after	>	Group C soil hardness after	t-test	0.02764
	Woody species diversity after	Positive correlation	Soil hardness	Pearson's product-moment correlation	0.04709
Soil permeability	Group A soil permeability	<	Group B soil permeability	t-test	0.01507
Water retention ability of soil	Group A water content of soil of field capacity (pF 1.8)	<	Group A water content of soil after 14.5mm precipitation in 24 hrs	Paired t-test	0.014
	Group A water content of soil after 14.5mm precipitation in 24 hrs	>	Group A water content of soil after 16.5mm precipitation in 48 hrs	Paired t-test	0.0001058
	Group B water content of soil of field capacity (pF 1.8)	<	Group B water content of soil after 14.5mm precipitation in 24 hrs	Paired t-test	0.001584
	Group B water content of soil after 14.5mm precipitation in 24 hrs	>	Group B water content of soil after 16.5mm precipitation in 48 hrs	Paired t-test	0.03147
	Group C water content of soil of field capacity (pF 1.8)	<	Group C water content of soil after 14.5mm precipitation in 24+D54 hrs	Paired t-test	0.0008536
	Group C water content of soil after 14.5mm precipitation in 24 hrs	>	Group C water content of soil after 16.5mm precipitation in 48 hrs	Paired t-test	0.02111
	Group C water content of soil of field capacity (pF 1.8)	<	Group C water content of soil after 16.5mm precipitation in 48 hrs	Paired t-test	0.0002117
	Group A water content variance of soil of field capacity (pF 1.8)	>	Group A water content variance of soil after 14.5mm precipitation in 24 hrs	F-test	0.02993
	Woody species diversity after	Negative correlation	Mean water content of soil	Pearson's product-moment correlation	0.0008532
	Introduced woody species diversity after	Negative correlation	Mean water content of soil	Pearson's product-moment correlation	6.87E-05
	Herbaceous species diversity after	Negative correlation	Mean water content of soil	Pearson's product-moment correlation	5.22E-05
	Introduced herbaceous species diversity after	Negative correlation	Mean water content of soil	Pearson's product-moment correlation	0.01601
	Spontaneous herbaceous species diversity after	Negative correlation	Mean water content of soil	Pearson's product-moment correlation	1.41E-06
Soil microbial diversity and activity	Herbaceous species diversity after	Positive correlation	Soil microbial diversity * vitality value	Pearson's product-moment correlation	0.0007458
	Introduced herbaceous species diversity after	Positive correlation	Soil microbial diversity * vitality value	Pearson's product-moment correlation	0.0006723
Decomposition and production of organic matters	Spontaneous woody species diversity after	Negative correlation	Tea bag index S value	Pearson's product-moment correlation	0.004487
	Group C tea bag index k value	Negative correlation	Group C tea bag index S value	Pearson's product-moment correlation	0.005975
	Group A soil permeability	Negative correlation	Group A tea bag index S value	Pearson's product-moment correlation	0.0021

Table 5. Harvest records of synecoculture farm in Japan and in Burkina Faso. Annual harvest is calculated in each currency based on the annual mean of the whole experiment period. Price rate refers to the pricing of synecoculture produce compared to conventional products in the market. Product species diversity describes the number of species actually sold as synecoculture products. Conventional harvest is based on (JA, 2015; Tindano and Funabashi, 2017)

Location	Surface	Period	Synecoculture Harvest	Conventional harvest	Price rate	Product species diversity
Ise, Mie prefecture, Japan	1000 m^2	June 2010 - May 2014	519,834 JPY/yr	250,000 JPY/yr	1.5	133 spp.
Mahadaga, province of la Tapoa, Burkina Faso	500 m^2	June 2015 - November 2016	7,572,000 CFA/yr	720,500 CFA/yr	2	37 spp.

A, B and C, respectively. These T scores correspond to empirical evaluation that group A: rich soil, good taste of produce, suppress diseases; group B: Very rich soil, very good taste of produce, little occurrence of diseases; and group C: Extremely rich soil, low occurrence of pest and possible to cultivate with less amount of fertilizer and less effort of weed control (DGC, 2015). The overall results could be positively linked with the effect of symbiotic gain promoted by active introduction of edible plants through the organization of ecological optimum.

Decomposition and production of organic matters: Spontaneous woody species diversity and group A soil permeability were negatively correlated with S value of tea bag index. Additionally, k and S values were negatively correlated only in group C. According to the definition, k represents short-term decomposition dynamics of labile compounds, and S is indicative for long-term carbon storage by environmental conversion to recalcitrant fraction (Keuskamp *et al*., 2013). Therefore, these results can be integrated into the hypothesis that the increased species diversity drives the material cycle of organic matters into decomposable fraction by eliminating recalcitrant stock. This dynamic conforms to the increased flow in the decomposition and production cycle of organic matters generally expected from high soil microbial diversity and activity through disease suppression (Yokoyama and Taguchi, 2013).

It is also reported that increased biodiversity is associated with the promotion of mineral cycle in synecoculture, showing high concentration in produce despite insufficiency in soil (Funabashi, 2013b). Spontaneous insect diversity is estimated to be the primary source of mineral concentration in the no-fertilizer culture environment.

Yield Performance

The summary of harvest record of 4-year (June 2010 – May 2014) and 1.5-year (June 2015-November 2016) experiments, respectively in Japan and Burkina Faso, is listed in Table 5. Compared to conventional market gardening in the same region, synecoculture result in Japan achieved about 2-fold productivity and 5-fold profitability after cost deduction (JA, 2015). In Burkina Faso, small-scale comparison on 500 m^2 in the same location attained more than 10-fold productivity and cost effectiveness with synecoculture. Furthermore, unit surface comparison with nation-wide statistics of conventional systems reached the estimation of 40 to 150-fold productivity. The outstanding performance in semi-arid tropic was also associated with a drastic recovery of local biodiversity, that reversed the local regime shift from uncultivable desert to mature vegetation composition of primary succession (Tindano and Funabashi, 2017).

Food and Nutrition Diversity of the Products

Product diversity reached 133 species from 4-year record in Japan and 37 species during 1.5 year in Burkina Faso. With nothing but 1000 and 500 m^2, respectively, these are comparable with the product diversity of regional scale and expected to largely contribute to promote food diversity with local production. Especially introduction to family garden in rural area could benefit effectively both in nutrition and generating income through utilization of neglected and underutilized species (Padulosi *et al*., 2012). Nutrition diversity of synecoculture products showed various expression of health-protective components, such as increased concentration of minerals and expression of secondary metabolites which potentially provide preventive effects on non-communicable diseases (Funabashi, 2013b; Funabashi, 2016a).

Implication for Agriculture in India

Synecoculture results out-performed conventional monoculture systems of market gardening both in the temperate region of Japan and semi-arid tropic in Burkina Faso. These results indicate promising possibilities for

the introduction of synecoculture to small-holding farms and family gardens in India.

In terms of latitude and climate, India is situated at the combination of Japan and Burkina Faso: The southern halves of Karnataka and Andhra Pradesh states mainly overlap to the latitude range of Burkina Faso (Bangalore is in close latitude with Ouagadougou), and the Himachal Pradesh state in Northern India corresponds to the Kyushyu island in the South of Japan.

With respect to the Köppen-Geiger climate classification based on vegetation types (Peel *et al*., 2007), the Southern and Western halves of India commonly share the Savanna climate (Aw), hot semi-arid climate (BSh), and hot desert climate (BWh) with Burkina Faso. On the other hand, the North-Eastern part of India belongs to the Monsoon-influenced humid subtropical climate (Cwa) and subtropical highland climate with dry winters (Cwb) where results in Japan with the humid subtropical climate (Cfa) could be applied with additional consideration for water management (the abbreviations represent the Köppen-Geiger climate classification scheme symbols).

Precipitation records show that the Western half of India corresponds to below 1000 mm/year (except the rain-abundant biodiversity hotspot in the South-Western coastal area), which can employ farming strategies developed under the 800-1000 mm annual rainfall in la Tapoa province in Burkina Faso (Survey of India, 2006; PICOFA, 2006).

These geographical and eco-climatic conditions located in India together with social-ecological states of poverty, malnutrition and environmental degradation as an important target in need for a larger-scale application of synecoculture in smallholding population. Indeed, the synecoculture performance achieved in the environmental reconstruction, food security and income generation especially in semi-arid tropic and weak infrastructure conditions, could possibly help in achieving Aichi Biodiversity Targets by 2020 and the Sustainable Development Goals 2015-2030 of the United Nations (Tindano and Funabashi, 2017). Successful replication requires the adaptation and improved access and benefit sharing to commercial and local plant genetic resources (PGR).

In terms of the diversity of plant genetic resources for food and agriculture (PGRFA), synecoculture farms can be considered as a novel example of "*in situ*/on-farm conservation through utilization." The collaboration with on-going international gene bank initiatives and coordination of farmers' seed system including exchange opportunities of local varieties and neglected/underutilized species could provide essential support for the propagation of synecoculture. These are expected to largely promote the global action plans for the conservation, sustainable use, institutional and human capacity building of PGRFA and climate resilience through the implementation to smallholders (Diulgheroff and Leskien, 2016; Sthapit *et al*., 2010).

In strengthening the crop portfolio, application of the plant science to produce non-GMO (non-genetically modified organism) varieties of crops could be important in accordance with synecoculture principles. Important features for dryland agriculture such as drought resistance and low nitrogen tolerance, as well as adaptations to marginal land and climate change such as by hybridization with wild perennials and extension of photoperiodic responses, could be better enhanced with traditional breeding and phenotypic selection than transgenic technologies (Funabashi, 2016a). The principle of non-GMO is also important in terms of the genetic pollution risk to PGR that support the water cycle. The creation of GMO only introduces at most 10 kinds of gene, and it contains the risk that could bring invasive outcome to the diversity of PGR in metapopulation, not only through introgressive hybridization but also interspecies gene transfer that is prevalent in the natural evolution of plant genome. On the other hand, genetic resources that support the provisioning and regulation services of water cycles are composed of all living organisms participating to the soil formation where surface flows are buffered and groundwater nurtured. These include plant, animal, and microbial species, which amounts to astronomical figures. Incorporation of water cycles in the management of farmland becomes cumulatively important at the vast watershed of large rivers for the downstream water quantity and quality, including impacts on marine ecosystems. Enhancing PGR of the regional environment through the diversification of PGRFA could be a more comprehensive solution than GMO-based systems in dryland agriculture where the majority of Indian smallholders subsist. This perspective also encompasses the diversity of medicinal plants used in traditional medicine such as Ayurveda, which is increasing its importance as a source of scientific discovery and the foundation of healthcare (*e.g.* IFDC, 2015).

For efficient promotion of PGRFA diversity among smallholders, ICT supports with open-source initiatives are featured to be an essential infrastructure. Modern open-source intermediaries are expected to increase the capacity to handle the future and spot exchange of diverse commodities, and become important hubs for rural businesses that might contribute to market efficiency and price stability (Gulati and Minten, 2008). This could further facilitate the prediction and reduction of subsidy bill of the Government, and connect the significant gap between data and policy to enhance the nutrition sensitivity of agriculture in India (Gillespie *et al.*, 2012).

More fundamentally, the spatial-temporal patterns of biodiversity in ecological optimum follow power-law distribution (see section Power-law surface distribution in synecoculture and natural vegetation), which requires the control by information rather than material inputs. The Access and Benefit-Sharing Clearing-House mechanisms regarding the PGRFA for the implementation of Nagoya Protocol substantially requires a nation-wide ICT network for an effective real-time management.

Conclusion

We reported experimental results of synecoculture in Japan and Burkina Faso in view of application to Indian contexts. In terms of productivity, promotion of biodiversity and sustainable use of PGRFA, social and ecological problematics, India is situated at one the largest target nations that synecoculture could potentially contribute to leverage small-holding agriculture. The application of synecoculture could be expected to bring higher positive impact in marginal dryland under weak infrastructure and low income conditions, as proved in Burkina Faso.

If successful convergence to ecologically optimum production was realized in small-holders that constitutes more than half of the national and about 80% of farming population, the nation could entirely break away from historically exacerbated biodiversity losses, recover multiple regulation services that strengthen adaptations to climate change, and substantially improve food security and malnutrition. Given its scale of the surface and biodiversity, such transformation could lead India to be a major actor to prevent the global regime shift anticipated before the middle of the century, as the realization of a true megadiverse country through anthropogenic augmentation of ecosystems (Funabashi, 2016a).

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

EO Manyasa[1,2], P Tongoona[2], P Shanahan[2], S Githiri[2], H Ojulong[1] and A Rathore[3]
[1]*International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), PO Box 39063, Nairobi 00623, Kenya.*
[2]*School of Agricultural, Earth and Environmental Sciences, University of KwaZulu-Natal, Private Bag X01, Scottsville, Pietermaritzburg 3209, South Africa.*
[3]*ICRISAT, Patancheru-502 324, Telangana, India.*

Eighty one finger millet germplasm accessions from East Africa were evaluated in eight environments in Kenya, Tanzania and Uganda for adaptation and grain yield stability, genotype and genotype x environment (GGE) models. 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. Seven genotypes were identified for yield stability across the eight environments, whereas nine genotypes had specific adaptation. Fourteen genotypes attained the highest grain yield 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 traits. The East African finger millet germplasm has high potential as a source of climate smart, high yielding genotypes for direct production and/or breeding.

Key Words: Finger Millet, Genetic Diversity, GGE, Yield Stability

Introduction

Finger millet in East Africa is mainly grown in the sub-humid to humid zones of Lakes Victoria and Tanganyika, where blast disease (caused by the fungus *Magnaporthe grisea*) thrives, the cool highlands with low temperatures and to a lesser extent in the low rainfall lowlands that suffer from moisture stress/drought. Finger millet has been reported to be sensitive to temperature extremes. Very high temperatures (38°/28°C compared to 32°/22°C), decrease panicle emergence, number of seeds per panicle, grain yield and harvest index (Opole, 2012) whereas low temperatures have been reported to affect pollination and fertilization processes (Bandyopadhyay, 2009). The improved cultivars available in the region have been derived mainly from germplasm selections (Oduori, 2008). The extent of significant genotype by environment (G×E) interactions determine the consistency of performance of genotypes across locations and seasons. Partitioning of G×E interaction into Genotype × Locations and Genotype × Years within Locations enables the identification of genotypes with specific adaptation to an environment or with wide adaptability (Yan and Tinker, 2006; Das *et al*., 2011). In East Africa, no G×E studies have been reported in finger millet and most cultivar selections have been based on individual location testing. This limits the appreciation of the performance potential of many cultivars in other agro-ecologies not used as test sites. Significant G×E interactions for grain yield and yield components in finger millet have been reported in India by, among others, Misra *et al.* (2010) and Joshi *et al*. (2005) and in Ethiopia by Bezaweletaw *et al*. (2006). This study was conducted to evaluate the G×E interaction and yield stability of 81 finger millet accessions selected from an East African germplasm pool.

Materials and Methods

Experimental Material

A total of 81 genotypes (which included five checks-U 15, KNE 814, KNE 479, Nakuru FM 1 and Kahulunge) with high productivity potential were used in this study (Table 1). These comprised selection from 420 accessions (340 landraces and 80 minicore set) previously phenotyped across four locations in Kenya.

Test Environments and Experimental Design

Trials were tested in eight environments (Table 2). They were planted in a 9 × 9 square lattice design with two replications per environment; each experimental plot comprising three 4 m length rows with inter-row and intra-row spacing of 0.4 m and 0.1 m, respectively. Seeds were manually drilled in furrows and thinned two weeks after emergence to 41 plants per row. Fertilizer application, weeding and pest control were done according to recommended practices. Data collected for

**Author for Correspondence: E-mail: e.manyasa@cgiar.org*

**Author for Correspondence: E-mail:hort_pradheep@yahoo.co.in*

Table 1. The finger millet genotypes (81) used for G × E evaluation

Genotype	Name	Origin	Genotype	Name	Origin	Genotype	Name	Origin
G1	Emiroit/Engeny	Uganda	G28	Gulu E	Uganda	G55	GBK-040468A	Kenya
G2	Ekama-white	Uganda	G29	GBK-011110A	Kenya	G56	GBK-043163A	Kenya
G3	Kal	Uganda	G30	GBK-011141A	Kenya	G57	Acc # 79	Minicore
G4	Kal	Uganda	G31	GBK-027145A	Kenya	G58	Acc # 3924	Minicore
G5	Kal Atari	Uganda	G32	GBK-027201A	Kenya	G59	P 224	Uganda
G6	Kal Atari	Uganda	G33	IE 4497	Minicore	G60	Unknown	Uganda
G7	Kal atari	Uganda	G34	Ekama	Tanzania	G61	Etiyo -brown	Uganda
G8	Ekamo	Uganda	G35	IE 5306	Minicore	G62	Ekama	Uganda
G9	Unknown	Uganda	G36	IE 6154	Minicore	G63	Kal	Uganda
G10	RW 127 (IE 6613)	Uganda	G37	KNE 1034	Kenya	G64	Otara chigal	Uganda
G11	GBK-008301 A	Kenya	G38	Acc # 3989	Minicore	G65	GBK-000352A	Kenya
G12	GBK-011116A	Kenya	G39	Eteke	Uganda	G66	GBK-011113A	Kenya
G13	GBK-011136A	Kenya	G40	Adalaka	Uganda	G67	GBK-011119A	Kenya
G14	GBK-029681A	Kenya	G41	Kal	Uganda	G68	GBK-027200A	Kenya
G15	Acc # 2954	Minicore	G42	GBK-000347A	Kenya	G69	GBK-029646A	Kenya
G16	Acc # 3656	Minicore	G43	GBK-000351A	Kenya	G70	GBK-029672A	Kenya
G17	Acc # 3779	Minicore	G44	GBK-000368A	Kenya	G71	GBK-029768A	Kenya
G18	Kafumbata	Tanzania	G45	GBK-000373A	Kenya	G72	GBK-043166A	Kenya
G19	Kaulunge	Tanzania	G46	GBK-000410A	Kenya	G73	IE 2430	Minicore
G20	3953	Tanzania	G47	GBK-011111A	Kenya	G74	IE 4121	Minicore
G21	Purple	Uganda	G48	GBK-011129A	Kenya	G75	Ngome	Uganda
G22	Engenyi	Uganda	G49	GBK-011133A	Kenya	G76	Katila	Uganda
G23	Unknown	.Uganda	G50	GBK-011137A	Kenya	G77	KNE 479	Kenya
G24	Acomomcomo	Uganda	G51	GBK-027149A	Kenya	G78	KNE 814	Kenya
G25	Lowa	Uganda	G52	GBK-027155A	Kenya	G79	Nakuru FM 1	Kenya
G26	Omunga	Uganda	G53	GBK-028590A	Kenya	G80	U 15	Uganda
G27	Kal	Uganda	G54	GBK-040463A	Kenya	G81	Kahulunge	Tanzania

Table 2. Characteristics of the eight test environments used in the evaluation of 81 finger millet accessions in 2011 and 2012

Location	Environment codes	Altitude (m)	Latitude	Longitude	Temperatures (°C)			Mean annual rainfall (mm)
					Min	Max	Mean	
Alupe (Kenya)	Alu11SR, Alu12LR	1189	0°28'N	34°7'E	17.7	30.3	24.0	1100
Lanet (Kenya)	Lan12LR	1920	0°30'S	36°0'E	10.0	20.0	15.0	850
Kiboko (Kenya)	Kib11SR, Kib12LR	9	2°20'S	37°45'E	16.6	29.4	23.0	604
Serere (Uganda)	Ser12LR	1000	1°31'N	33°27'E	18.0	30	24.0	1378
Miwaleni Tanzania)	Miw12LR	500	3°25'S	37°27'E	16.5	27.0	21.7	650
Uyole (Tanzania)	Uyol12	1800	8°55'S	33°34'E	7.9	19.3	13.5	870

Al11SR - Alupe 2011 short rains, Alu12LR - Alupe 2012 long rains, Kib11SR - Kiboko2011 short rains, Kib12LR - Kiboko 2012 long rains, Lan12LR-Lanet 2012 long rains, Miw12LR - Miwaleni 2012 long rains, Uyol12 - Uyole 2012, Ser12LR - Serere 2012 long rains

days to 50% flowering (when half of the plants in the plot had started flowering) plant height (from the base of the stem to the tip of the panicle at hard dough stage in cm), grain yield t ha^{-1}). The trials were conducted under rain grown conditions at all environments except at Kiboko and Miwaleni where supplementary irrigation was applied during very dry periods up to flowering.

Data Analysis

GGE Biplot Analysis

For GGE biplot analysis, Yan (2002) model based on the singular value decomposition (SVD) of the first two principal components was used in Genstat 15.0 (http://www.genstat.co.uk). The GGE biplots were interpreted

according to Yan *et al*. (2001) and Yan (2002) and used to discriminate the environments.

Results

Discriminatory Ability and Representativeness of Test Environments

The GGE biplot explained 46.1% of the total G×E interaction for grain yield (Fig. 1). High correlations were detected between Miw12LR, Kib11SR, Kib12LR, Alu11SR and Alu12LR and between Lan12LR and Uyol12. The environments were placed in three groups based on inter-environment distances (Fig. 1). Group one comprised the Alu11SR, Alu12LR, Kib11SR, Kib12LR and Miw12LR, group two comprised the two cool highlands environments Lan12LR and Uyol12, and Ser12LR stood alone. Although Ser12LR grouped alone, it was significantly ($P \leq 0.01$) positively correlated to Alu12LR. The most discriminative environment for grain yield was Lan12LR. The best performing genotypes for grain yield per mega-environment (and furthest from the biplot origin) were genotypes 74, 32, 71 and 28 for Ser12LR (74 best adapted), genotypes 1, 21, 20, 23 for Alu11SR, Alu12LR, Kib11SR, Kib12LR and Miw12LR (1 best adapted), and genotypes 37, 35, 71 and 75 for Lan12LR and Uyol12 (37 best adapted) (Fig. 1).

Genotype Ranking Based on Mean Grain Yield and Stability

Genotypes 74, 32, 71 and 28 had the highest mean yield regardless of stability and 5, 12, 25, 27, 30, 33, 48, 56 and 76, were most stable regardless of yield. Genotypes 3, 5, 17, 25, 28, 36, 42, 45, 56 and 71 were highly stable with grain yield above the grand mean across environments (Fig. 2 and Table 3). Genotypes 15 and 70 were unstable with the lowest grain yield whereas genotypes 27, 30, 33, 48, 54, 65 and 78 were stable but with low yield.

Discussion

Discriminatory Power and Representativeness of Test Environments

The most discriminating environment will give the most information about the genotypes and it is characterized by long vectors from the biplot origin (Yan and Tinker, 2006). For grain yield, Lan12LR followed by Miw12LR and Ser12LR were the most informative

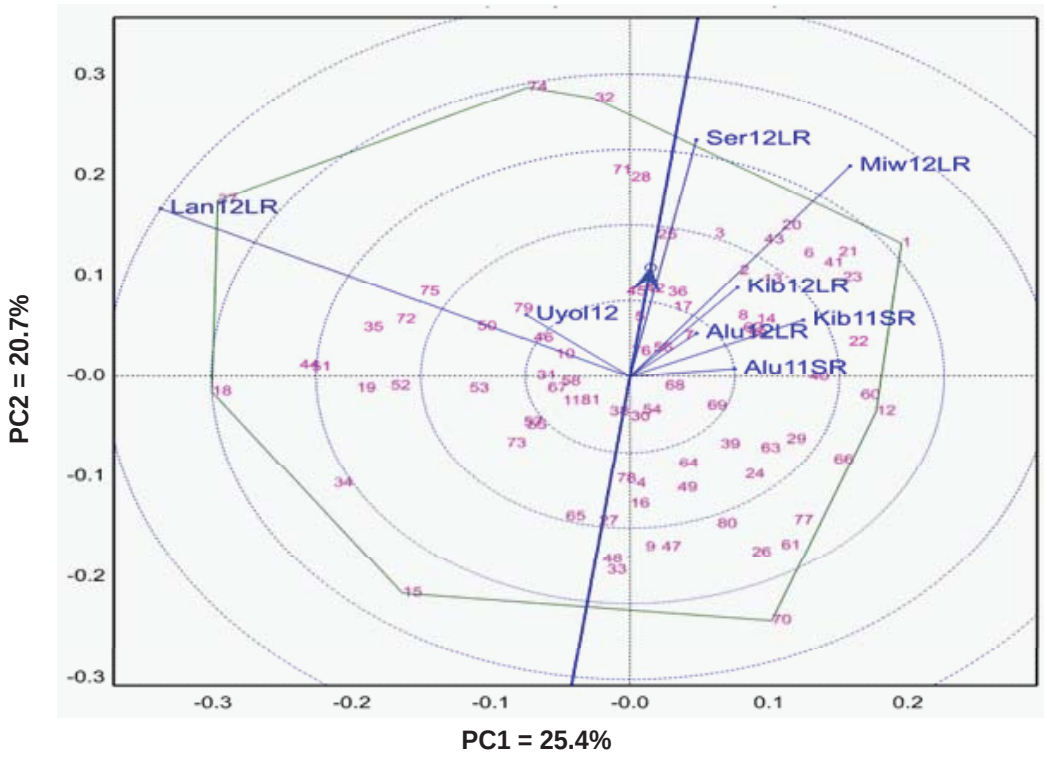

Fig. 1. Discriminatory ability and representativeness of the eight test environments for grain yield (t ha^{-1})

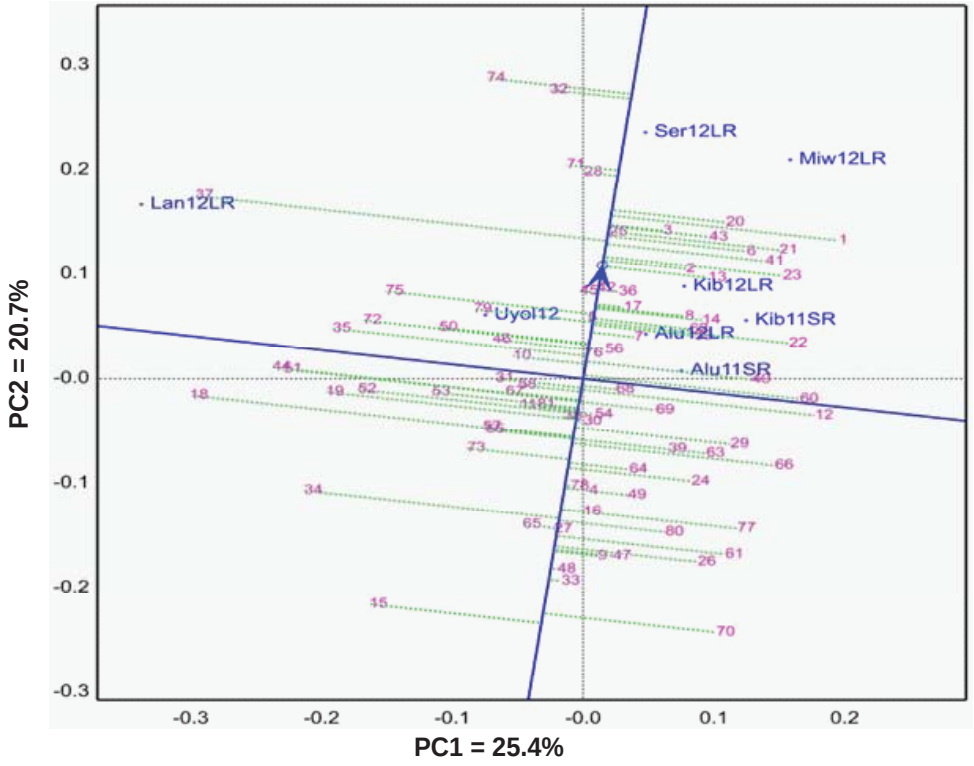

Fig. 2. Genotype ranking based on mean grain yield and stability across the environments

Table 3. Grain yield, plant height, days to flowering of stable genotypes

Genotype	Grain yield (t ha^{-1})[a]	Plant height (cm)[a]	Days to flowering[a]
G3	3.13	71.5	81
G5	2.75	75.0	76
G17	2.79	83.0	82
G25	2.52	78.0	82
G28	2.90	81.7	87
G30	2.45	74.4	75
G36	2.51	78.5	81
G56	2.34	79.5	83
G71	2.66	81.0	97
Grand mean (N = 81)	2.14	86.7	78

[a]Across eight environments, Al11SR - Alupe 2011 short rains, Alu12LR - Alupe 2012 long rains, Kib11SR - Kiboko2011 short rains, Kib12LR - Kiboko 2012 long rains, Lan12LR - Lanet 2012 long rains, Miw12LR - Miwaleni 2012 long rains, Uyol12 - Uyole 2012, Ser12LR - Serere 2012 long rains

environments whereas Alu12LR and Alu11SR were the least informative. Based on polygon biplot, there were three mega-environment groups with the cool high elevation environments Lan12LR and Uyol12 in one mega-environment; Alu11SR, Alu12LR (sub-humid, mid-altitude), Kib11SR, Kib12LR and Miw12LR (dry lowlands) in another group; and Ser12LR (sub humid mid-altitude) on its own. Although, Ser12LR formed its own mega-environment, its significant positive correlation with Alu12LR was more realistic as these two environments fall within the same sub-humid zone with similar mean temperatures and rainfall. Ser12LR was the most representative test environment in terms of average interaction effects with the genotypes in terms of PC1 and PC2 and relative to environments and genotypes evaluated whereas Lan12LR and Alu12SR were the least representative for grain yield. Ser12LR was also highly discriminating for grain yield and hence useful for carrying out selection for both general and specific adaptation to sub-humid environments. Hopkins

(1938) alluded to the fact that phenological development of plants can differ by four days for every degree of latitude. Therefore, Lan12LR would be ideal for low temperature genotype discrimination, it should be utilized separately from Uyol12 when selecting for specific and general adaptation considering the differences in latitude (5°) between the two environments.

Genotype Ranking Based on Mean Yield and Stability Indices

The vertex (winning) genotypes in each environment based on polygon rays of GGE biplots were: 1 in the mega-environment grouping of Alu11SR Alu12LR, Kib11SR, Kib12LR and Miw12LR environments, genotype 74 in Ser12LR and genotype 37 in Lan12LR and Uyol12. The highest yielding genotypes in each of the three mega-environment were 74, 32, 71 and 28 in Ser12LR; 1, 21, 20, and 23 in Alu11SR, Alu12LR, Kib11SR, Kib12LR and Miw12LR; and 37, 35, 71 and 75 in Lan12LR and Uyol12. Selection of suitable genotypes is based on both yield *per se* and stability. Yan and Kang (2003) described an ideal genotype as one having the highest mean and stability represented by the longest vector from origin and short AEC ordinate and zero GEI in a GGE biplot. High stability and above average mean grain yields were recorded in genotypes 3, 5, 17, 25, 28, 36, and 71. These genotypes were early to medium in flowering, had average height and moderate resistance to blast. However genotypes 25, 30, and 71 may be best utilized in environments with low incidence of blast as they were susceptible to all three blast types.

Conclusions

The high elevation low temperature finger millet production environments were distinctly separated from the warmer mid-altitudes and lowlands environments. Lan12LR was identified as an ideal environment to discriminate low temperature adapted genotypes, Ser12LR for sub-humid environments and Miw12LR for the dry lowlands for grain yield. Adaptation testing for the low temperature environments Lan12LR and Uyol12 may be handled separately considering large differences in latitude between them. Genotypes 3, 5, 17, 25, 28, 36 and 71 were identified to be stable across the eight environments based on grain yield. Genotypes 1, 18, 19, 37, 54, 61, 74, 75 and 77 were identified for specific adaptation.

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Characterization of Some Aromatic Farmers' Varieties of Rice (*Oryza sativa* L.) from West Bengal and Adjoining States

Sudhansu Mahato[1], Dinesh Tulsiram Surje[1], Swarnajit DebBarma[1] and Bidhan Roy[2*]
[1]Department of Genetics and Plant Breeding, [2]Department of Seed Science and Technology, Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar-736165, India*

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The genetic variability was assayed in 35 aromatic Farmers' Varieties (FVs). High magnitude of variability was observed for all the characters under study. High heritability was observed for days to 50% flowering, plant height, number of panicles per plant, panicle length, number of grains per panicle, 100-grain weight, grain length, grain breath and grain yield. The collective contribution of the yield contributing characters resulted in high yield for Rampha, Laldhyapa-1, A-1-1, Kauka, Kalakali and Joha Bora. Khasa, Radhunipagul, Mohanbhog, Gobindobhog, Kalojeera, Badshahbhog, Tulsibhog, Tulaipanji, Bora, Joha Bora, Silathia Bora, Jailung Lal Komal, Ghee Bora, Birai, Kabra, Rampha, Kolajoha-Big, Kolajoha-Small and Konkoni Joha were classified as the FVs having strong aroma. Grain yield showed highly significant positive association with number of panicles per plant, 100-grain weight and grain thickness. Positive direct effect on grain yield/plant was observed in number of panicles/plant, 100-grain weight, and grain length and breadth.

Key Words: Aroma, Farmers' variety, Heritability, Path analysis, Variability

Introduction

Rice (*Oryza sativa* L.) is one of the most important food crop in the world, grown in over 164 million hectares of land with overall worldwide production of 731.2 million tonnes per annum (FAO, 2013). Countries in Southeast Asia are heavily reliant upon rice. Among the rice growing countries, India has the largest area accounting for about 31% of the global area. India accounts for nearly one-fourth (22%) of the rice produced in the world with the first place occupied by China. Rice varieties have different productivities, grain qualities, grain appearance and aroma. Many aromatic rice varieties are produced in India, Thailand, Pakistan, Bangladesh, Nepal, Iran, Afghanistan, Myanmar and Indonesia. Aromatic rice cultivars that are popular in Thailand are Thai Hom Mali rice, Jasmine rice, and Thai Fragrant rice. In India the famous aromatic rice is Basmati, which has medium texture with a slender shape and long grain and less chalkiness (Kamath *et al*., 2008). Besides the much sought after Basmati types, which get premium price in international markets, the hundreds of indigenous short grain aromatic cultivars and landraces are grown in pockets of different states of India. Almost every state has its own collection of aromatic rices, which perform well in native areas (Shobha Rani and Krishnaiah, 2001). These aromatic rice varieties possess exemplary quality traits like aroma, fluffiness and taste. However, the genetic improvement in these rice varieties is very much neglected as they lack export value *per se*.

The aroma of rice plays a role in its consumer acceptability. Aroma of rice is caused by chemical compounds that can easily evaporate. More than 100 compounds that contribute to the aroma of rice have been identified. Some of these volatile compounds contribute to consumer acceptance of certain types of rice, whereas other compounds contribute to consumer rejection. The popcorn-like smell of aromatic rice stemming primarily from its 2-acetyl-1-pyrroline (2-AP) content is preferred by many consumers. The 2-AP was detected in one of the famous aromatic rice 'Khaw Dawk Mali-105' (Laksanalamai and Ilangantileke, 1993; Bourgis *et al.*, 2008). Weber *et al.* (2000) stated that 2-AP content in aromatic rice is 15 times greater than that of non-aromatic rice. Gene controlling the level of 2-AP expression is *OsBADH*2 (Niu *et al.*, 2008). More recently, an eight base pair-deletion and three SNPs in exon 7 of the gene encoding betaine aldehyde dehydrogenase 2 (*BADH*2) on chromosome 8 of rice were identified as the probable cause of aroma in aromatic rice (Bradbury *et al.*, 2005).

**Author for Correspondence: Email- bcroy10@yahoo.com*

Rice aroma also depends on environmental conditions and cultivation management. Aroma in scented rice depends on the levels of 2-AP content and it varies with genetic background and environmental conditions (Nadaf *et al*., 2006). Basmati variety will be more aromatic if cultivated in area having relatively cool temperature in the afternoon (25-32 °C) and night (20-25 °C) with humidity of about 70-80% during primordial and grain filling stages (Singh, 2000). In view of the importance of the aromatic rice in the national and international markets, the aim of present study was to quantify genetic variability in important yield contributing characters in a set of 35 aromatic FVs and assessment of character associationships through correlation and path coefficient analyses under the humid sub-tropics of Terai Zone of Cooch Behar, West Bengal.

Materials and Methods

Germplasm Collections

Thirty-five aromatic Farmers' Varieties (FVs) of rice were used in this study. These FVs were collected from West Bengal, Assam and Manipur. Details of the genotypes are given in Table 1. The field experiment was carried out at the Instructional Farm of Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar, West Bengal. The farm is situated at 26º19′86″ N latitude and 89º23′53″ E longitude, at an elevation of 43 meter above mean sea level. The climatic condition of *Terai* Zone is sub-tropical in nature with high rainfall, high humidity and prolong winter season.

Morphological Characterization

Thirty days old seedlings were transplanted (single seedling per hill) in plots measuring 3 × 1.5 m area in randomized block design with two replications. Row to row and plant to plant spacing were 30 and 20 cm, respectively. Standard agronomic practices compatible to the humid tropic of *Terai* Zone were followed to obtain good crop stand. Five random plants were selected from each entry from each replication for recording the data using the guidelines of IRRI (IRRI, 2002). Observations were recorded on days to 50% flowering, plant height (cm), number of panicles per plant, panicle length (cm), grain density, number of filled grains per panicle, filled grain percentage, number of chaffy grains per panicle, grain sterility (%), total grains per panicle, 100-seed weight (g), grain length (mm), grain width (mm), grain thickness (mm) and grain yield per plant (g).

Aroma Testing

Aroma was evaluated through cooked rice aroma test following the method as described by Allidawati (1989). One gram of rice was placed in test tube of 15 mm × 150 mm containing 10 ml of dH_2O. The test tube was then covered with aluminum foil and cooked in boiling water for 15 minutes. After the samples were cooled down, the aluminum foil was opened and the score of each sample was recorded by a panel of experts (panelists) who have experience in evaluation of aroma and quality of rice. The scores were averaged and classified into aromatic, slightly aromatic and not aromatic.

Table 1. Name of the Farmers' Varieties of rice used in this study and their place of collection

S.No.	Name of the FV	District/ State of cultivation	S.No.	Name of the FV	District/ State of cultivation
1.	Khasa	Maldah, W.B.	19.	Konkoni Joha	Assam
2.	Radhunipagal	Nadia, W.B.	20.	Sial Bhomra	Assam
3.	Mohanbhog	Nadia, W.B.	21.	Jhagrikartik	Assam
4.	Gobindobhog	Nadia, W.B.	22.	Sadanunia	Cooch Behar, W.B.
5.	Kalojeera	Cooch Behar, W.B.	23.	Kataribhog	Alipurduar, W.B.
6.	Badshabhog	Maldah, W.B.	24.	Khama	Alipurduar, W.B.
7.	Tulsibhog	Alipurduar, W.B.	25.	Bhiganmachhuya	Assam
8.	Tulaipanji	Uttar Dinajpur, W.B.	26.	A-1-1	Alipurduar, W.B.
9.	Bora	Assam	27.	Laldhyapa-1	Alipurduar, W.B.
10.	Joha Bora	Assam	28.	Singra	Alipurduar, W.B.
11.	Silathia Bora	Assam	29.	Kalakali	Alipurduar, W.B.
12.	Jailung Lal Komal	Assam	30.	Marichsal	Alipurduar, W.B.
13.	Ghee Bora	Assam	31.	Kauka	Alipurduar, W.B.
14.	Birai	Assam	32.	Laghidhan	Alipurduar, W.B.
15.	Kabra	Assam	33.	Dubari Komal	Assam
16.	Rampha	Assam	34.	Hatidat Komal	Assam
17.	Kolajoha Big	Assam	35.	Ranga Komal	Assam
18.	Kolajoha Small	Assam			

Table 2. Analysis of variance for different characters in rice

Characters	Source of variation with d.f.		
	Replication (1)	Treatment (34)	Error (34)
Plant height	0.6071	471.2316**	0.7285
Days to 50% flowering	-0.0357	362.8456**	0.1922
No. of panicles/ plant	0.2057	49.9270**	0.0478
Panicle length	0.0975	7.5545**	0.0179
Grain density	0.7560	11.1154**	0.0425
No. of filled grains/ panicle	595.9714	5237.0771**	26.8905
Filled grain (%)	9.9804	28.7132**	0.6734
No. of chaffy grains/ panicle	6.4129	181.7336**	1.7212
Grain sterility (%)	10.0338	28.7144**	0.6723
No. of total grains/ panicle	478.8286	6265.3311**	27.1374
100 grains weight	0.0084	0.5740**	0.0052
Grain length	0.1843	3.5144**	0.1274
Grain breadth	0.0112	0.2704**	0.0152
Grain L/B ratio	0.0835	0.6641**	0.0365
Grain thickness	0.0066	0.1069**	0.0167
Grain yield/ plant	13.9214	258.9746**	6.5962

Statistical Analysis

The experimental design used was RBD using 35 treatments (genotypes) with two replications. The data were subjected to standard statistical methods of analysis of variance (ANOVA), correlation and path analysis using AgRes Statistical Software, (c) 1994 Pascal Intl Software Solutions, Version 3.01. Path coefficient analysis is simply standardized partial regression coefficient, which splits this correlation coefficient into measures of direct and indirect effects of a set of independent variables on these dependent variables.

Results and Discussion

Genetic Variability

The present investigation was undertaken to quantify the nature and magnitude of variability, heritability and genetic advance in respect of 16 agronomic and grain characters in a set of 35 aromatic FVs of rice. Efforts were also made to understand character associationship through correlation and path analyses. Genotypes were found to be significantly different from each other in respect of all the characters studied (Table 2).

Classification Based on Grain Type

Based on classification of Govindaswami (1985) the grains of these 35 FVs were classified into four groups *viz*., long slender (LS), medium slender (MS), long bold (LB) and short bold (SB). Eleven FVs were classified under long slender, five FVs were medium slender, 13 were long bold and six FVs were short bold (Table 3). Grain shape determines the selling price of this important commodity. This character largely depends on grain length, breadth and L:B ratio. Long slender grain influences the consumers' acceptance of the genotype in the market.

Classification Based on Strength of Aroma

The Indian subcontinent has the *Nature's Gift* of Basmati rice that has been accepted as the best scented, long and slender grain in the national and international markets and gets premium price. In addition to Basmati, many local landraces are grown traditionally which excel in aroma, grain quality and cooking quality. 'Tulaipanji' of Daskhin Dinajpur district of West Bengal equally satisfies the grain quality as that of Basmati rice.

Table 3. Classification of FVs based on grain type as per the recommendation of Govindaswami (1985)

Classes	Name of the Farmers' Varieties	No. of FVs
Long Slender	Tulaipanji, Jailung Lal Komal, Birohi, Kabra, Kolajoha Big, Kataribhog, A-1-1, Kalakali, Dubari Komal, Hatidat Komal, Sadanunia	11
Medium Slender	Tulsibhog, Joha Bora, Silathia Bora, Kolajoha Small, Sial Bhomra	5
Long Bold	Radhunipagal, Bora, Ghee Bora, Rampha, Jhagrikartik, Khama, Bhiganmachhuya, Laldhyapa-1, Singra, Marichsal, Kauka, Laghidhan, Ranga Komal	13
Short Bold	Khasa, Mohanbhog, Gobindobhog, Kalojeera, Badshabhog, Konkoni Joha	6

Many FVs have strong aroma, but their other plant characters and/or grain characters may not be *at par* with the modern high yielding varieties. Most of those aromatic FVs are poor yielders, for examples, Kalonunia, Tulaipanji (Mandal *et al*., 2013), Kalojeera and Mohanbhog. On the other hand, few aromatic FVs possess high yielding ability, such as Gobindobhog and Badshabhog. Those FVs may be brought under cultivation through improved agronomic practices. In West Bengal, those strongly scented rices are generally used in preparation of *Khir* during special occasions and also offered during different auspicious occasions.

The collected germplasm was classified under two groups based on aroma as per the guidelines of (Allidawati, 1989; Anonymous, 2004; Lestari, 2011) (Table 4). A sizable numbers of aromatic FVs possessed strong aroma and those cultivars also fetched high prices in the local market. These cultivars may be released with modern agronomic practices to improve yield potential and subsequently popularization of their cultivation.

Khasa, Radhunipagul, Mohanbhog, Gobindobhog, Kalojeera, Badshahbhog, Tulsibhog, Tulaipanji, Bora, Boha Bora, Silathia Bora, Jailung Lal Komal, Ghee Bora, Birai, Kabra, Rampha, Kolajoha-big, Kolajoha-Small and Konkoni Joha were classified as the FVs having strong aroma. Few of these FVs are very popular in Assam (Ghee Bora, Silathia Bora, Kolajoha-big and Kolajoha-Small) and West Bengal (Gobindobhog, Badshabhog, Khasha, Tulaipanji, Kalobhog etc.). Rest all the other FVs have been recorded as mild aromatic cultivars, namely, Sial Bhomra, Jhagrikartik, Sadamunia, Kataribhog, Khama, Baigon Machhuya, A-1-1, Laldhyapa-1, Singara, Kalakali, Marichsal, Kauka, Dubari Komal, Hatidat Komal and Ronga Komal.

Donor's Identification for Different Argonomic Characters

The FVs showed desirable characteristics based on individual character were listed in Table 5. The FV, such as, Sadanunia was found to be superior for the important plant characters (days to 50% flowering, plant height, number of panicles per plant, grain type and grain yield per plant). The FV Rampha was found better for the characters, such as, panicle length, 100-grain weight, grain type and yield. The FV A-1-1 was found to be superior in respect of number of panicles per plant, lower percentage of chaffy grains per panicle, grain type and yield per plant.

The most important desirable characters for the rice cultivation under multiple cropping system are days to 50% flowering, plant height, number of panicles per plant, panicle length, number of filled grains per panicle, spikelet sterility, 100-grains weight, grain type and finally the yield per plant. The FVs Tulsibhog and Sadanunia showed earliness for grain maturity. Generally the FVs are long duration, but these two FVs were found to be of medium duration. Sadanunia also have some other desirable characters like, plant height, number of panicles per plant, grain type and grain yield per plant.

High number of panicles per plant was recorded for Rampha, Kalakali, Khasha, Laldyapa-1, Sadanunia and A-1-1. Longer panicles were observed for the FVs namely, Marichsal, Birohi, Kolajoha Big, Rampha, Khama, Singara and Gobindobhog. The FVs which showed higher number of filled grains per panicle were Badshabhog, Mohanbhog, Sial Bhomra, Kolajoha Small, Khama, Gobindobhog and Bhiganmachhuya. Low spikelet sterility was observed for Tulaipanji, A-1-1, Kamar, Mohanbhog, Silathia Bora and Radhunipagal. Higher 100-grains weight was documented for Hatidat Komal, Rampha, Dubari Komal, Laldhyapa, Ghee Bora, Joha Bora, Rongakomal and Silathia Bora. Long slender grain was witnessed for Tulaipanji, Jailung Lal Komal, Birohi, Kabra, Kolajoha Big, Kataribhog, A-1-1, Kalakali, Dubari Komal, Hatidat Komal and Sadanunia.

The collective contribution of the yield attributing characters resulted high yield for the FVs namely, Rampha, Laldhyapa-1, A-1-1, Kauka, Kalakali, Joha Bora, Khama, Sadanunia, Hatidat Komal, Marichsal and Dubari Komal. High yield of these genotypes were probably governed by moderate to high number of panicles per plant, grains per panicle and 100-

Table 4. Genetic variability of the collected Farmers' Varieties of rice in respects of aroma

Classes	Name of the farmers' varieties	No. of FVs
Strong aroma	Khasa, Radhunipagul, Mohanbhog, Gobindobhog, Kalojeera, Badshahbhog, Tulsibhog, Tulaipanji, Bora, Boha Bora, Silathia Bora, Jailung Lal Komal, Ghee Bora, Birai, Kabra, Rampha, Kolajoha-big, Kolajoha-Small, Konkoni Joha	19
Mild aroma	Sial Bhomra, Jhagrikartik, Sadamunia, Kataribhog, Khama, Baigon Machhuya, A-1-1, Laldhyapa-1, Singara, Kalakali, Marichsal, Kauka, Dubari Komal, Hatidat Komal, Ronga Komal	16

Table 5. Donors identification for different argonomic characters among 35 famers' varieties of rice

Character	Genotype
Days to 50% flowering	Tulsibhog, Sadanunia
Plant height	Sadanunia, Mohanbhog, Katarybhog, Jailung Lal Komal, Bora, Jhagrikartick
No. of panicle per plant	Rampha, Kalakali, Khasha, Laldyapa-1, Sadanunia, A-1-1
Panicle length	Marichsal, Birohi, Kolajoha Big, Rampha, Khama, Singara, Gobindobhog
No. of filled grains per plant	Badshabhog, Mohanbhog, Sial Bhomra, Kolajoha Small, Khama, Gobindobhog, Bhiganmachhuya
Filled grain percentage	Mohanbhog, Silathia Bora, Radhunipagal, Kalojeera, Badshabhog, Kabra, Gobindobhog
Number of chaffy grains per panicle	A-1-1, Tulsibhog, Kalojerra, Radunipagal, Kabra, Kauka
Spikelet sterility (%)	Tulaipanji, A-1-1, Kamar, Mohanbhog, Silathia Bora, Radhunipagal
Total number of grains per panicle	Badshabhog, Mohanbhog, Sial Bhomra, Konkoni Joha, Kolajoha Small
Grain density	Badshabhog, Mohan bhog, Sial Bhomra, Kolajoha Small, Bhiganmachhuya, Silathia Bora, Joha Bora
100-grain weight	Hatidat Komal, Rampha, Dubari Komal, Laldhyapa, Ghee Bora, Joha Bora, Rongakomal, Silathia Bora
Grain length	Khama, Dubari Komal, Ranga Komal, Sial Bhomra, Kolajoha Big, Rampha
Grain breadth	Badshabhog, Tulaipanji, Tulsibhog, Kataribhog, Sadanunia, Kolajoha Small
Grain L:B ratio	Tulaipanji, Kataribhog, Jailung Lal Komal, Birohi, Kalakali, Kalojeera, Kabra, A-1-1, Dubari Komal, Hatidat Komal
Grain type (Long Slender)	Tulaipanji, Jailung Lal Komal, Birohi, Kabra, Kolajoha Big, Kataribhog, A-1-1, Kalakali, Dubari Komal, Hatidat Komal, Sadanunia
Grain yield/plant	Rampha, Laldhyapa-1, A-1-1, Kauka, Kalakali, Joha Bora, Khama, Sadanunia, Hatidat Komal, Marichsal, Dubari Komal

grain weight. For genetic improvement of rice several promising donors were identified (Table 5), which may be used in the breeding programmes.

Genetic Parameters

The estimates of different genetic parameters *viz*., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (H^2) and genetic advance (GA) were presented in Table 6.

The PCV estimates were found to be higher than corresponding GCV estimates for all the characters under consideration, which suggested their involvement in influencing the expression of these characters (Table 6). Similar result was also reported by Suresh and Anbuselvam (2005), Hasib (2005), Karad and Pol (2008), Kumar and Senapati (2013). GCV and PCV for grain thickness differed significantly and was found to be more prone to environmental changes than other characters. This abreast with the findings of Reddy *et al.* (1997a-b).

Impact of environment on the expression of any character is studied by estimating GCV and PCV. It was revealed less difference in corresponding GCV and PCV values for all the characters studied for associationship except grain thickness. It indicates marginal control of environment in governing these characters. Ramalingam *et al*. (1994) and Borbora and Hazarika (1998) also reported similar results.

Heritability estimates were found to be high for days to 50% flowering (99.0%), plant height (99.0%),

Table 6. Variability and genetic parameters for different characters in rice

Character	Variance			GCV	PCV	h2 (BS)	G.A. as % of mean
	Phenotypic	Genotypic	Environmental				
Plant height	235.98	235.252	0.728	10.30	10.32	0.99	21.19
Days to 50% flowering	181.59	181.327	0.192	10.01	10.02	0.99	20.62
Number of panicles/plant	24.97	24.940	0.048	27.46	27.49	0.99	56.53
Panicle length	3.76	3.768	0.018	7.690	7.70	0.99	15.80
No. of filled grain/panicle	2631.98	2605.093	26.891	31.60	31.76	0.98	64.76
No. of chaffy grain/ panicle	91.72	90.006	1.721	38.69	39.05	0.98	78.95
100-grain weight	0.29	0.284	0.005	28.89	28.57	0.98	57.81
Grain length	1.82	1.693	0.127	18.89	19.59	0.93	37.53
Grain breadth	0.14	0.128	0.015	14.08	14.89	0.89	27.42
Grain thickness	0.06	0.045	0.017	11.64	13.63	0.72	20.49
Grain yield/plant	132.78	126.189	6.596	39.50	40.42	0.95	79.32

number panicles per plant (99.0%), panicle length (99.0%), number of filled grains per panicle (98.0%), 100-grain weight (98.0%), grain length (93.0%), grain breath (89.0%) and grain yield (95.0%). High heritability along with high genetic advance for number of filled grains per panicle, number of panicles per plant and 100-grains weight were also reported by Tripathi *et al*. (1999), Sarkar *et al*. (2005), Suresh and Anbuselvam (2005), Karad and Pol (2008), Mulugeta *et al.* (2012), Kumar and Senapati (2013).

H^2 in broad sense indicates the extent of genetic control of a character and it reflects the efficiency of selection to improve upon a particular character. Thus, characters endowed with high values may be used as selection criteria in genetic improvement of grain yield. High H^2 for quantitative characters are useful as it enables in effective selection based on the phenotypic performance. It also indicates the correspondence between genotype and phenotype. Similar results were also reported by Roy and Kar (1992), Ramalingam *et al*. (1994), Sarawgi and Soni (1994), Yadav (1992) and Reddy *et al*. (1997 a-b) for days to 50% flowering and plant height, Sarma and Roy (1993), Sawant and Patil (1995), and Roy *et al* 2001) for number of filled grains per panicle and 100-grain weight. High GCV coupled with high heritability indicating effectiveness of selection based on these characters.

High genetics advance was observed for number chaffy grains per panicle (78.95), number of filled grains per panicle (64.76), grain yield per plant (79.32), 100-grains weight (57.81) and number of panicles per plant (56.53) (Table 6).

A character attracts more attention which displays high degree of heritability for genetic improvement through simple selection. But to assess the maximum effect of selection, GA is simultaneously computed. Johnson *et al*. (1955) and Panse (1957) opined that H^2 estimate with simultaneous consideration of GA values would be more useful than H^2 alone in predicting the efficiency of selection. High GA coupled with high H^2 were observed for number of filled grains per panicle, grain yield per plant, 100-grains weight and number of panicles per plant. Ghosh *et al*. (1981), Kaul and Kumar (1982), Sawant *et al*. (1995) also reported similar result for number of field grains per panicle, 100-grain weight and grain yield per plant. High heritability coupled with high GA indicates the predominance of additive gene action and selection for these characters based on phenotypic value would result in more efficient breeding programmes. Simple selections like mass and family selections would be effective to accumulate such additive genes, which may further improve upon their performances.

Character Associationship

For analysis of character associationship, 11 characters were considered instead of 16 characters. The characters derived from other basic characters such as grain density, filled grain percentage, spikelet sterility (%), total grains per panicle and grain L:B ratio were not included here. The genotypic and phenotypic coefficients of correlation between the characters in all possible combinations are presented in Table 7.

Grain yield showed high significant positive association with number of panicles per plant (0.668, 0.651), 100-grains weight (0.617, 0.598) and grain thickness (0.449, 0.410) both at genotypic and phenotypic levels. This character showed significant positive correlation (0.334) with grain length at genotypic level, whereas it showed positive insignificant association with grain length. Grain yield per plant also showed positive correlation with plant height and grain thickness. It showed negative association with days to 50% flowering, panicle length and number of filled grains per panicle. Grain yield per plant registered high significant negative association with number of chaffy grains per panicle. This is very desirable characters association, because with decrease in number of chaffy grains per panicle will increase grain yield of rice.

Most of the plant characters of economic importance such as grain yield per plant are extremely complex in inheritance and generally associated with several other characters. Furthermore, expression of such characters by and large is influenced by the environment, which increases the complexity of inheritance pattern and in shaping such characters in breeding programmes. Hence, knowledge of the degree of genotypic and phenotypic correlations between yield and other component characters as-well-as among themselves becomes imperative. Correlation studies provide better insight in understanding yield components, which help in choosing proper selection criteria (Johnson *et al*., 1955). Maximum combinations of heritability and correlation coefficient values are necessary to execute more efficient selection than direct selection for improved grain yield *per se*. Genotypic correlation generally

Table 7. Genotypic (G) and phenotypic (P) correlations among yield and its attributes in rice

Char.		X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
X1	G	0.321	0.085	0.236	0.024	0.021	-0.029	0.278	0.107	0.130	0.079
	P	0.320	0.085	0.235	0.025	0.028	-0.028	0.265	0.101	0.103	0.074
X2	G		-0.112	0.0980	0.270	0.196	0.020	0.116	0.135	-0.200	-0.060
	P		-0.112	0.097	0.269	0.194	0.019	0.111	0.128	-0.175	-0.059
X3	G			-0.189	-0.235	-0.211	-0.157	0.094	-0.174	-0.186	0.668**
	P			-0.189	-0.233	-0.208	-0.155	0.090	-0.166	-0.160	0.651**
X4	G				-0.337**	0.037	0.087	0.252	0.071	0.152	-0.108
	P				-0.336**	0.037	0.083	0.243	0.064	0.132	-0.103
X5	G					0.438**	-0.260	-0.280	-0.143	-0.084	-0.298
	P					0.430**	-0.255	-0.276	-0.137	-0.067	-0.293
X6	G						-0.249	-0.199	-0.069	-0.162	-0.341*
	P						-0.241	-0.182	-0.066	-0.131	-0.332*
X7	G							0.344*	0.708**	0.433**	0.617**
	P							0.328*	0.667**	0.364**	0.598**
X8	G								0.310	0.275	0.334*
	P								0.283	0.221	0.318
X9	G									0.684**	0.449**
	P									0.579**	0.410**
X10	G										0.242
	P										0.239

X1: Plant height
X2: Days to 50% flowering
X3: Number of panicles/plant
X4: Panicle length
X5: No. of filled grains/panicle
X6: No. of chaffy grains/ panicle
X7: 100-grains weight
X8: Grain length
X9: Grain breadth
X10: Grain thickness
X11: Grain yield per plant

appears due to linkage, pleiotropic effect of the genes and effect of selection. These act either singly or in combination. Estimates of genetic association along with phenotypic correlationships not only display a clear picture of the extent of inherent association but also indicate the quantum of phenotypically expressed correlation influenced by the environment. When any variables are involved in a study, correlation becomes complex, however, meaningful conclusions generally emerge. Genotypic correlationships obtained from a number of genotypes are likely to be higher than those obtained from segregating population in view of the fact that the genotypes stabilize when established under continuous selection process in relation to independent set of genes.

Genotypic correlations were slightly higher than their corresponding phenotypic correlations in this study, which indicated that there is better association between two characters genetically, but the phenotypic value reduced due to significant interaction of the genotype with environment. Johnson *et al*. (1955) also suggested that the low phenotypic correlations might be due to masking/modifying effect of the environment in genetic association between characters. Similar results were observed in several crops including rice (Reddy *et al*., 1997a). For selection purpose, phenotypic correlation is of little practical value unless genotypic and environmental correlations are concurrently considered for pairs of characters. Genotypic correlation is generally used in selecting a character as a means to improve other character. Environmental correlation has no general value as such in selection process except it provides information about the relationship of characters irrespective of genetic differences among the genotypes.

Grain yield showed significant positive association with plant height, number of panicles per plant, 100-grain weight, grain length, grain breadth and grain thickness at genotypic and phenotypic levels. These results indicate that increase in one variable will cause increase in the other and *vice versa*. Similar results were also reported by Yadav (1992), He and Chen (1992), Rao and Saxena (1999) and Meenakshi *et al*. (1999), for number of panicles per plant; Chauhan and Tandon (1984), Paramasivam (1991), Surek *et al*. (1998) and Bagali *et al*. (1999) for 100-grain weight. A positive correlation between desirable characters is essential, which may help in simultaneous improvement of both characters. Very high value of association of grain yield per plant was found with 100-grains weight. Yuan *et al*. (1995) also suggested that the most important character affecting

grain weight per panicle was found to be the number of filled grains per panicle. The genetic improvement in respect of an independent character can be achieved by applying strong selection to a particular character, which is genetically correlated with the dependent character. Grain length, grain breadth and grain thickness showed insignificant positive association with grain yield indicating the independent nature of the two characters (Singh and Narayanan, 1993). Chakraborty and Hazarika (1994) reported positive and significant association of grain breadth with yield.

A positive correlation between important characters is desirable since it helps in simultaneous improvement of both the characters (Simmonds, 1979). They may be used as selection criteria to improve upon the grain yield in rice. Therefore, selection for number of panicles per plant and 100-grain weight could be effective in improving grain yield per plant. Deosarkar *et al*. (1989), Luzi-Kihupi (1998) also suggested that grain weight were used as efficient selection criteria for increased grain yield in rice.

Path Coefficient Analysis

Yield is the multiplicative end product of several component characters (Whitehouse, 1958; Grafius, 1959). These are mutually associated which in turn impair the true association existing between a component character and grain yield. The complexity of character relationship among themselves and with grain yield do not provide comprehensive picture of relative importance direct and indirect influence of each characters to the yield since resultant yield is the combined effects of various factors complementary or counteracting. Path coefficient analysis provides an effective means of untangling direct and indirect causes of association and permits a critical examination of specific forces acting to produce a given correlation. It measures the direct and indirect contributions of independent variables on dependant variables. Therefore, to understand the relationship between yield per plant and related characters, path analysis was computed using simple genotypic correlation coefficient values between characters and has been presented in Table 8.

Maximum positive direct effect on grain yield per plant was observed in number of panicles per plant (0.829) followed by 100-grains weight (0.672), grain length (0.127) and grain breadth (0.074). The correlation coefficients between grain yield and direct effect of number of panicles per plant and 100-grains weight did not differ much. This explains the true relationship and a direct selection through these characters will be more effective.

The direct effect of plant height (-0.009) and grain thickness were found to be negative. However, the correlation coefficients were found to be positive, which indicates that the direct effects seem to be the cause of correlation. In such situation, the indirect casual factors are to be considered simultaneously for efficient selection.

Residual effect indicates the involvement of the other associated characters in governing grain yield, which was not considered in this study. The residual effect was 44.82%, so, independent variables could explain only 55.18% of the variability for grain yield per plant. The reason seems to be due to the presence of low and

Table 8. Path coefficient (Genotypic) analysis showing direct (Bold) and indirect effects of component traits in rice genotypes

Cha.	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	Yield Corrl.
X1	-0.009	-0.010	0.070	-0.005	-0.053	-0.005	-0.194	0.035	0.007	-0.006	0.079
X2	-0.003	-0.031	-0.092	-0.002	-0.611	-0.047	0.013	0.015	0.010	0.009	-0.060
X3	-0.001	0.003	0.829	0.004	0.532	0.051	-0.105	0.012	-0.013	0.008	0.668
X4	-0.002	-0.003	-0.157	-0.023	0.763	-0.009	0.056	0.032	0.005	-0.007	-0.108
X5	-0.000	-0.008	-0.195	0.008	-2.264	-0.105	-0.176	-0.035	-0.010	0.004	-0.298
X6	-0.000	-0.006	-0.174	-0.000	-0.991	-0.240	-0.166	-0.025	-0.005	0.007	-0.341
X7	0.000	-0.001	-0.130	-0.002	0.593	0.060	0.672	0.044	0.052	-0.019	0.617
X8	-0.002	-0.003	0.776	-0.006	0.634	0.048	0.231	0.127	0.023	-0.012	0.334
X9	-0.001	-0.004	-0.145	-0.002	0.323	0.017	0.476	0.039	0.074	-0.308	0.449
X10	-0.001	0.006	-0.154	-0.004	0.191	0.039	0.291	0.035	0.053	-0.045	0.242

Residual Effect = 44.823%

X1: Plant height **X2:** Days to 50% flowering **X3:** Number of panicles/plant
X4: Panicle length **X5:** No. of filled grain/panicle **X6:** No. of chaffy grain/ panicle
X7: 100-grain weight **X8:** Grain length **X9:** Grain breadth
X10: Grain thickness **X11:** Grain yield per plant

insignificant correlations of plant height, days to 50% flowering, panicle length, number of filled grains per panicle and number of chaffy grains per panicle with grain yield. Besides the characters considered in this study, inclusion of some other additional characters might have covered the full range of variation for grain yield per plant.

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Estimation of Genetic Diversity among the Rice (*Oryza sativa* L.) Genotypes using Microsatellite Markers

Megha Joshi[1], PK Singh[1*], Pallavi[2], Showkat A Waza[1] and Aparajita Singh[1]
[1]*Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi-221005, Uttar Pradesh, India*
[2]*Department of Botany, Institute of Science, Banaras Hindu University, Varanasi-221005, Uttar Pradesh, India*

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Sixteen microsatellite markers were used to study the genetic diversity among 73 genotypes of rice from geographically diverse locations. Thirteen markers revealed polymorphism, while three were observed to show the monomorphic amplicons. The polymorphic markers produced total of 34 alleles with an average of 2.62 alleles per locus. Amplification products ranged from 100 bp produced by marker K39512 to 220 bp produced by marker RM536. Polymorphism Information Content (PIC) value varied from 0.225 to 0.743 and the marker RM336 was observed to be most suitable for discriminating the genotypes owing to its highest PIC value. The UPGMA cluster diagram grouped the genotypes into eight major clusters. The Jaccard's similarity coefficients ranged from 0.16 to 1.00.

Key Words: Dendrogram, Diversity, Microsatellite markers, PIC value, Rice

Introduction

Rice (*Oryza sativa* L.) is a staple food for more than half of the world population and is one of the most important food crops grown worldwide. It is also a model monocot plant for genetic and genomic studies. However, the annual increase in rice yield has decreased from 2.4% (in the late 1980s) to 1.0% at present (Fischer *et al.*, 2014). One of the possible causes in low genetic gains of rice crop is the continuous use of genetically related elite germplasm in breeding programmes. Exploitation of genetic diversity among parental genotypes is one of the major approaches to maximize genetic gains in rice breeding programmes. Genetic diversity study helps in estimating and establishing the genetic relationship in germplasm collections for identifying diverse parental combinations to create segregating progenies with maximum genetic variability. It helps in the identification of superior recombinant lines for further selection and introgressing desirable genes from diverse germplasm (Thompson *et al.,* 1998; Islam *et al.,* 2012).

Genetic diversity is commonly estimated by genetic distance or similarity analyses, both of which entail that there are either differences or similarities at the genetic level (Weir, 1990). It can be evaluated using morphological traits, biochemical and molecular markers. However, DNA polymorphism based genetic variations are abundant and independent of environmental factors. Molecular Marker based Genetic Diversity Analysis (MMGDA) also has potential for assessing changes in genetic diversity over time and space (Duwick, 1984). Among various types of molecular markers, simple sequence repeats (SSRs) are efficient in detecting genetic polymorphisms and discriminating among genotypes from germplasms of various sources. These markers can detect finer levels of variation among closely related breeding lines even within a same variety (Lapitan *et al.,* 2007).

A number of studies have been carried out to study genetic diversity within the rice genotypes belonging to *indica* and *japonica* types using a set of SSR markers (Ravi *et al.,* 2003; Herrera *et al.,* 2008; Singh *et al.,* 2014; Waza *et al.,* 2013). The results revealed that the SSR markers showed distinct polymorphism among the cultivars studied indicating the robust nature of microsatellites in revealing polymorphism. In the present study, an attempt has been made to classify and understand the nature and magnitude of genetic diversity among various genotypes of rice using SSR markers.

Materials and Methods

The research material consisted of 73 morphologically diverse rice genotypes from geographically variable locations (Table 1). DNA was extracted from the leaves

**Author for Correspondence: Email- pksbhu@gmail.com*

Table 1. List of genotypes evaluated in the present study

S.No.	Genotype	Source	S.No.	Genotype	Source
1.	IC 260937	DBT, Networking project, BHU, Varanasi	37.	IC 356431	DBT, Networking project, BHU, Varanasi
2.	IC 260961		38.	IC 356432	
3.	IC 260964		39.	IC 356448	
4.	IC 267416		40.	IC 362206	
5.	IC 278777		41.	IC 382604	
6.	IC 280466		42.	IC 383396	
7.	IC 281785		43.	IC 383404	
8.	IC 281786		44.	IC 383441	
9.	IC 282418		45.	IC 383559	
10.	IC 282443		46.	IC 384176	
11.	IC 282463		47.	IC 384190	
12.	IC 282471		48.	IC 384260	
13.	IC 282514		49.	IC 391524	
14.	IC 282808		50.	IC 418382	
15.	IC 282815		51.	IC 426012	
16.	IC 282816		52.	IC 426013	
17.	IC 282822		53.	IC 426017	
18.	IC 282824		54.	IC 426058	
19.	IC 331196		55.	IC 426060	
20.	IC 334180		56.	IC 426061	
21.	IC 337051		57.	IC 426137	
22.	IC 337367		58.	IC 438644	
23.	IC 337558		59.	IC 446975	
24.	IC 337578		60.	EC 545051	
25.	IC 337582		61.	EC 545061	
26.	IC 337588		62.	EC 545165	
27.	IC 337593		63.	Koshihikari	IRRI, Philippines
28.	IC 341351		64.	Mars	
29.	IC 346002		65.	Sang khla	
30.	IC 346004		66.	Swarna	
31.	IC 346813		67.	HUR-W-1	BHU, Varanasi
32.	IC 346880		68.	S-183	CRRI, Cuttack
33.	IC 356117		69.	Sarjoo-52	NRCPB, New Delhi
34.	IC 356419		70.	S-148	CRRI, Cuttack
35.	IC 356422		71.	S-155	
36.	IC 356429		72.	Nirboi	IRRI, Philippines
			73.	Tetep	

of 15 days old seedlings according to CTAB method with little modifications (Doyle and Doyle, 1987). DNA quality was evaluated by electrophoresis in 0.8% agarose gel and quantification was accomplished using spectrophotometer.

For molecular analysis, 16 randomly selected SSR markers were used (Table 2). DNA amplification was carried out in 10 µl reaction mixtures containing 5 ng /10µl template DNA, 1x PCR buffer, 2.4 mM $MgCl_2$, 0.12 mM dNTPs, 0.7 pM of each primer (forward and reverse) and 0.6 U of Taq DNA Polymerase. Polymerase chain reaction (PCR) was carried out in a thermal cycler (Eppendorf, USA) with the following temperature cycle profile: Initial denaturation at 94°C for 4 min, 40 cycles each of 1 min denaturation at 94°C followed 30 sec annealing at 55°C to 65°C (depending on the primer used) and 1 min extension at 72°C, and finally 4 min at 72°C for the final extension.

Table 2. Allele size (bp) and polymorphism information content (PIC) of the SSR primers used in the present study

S.No.	Primer	PIC	No. of alleles amplified	Approximate size of amplified product (bp)
1.	Sbq1	0.00	1	210 (monomorphic)
2.	sbq 11	0.42	2	150-160
3.	RM 3691	0.26	2	130-160
4.	RM 3428	0.24	2	140-170
5.	K 39512	0.23	2	100-110
6.	RM 536	0.34	2	210-220
7.	RM5481	0.00	1	100 (monomorphic)
8.	RM 224	0.66	3	125-160
9.	RM 306	0.52	3	150-210
10.	RM 338	0.00	1	180 (monomorphic)
11.	RM 257	0.32	2	110-150
12.	RM 210	0.64	4	110-210
13.	RM 202	0.36	2	160-180
14.	RM 209	0.69	3	110-150
15.	RM 336	0.74	4	140-210
16.	RM 251	0.67	3	140-190

The amplified products were separated in 2.5 percent agarose gel prepared in 1x TAE (Tris-acetate-EDTA) buffer and stained with ethidium bromide. The gels were run in 1x TAE buffer at constant voltage of 65 V for 3 hours. They were visualized and photographs taken using gel documentation instrument (BioRad). Clearly resolved and unambiguous bands for each primer were scored in the form of matrix as 1 (presence) and 0 (absence) for each genotype.

Statistical analysis was carried out using the software NTSYS-pc version 2.1 (Rohlf, 1998). The data from all the markers were analyzed to estimate similarity based on the number of shared bands. Similarity was assessed with SIMQUAL module of NTSYS that calculates various types of similarity and dissimilarity coefficients for qualitative data. The similarity matrix estimates based on Dice coefficient of similarity were estimated. The dendrogram based on Unweighted Pair Group Method based on Arithmetic Average (UPGMA) was generated using the similarity matrix. Polymorphic information content (PIC) was estimated using the formula proposed by Nei (1973).

$$PIC = 1-\sum x^2_k$$

Where, x^2_k represents the frequency of the k^{th} allele.

Results and Discussion

Seventy three rice genotypes were analysed using SSR markers to assess genetic diversity. Out of the sixteen primers used, thirteen produced reproducible and polymorphic DNA banding pattern, while three primers (sbq1, RM5481 and RM338) were found to be monomorphic. The thirteen polymorphic primers produced total of 34 fragments, whose size varied from 100bp (marker K39512) to 220bp (marker RM536). Among the polymorphic markers, 7 revealed 2 alleles each, 4 showed 3 alleles each and 2 produced a maximum of 4 alleles each. Maximum of four fragments were produced by primers RM336 and RM210. An average of 2.6 fragments were produced by the primers showing polymorphic amplification. The value is lower than that of 5.89 and 5.66 per microsatellite locus as reported by Lapitan *et al.* (2007) and Hoque *et al.* (2014), respectively. Gel images showing SSR banding profiles obtained by primer RM224 are presented in Fig. 1.

Polymorphism information content (PIC) provides information about allele diversity and frequency among the genotypes. Its value for each marker can be evaluated on the basis of alleles, which varied among the SSR loci tested. Higher the PIC value of a locus, higher the number of alleles detected. The PIC value of SSR markers in present study ranged from 0.225 to 0.743 with an average value of 0.47. Markers RM336, RM209, RM251 and RM224 were most informative on the basis of high PIC value of 0.743, 0.694, 0.668 and 0.656, respectively. SSR marker K39512 showed least PIC value of 0.225. The early studies on PIC values ranged from 0.24 to 0.92 with an average of 0.61 (Jain *et al.,* 2004), 0.19 to 0.90 with an average of 0.75 (Borba *et al.,* 2009), 0.356 to 0.798 with an average of 0.543 (Hoque *et al.,* 2014), which is relatively higher

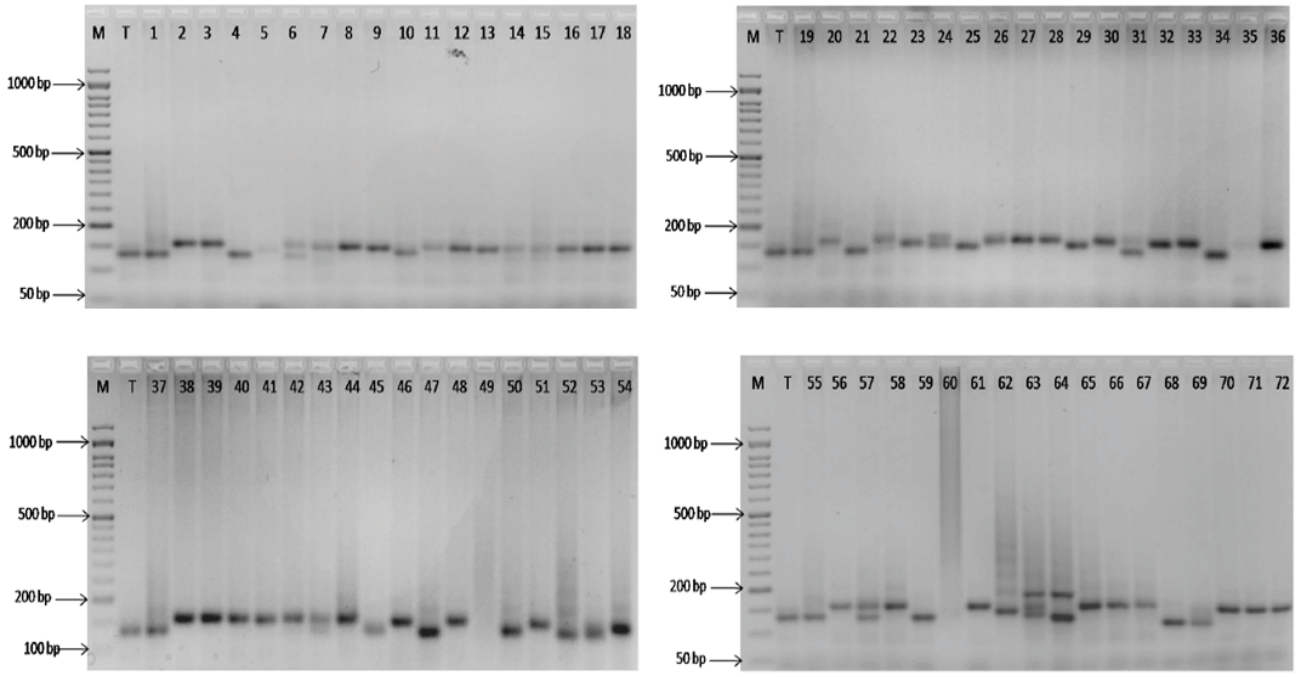

Fig. 1. Gel images showing SSR banding profile obtained by primer RM224. Lanes 1-72 represents the rice accessions as listed in Table 1; M = 100bp DNA size marker and T = Tetep variety (73rd rice accession in Table 1)

than that of present study. RM336 was found to be the most appropriate marker for discriminating various rice genotypes owing to its highest PIC value of 0.743.

A UPGMA cluster diagram obtained by all the 34 alleles (amplification products) generated by 13 polymorphic SSR markers grouped the genotypes into eight major clusters (Fig. 2). Cluster I, consisted of 38 genotypes, which were again subdivided into two sub clusters, *viz.*, Ia (14 genotypes) and Ib (24 genotypes). Cluster II includes only 3 genotypes. Cluster III contained twelve genotypes which were further divided into two sub clusters IIIa (6 genotypes) and IIIb (6 genotypes). Two genotypes were present in Cluster IV and six in Cluster V. Cluster VI includes five genotypes, whereas cluster VII consisted of six. The cluster VIII was monogenic containing only one genotype. Diversity studies involving cluster analysis have also been revealed by the earlier studies of Pervaiz *et al.* (2010), Tabkhkar *et al.* (2012) and Hoque *et al.* (2014). Kumar *et al.* (2014) reported that the genotypes studied were divided into five clusters, each consisting of accessions with distinct features. El-Malky *et al.* (2007) employed SSR makers for diversity studies and observed that genotypes evaluated were divided into two groups, one included the *indica* varieties and the other consisting of *japonica* types. Zeng *et al.* (2004) reported that the genotypes studied were grouped into two major branches in the dendrogram, one branch represents *japonica* rice and another represents the indica or the hybrids between *japonica* and *indica*.

The Jaccard's similarity coefficients in the present study ranged from 0.16 to 1.00. Hoque *et al.* (2014) observed the similarity coefficient range of 0.21 to 1.00 in the genotypes they evaluated. The pairwise similarity indices revealed 100% genetic similarity between the genotypes IC 282822 and IC 282824. These genotypes were found to be duplicate with respect to the loci studied. Sajib *et al.* (2012) also reported Deepa and Patnai-23 as duplicate accessions. Moreover, findings of the present study suggested that variety Tatep has least similarity with the genotype IC 267416 followed by IC 334180, IC 337578, IC 384176, IC 391524, IC 418382 and IC 446975.

The information regarding genetic diversity by microsatellite markers provides greater confidence for assessment of distinctness and relationships among various genotypes, which can be exploited in rice breeding programmes. With the help of microsatellite makers and clustering data, various distantly related rice genotypes may be combined by intercrossing to get hybrid varieties with highest heterosis and to screen

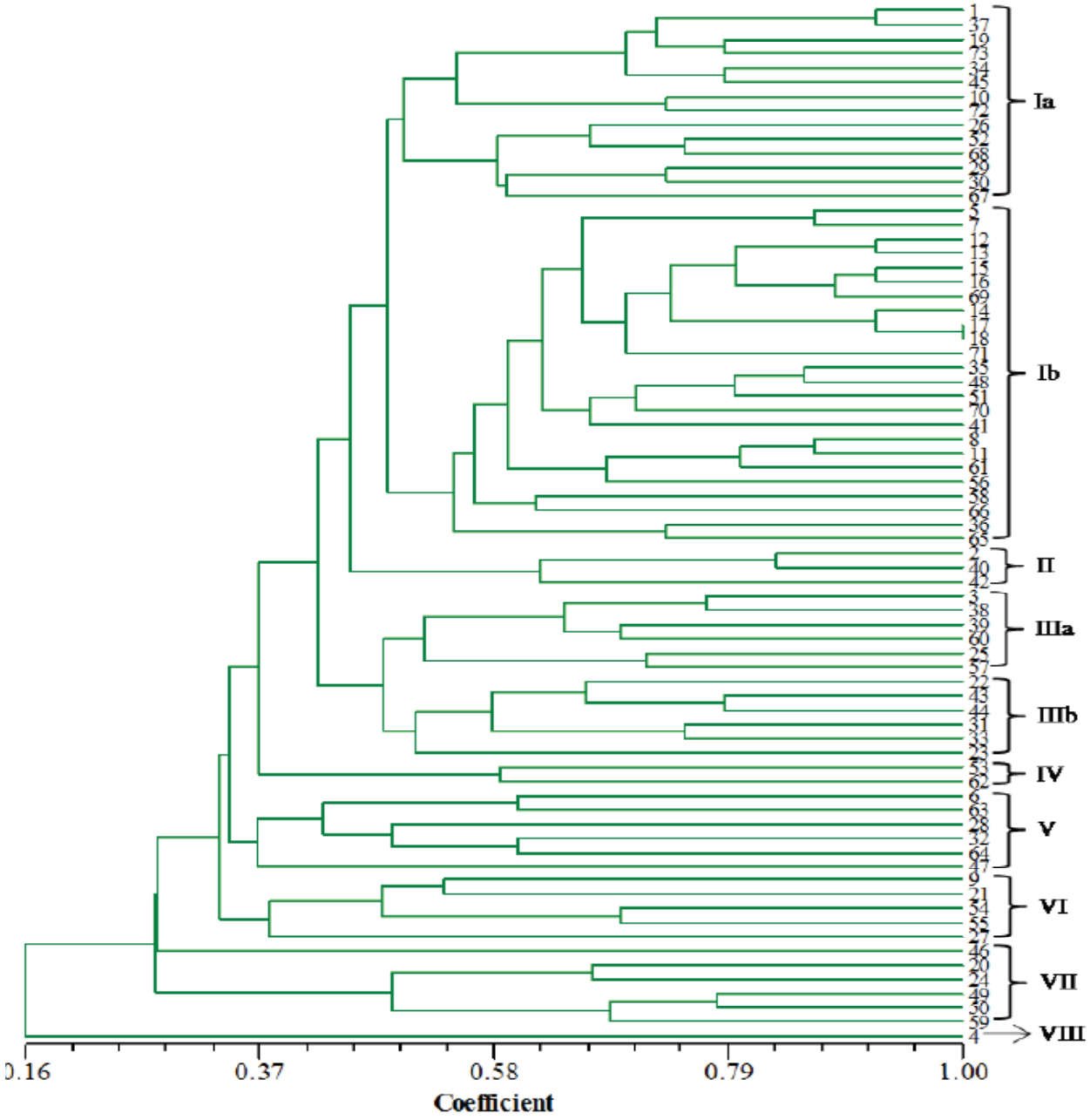

Fig. 2. UPGMA cluster dendrogram showing genetic relationship among various rice genotypes

out desirable genotypes from segregating generations. Moreover, the results can be used for fingerprinting and purity testing of genotypes.

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Variability in Mineral Content of *indica* Rice Genotypes of Assam, India

Khanin Pathak[1], S Rathi[1], S Baishya[1], H Verma[2], SW Rahman[3] and RN Sarma[2]
[1]*Department of Biochemistry and Agricultural Chemistry, Assam Agricultural University, Jorhat-785013*
[2]*Department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat-785013*
[3]*Department of Agricultural Biotechnology, Assam Agricultural University, Jorhat-785013*

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Significant genetic variations for grain concentration of all 9 mineral elements were observed. The range of macro elements like, phosphorous (P), sodium (Na), potassium (K), calcium (Ca) and magnesium (Mg) were recorded in the range of 0.272-0.412 per cent, 0.051-0.065 per cent, 0.190-0.232 per cent, 0.023-0.036 per cent and 0.039-0.049 per cent, respectively. The micro elements like iron (Fe), manganese (Mn), copper (Cu) and zinc (Zn) were found to be 2.34-4.21mg/100g, 1.02-3.87 mg/100g, 0.400-1.64 mg/100g and 2.10-4.66 mg/100g respectively. On average, the nine mineral content in rice genotypes were followed an order as P>K>Na>Mg>Ca>Zn>Fe>Mn>Cu. There is a significant correlation observed among different minerals. Highest estimate of GCV and PCV was recorded for Cu, which indicate plentiful variability of Cu content for genetic improvement. High heritability coupled with high genetic advance were observed for Cu, Mn, Zn and Fe which indicate preponderance of additive genetic effect in control of these minerals, which suggested the scope of genetic improvement of these minerals based on phenotypic performance.

Key Words: *Indica,* Rice, Mineral, Assam, Micronutrient

Introduction

With about half the world's human population dependent on rice (*Oryza spp*. L.) as a staple food, the grain provides the majority of dietary nutrients to billions of people (Shannon *et al.*, 2015). The deficiency of minerals and vitamins may result in various human disorders such as anemia, blindness, birth defects, retarded growth, diminished mental development and other health related problems (Darnton-Hill, 2005).Micronutrient deficiencies, particularly those involving iron (Fe) and zinc (Zn) are the most prevalent deficiency-related health disorders in the world (WHO, 2006). They also significantly and negatively impact on socio economic development at the individual, community and national levels (Darnton-Hill, 2005). The most prevalent nutrient deficiencies worldwide are Fe and Zn, with estimates that more than 25% of the world's population are at risk of mild to severe deficiency in one or both elements and with each element attributable for the deaths of 0.8 million persons per year (WHO, 2009; Maret and Sandstead, 2006). Low micronutrient densities in staple foods are generally the major reasons for human micronutrient malnutrition in developing countries (Cakmak, 2009; Gibson, 2006; Welch and Graham, 2004). Iron deficiency is responsible for up to 50% of the anaemia burden, making it the most widespread nutritional deficiency in the world (Stoltzfus 2011). It has been observed that the zinc deficiency is responsible for approximately 4% of child mortality (Black, 2008).

Assam is traditionally a rice growing state within North-East India and it plays a pivotal role in the economic and socio-cultural life of the people of the entire region. The *indica* type has enormous diversity in this region, which has resulted due to highly variable rice growing ecosystems and different cultural practices adapted by the local farmers. Unknowingly local farmers have selected many useful *indica* type cultivars, which have huge commercial prospects apart from being a staple food. Some of the special classes of *indica* rice in the region include aromatic rice, waxy or glutinous rice and soft rice. Wide variation of physiographic features and climatic characteristics have resulted three distinct growing seasons of *indica* type rice viz., *ahu* (Feb./March-June/July), *sali* (June /July-Nov /December) and *boro* (Nov/December-May /June).

Thus, the enhancement of rice grain micronutrient contents is viewed to be an important goal as part of global strategies for improving the nutritional quality of human diet. Rice varieties rich in micronutrients often

**Author for Correspondence: Email- khanin_bio@yahoo.in*

seems to have other desirable qualities such as high yield, good tolerance to nutrition deficiency stress, and pest resistance. Moreover, rice improvement in grain mineral elements content is always one of the major targets for rice breeders. Enhancement of the rice grain's nutritional value through genetic improvements could include both increasing concentrations of desirable elements (e.g. Fe, Zn or Ca) and decreasing concentrations of undesirable elements (e.g., As or Cd) and could create new marketing strategies for nutritionally enhanced and value-added products.

The breeding efforts in Assam are mainly directed towards yield traits such as morphological and physicochemical characteristics of the grain without focusing on mineral content of various traditionally grown rice landraces. A clear understanding of genetic base, through the characterization of local landraces for their mineral content is essential to use them in a rice nutrient breeding programme. The information regarding those aspects in case of different local rice landraces of Assam is scanty and sporadic. Therefore, the present investigation was conducted to evaluate the extent of variability in terms of mineral content of *indica* rice genotypes to be used in rice nutrient breeding from Assam.

Materials and Methods

For the present investigation, 100 different *indica* rice genotypes including another popular high yielding variety viz. Ranjit were collected from the Regional Agricultural Research Station (RARS), Titabar (Upper Brahamputra Valley Zone, UBVZ) and Regional Agricultural Research Station (RARS), Karimganz (Barak Valley Zone , BVZ) during the harvesting season in December-January, 2015. The grains of brown rice were grinded and converted into fine powder and oven dried at 100°C (± 2°C) and kept in a desiccator for mineral estimation.

For mineral estimation, the ash content was determined as described in the AOAC (1970). The mineral solution was prepared according to the method described by AOAC (1970). The all nine minerals (P, K, Na, Mg, Ca, Zn, Fe, Mn and Cu) were estimated using Atomic Absorption Spectrophotometer (Chemito, AA203D, Double beam atomic absorption spectrophotometer). The different standards were prepared for different minerals like, 1-2 ppm (P), 0.1 -0.6 ppm (Na), 0.5-2.0 ppm (K), 2-10.0 ppm (Fe), 2-8 ppm (Cu), 0.2-1.0 ppm (Zn), 1-4.0 ppm (Mn), 1-4.0 ppm (Ca) and 0.1-0.5 ppm (Mg).

Result and Discussion

The analysis of variance (ANOVA) revealed significant variation among genotypes for different minerals studied (Table 1), indicating abundant genetic variation in the genotypes under investigation. Choice of parents is a significant criterion for the successful breeding programme. Sometimes the *per se* performance of genotypes are used for choosing parents. The *per* se performance of genotypes for different minerals under investigation are shown in Table 2. Any crop improvement programmes mainly depend on extent of genetic variation and heritability for desirable characters in the genotypes, therefore conservation of variability has enormous potential in breeding programmes for future generations.

In the present investigation, the range of ash content of rice cultivars (1-2%) was almost similar with the findings of Yodmanee *et al.* (2011) and Oko *et al.* (2012). Oko and Ugwu (2011) reported similar ash content with the present study for some major rice varieties of South East Nigeria. However, a higher range of 3.16 to 3.79 per cent of ash in rice had been reported by Anjum *et al.* (2007).The variation in the ash content of different rice grains may primarily be due to cultivar differences, climatic condition as well as nutrient status of soil.

In the present study, analysis of variance indicated that the varietal effect on each of the minerals is highly significant. Correlation among the minerals themselves and with other parameters studied is shown in the Table 3.

Table 1. Analysis of variance for mineral content in *indica* rice genotypes from Assam, India

Characteristics	Sources of variation		
	Replication	Genotype	Error
df	2	99	198
Ash %	0.83253	0.19612*	0.043779
P %	0.9243	0.00649*	0.003795
K%	0.90501	0.00296*	0.003889
Na %	0.00133	0.00083*	0.000812
Mg %	0.01	0.00002*	0
Ca %	0.01	4.1E-05*	0
Zn (mg/100 g)	0.88649	0.76806*	0.003975
Fe (mg/ 100 g)	0.9243	0.51543*	0.003795
Mn (mg/100 g)	0.90501	0.74978*	0.003889
Cu (mg/100 g)	0.9243	0.19594*	0.003795

Df: Degrees of freedom; * Significant at 5% level. Data for mineral content are mean sum of square.

Table 2. Estimates of genetic parameters for mineral content in 100 indica rice genotypes from Assam, India

	Maximum	Minimum	Mean±SE	PCV (%)	GCV (%)	Heritability in broad sense (%)	Genetic advance (5%)
Ash %	2	1	1.4617	21.3298	15.6308	0.537	23.5963
P %	0.412	0.272	0.3476	19.3733	8.472	0.1912	7.632
K%	0.232	0.19	0.2098	27.7207	8.1523	-0.0865	-4.9388
Na %	0.065	0.051	0.0594	46.5783	3.9045	0.6742	0.007
Mg %	0.049	0.039	0.0445	5.8214	5.8214	1	11.992
Ca %	0.036	0.023	0.0297	12.5131	12.5131	1	25.777
Zn (mg/100 g)	4.661	2.103	3.4834	14.5765	14.4641	0.9846	29.5662
Fe (mg/ 100 g)	4.21	2.34	3.3154	12.572	12.4344	0.9782	25.3346
Mn (mg/100 g)	3.874	1.02	2.277	22.0131	21.843	0.9846	44.6487
Cu (mg/100 g)	1.64	0.4	0.7592	34.0477	33.0817	0.9441	66.2149

Table 3. Correlation among the minerals at their genotypic level

	Ash %	P %	Fe (mg/100 g)	Mn (mg/100 g)	Cu (mg/100 g)	Zn (mg/100 g)	Na %	K%	Ca %	Mg %
Ash %	1	0.0188	-0.0963	0.0375	-0.064	-0.0628	0.4189**	-0.0004	-0.0601	0.0767
P %		1	-0.1096	-0.0004	-0.0279	-0.3614**	-0.0235	0.1979*	-0.1127	0.1874*
Fe (mg/ 100 g)			1	-0.0547	0.1732*	0.2261*	0.2964**	-0.001	-0.2004*	0.0433
Mn (mg/100 g)				1	-0.2977**	0.007	-0.1193	-0.0003	0.1167*	-0.1602
Cu (mg/100 g)					1	0.0965	-0.5329**	-0.001	-0.2904**	0.1121
Zn (mg/100 g)						1	-0.1267	-0.0056	-0.0533	-0.0142
Na %							1	0	-0.7792**	0.444**
K%								1	0	0
Ca %									1	0.0181
Mg %										1

*Significant at 5% level and ** Significant 1% level

Phosphorous

The phosphorus content in the rice cultivars varied widely from 0.272 to 0.412 per cent, with a mean value of 0.348 per cent. The highest value was recorded in Mouguti Bora and the lowest one in Sukoni Bora-2. The findings of the present study were almost similar with the findings of Singh *et al.* (1998). However, phosphorous content was found lower than the findings of Oko *et al*. (2012). The Phosphorous content of Ranjit was 0.393 per cent. Phosphorus was found to be the highest among all the minerals estimated for the rice samples.

Potassium

The potassium content was found to be highest (0.232%) in the cultivar Kmj Bora-5 and the lowest (0.190%) in the Kola Bora-5 and Kmj Bora-11 with an average content of 0.209 per cent in the rice cultivars under study .The present result is in good agreement with the result of Oko *et al.* (2012) who reported the potassium content of Nigerian rice cultivars within the range of 0.15-0.23 per cent. However, the range of K content was found lower than the findings of Tinalin and Hashmi (2008), who reported the K content of husked rice within the range of 263.33-438.33 (mg/100 g) in some Malaysian rice varieties. Zeng *et al.* (2004) gave even a wider range of K content (0.172-0.452%) in core collection of Yunnan rice. The check variety, Ranjit contained 0.212 per cent of potassium.

Sodium

In the present investigation, the range of Na content in 100 rice cultivars was 0.051-0.065 per cent with an average of 0.060 per cent. The values for Na content was found higher than the reported values by Sotelo *et al.* (1989) and Tinalin and Hashmi (2008). Ranjit had 0.059 per cent of sodium. Oko *et al*. (2012) reported much higher sodium content with a wider range of 0.09-0.17 per cent for some Nigerian rice varieties. The variation might be mainly because of the differences in the genetic makeup of the rice cultivars and to certain extent geographical location, cultural practices adopted and the environmental factors.

Magnesium

Magnesium content of 100 rice cultivars used in the present study was found to vary between 0.039-0.049

per cent with the average of 0.044 per cent. The Mg content in rice cultivars was found to be higher than those reported by Tinalin and Hashmi (2008) and Sharma *et al.* (2012). Oko and Ugwu (2011) reported a higher range of magnesium content (0.19-0.26%) in some rice varieties from South East Nigeria. Zeng *et al.* (2004) reported average magnesium content for 653 accessions from core rice collection of Yunan to be 0.159 per cent. Check variety, Ranjit was statistically with 0.44 per cent magnesium content.

Calcium

The average calcium content for all the 100 cultivars used in the study was 0.030 percent with maximum in Kmj Bora-92 (0.036%) and minimum in Pokor Kola Bora (0.023%). The result is in good agreement with the results of Dutta and Baruah (1978) and Bhagabati (2000) who worked with glutinous rice varieties of Assam. However, there are several reports with much higher calcium content with a greater range (Oko and Ugwu, 2011; Oko *et al.*, 2012). Average calcium content for 465 glutinous rice landraces was reported to be 0.015 per cent against 0.013 per cent for non glutinous rice (Zeng *et al.*, 2004). The Ca content of Ranjit was found to be 0.028 per cent.

Zinc

In the present investigation, the range of Zn content in the rice cultivars was 2.103-4.66 mg/100 g with an average of 3.483 mg/100 g was almost similar with the findings of Jiang *et al.* (2007), Tinalin and Hashmi (2008). Tinalin and Hashmi (2008) reported that Zn content of husked rice was 2.52 to 3.42 mg/100 g in some Malaysian rice varieties. Thongbam *et al.* (2012) found the Zinc content to range from 1.33 to 3.42 mg/100 g in some indigenous rice cultivars from Tripura. Moreover, some Pakistani coarse rice varieties were also reported to have lower Zn content with a range between 1.44-2.97 mg/100 g (Anjum *et al.*, 2007). A comparable average Zn contents (3.68 mg/100 g) was reported by Zeng *et al.* (2004) for the glutinous rice landraces from Yunnan province. Ascheri *et al.* (2012) found Zn content in semi polished red rice grains to be 2-2.5 mg per 100 g. Zinc content in 100 rice cultivars was found to have significant positive correlation with Fe content and this was supported by earlier results (Abilgos *et al.*, 2002; Zeng *et al.,* 2004; Cheng *et al.*, 2006; Jiang *et al*., 2007). Ranjit had 3.12 mg/100 g of zinc.

Iron

The range of iron content in 100 rice cultivars (2.34-4.21 mg/100 g) was almost similar with the findings of Singh *et al*. (1998), Ahmed (2004) and Borua *et al.* (2004). A much lower range of iron content of 1.37-1.94 mg/100 g was reported by Anjum *et al.* (2007) for some Pakistani coarse rice varieties. The average iron content of 3.31 mg/100 g observed in the present study was much lower than the average value of 5.58 mg/ 100 g for the glutinous rice landraces of Yunnan province (Zeng *et al.*, 2004). Significantly positive correlations were recognized between Fe and Zn by many workers (Abilgos *et al.*, 2002; Zeng *et al.,* 2005; Cheng *et al.*, 2006; Jiang *et al*., 2007) which holds good for the present investigation also. These results suggested that high Fe content might be accompanied with high Zn contents of rice. The iron content of Ranjit was 2.94 mg/100 g.

Manganese

Manganese content of 100 rice cultivars was found in the range between 1.02-3.87 mg/100 g with an average of 2.277 mg/100 g. Stork *et al.* (2005) reported that the polished white rice had manganese content in the range of 0.7 to 2.0 mg/100 g. The average manganese contents of core collection, glutinous and non glutinous rice landraces of Yunnan province were reported as 1.52, 1.47 and 1.52 mg/100 g respectively (Zeng *et al.*, 2004). Anjum *et al.* (2007) reported a range of 1.57-2.33 mg/100 g of manganese for Pakistani coarse rice varieties. The Mn content of Ranjit was 2.684 mg/100 g.

Copper

The average copper content in 100 rice cultivars was 0.759 mg/100 g with highest in cultivar Kmj Bora-50 (1.64 mg/100 g) and the lowest in Kmj Bora-9 (0.4 mg/100 g). A wider and higher range of copper content (0.7 to 2.7 mg/100 g) in polished white rice was reported by Stork *et al.* (2005). Jiang *et al.* (2007) reported copper content in milled rice to vary between 0.3-2.5 mg/100 g. The glutinous and non glutinous rice landraces from Yunnan province had the average copper content as 1.58 and 1.7 mg/100 g, respectively (Zeng *et al.*, 2004). Thus, Assam cultivars were having lower copper contents as compared to rice from different sources. This difference might be because of the differences in the rice cultivars used for the studies. The Cu content of the check variety Ranjit was 1.08 mg/100 g.

Genetic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) provides reliable estimate of magnitude of genetic variability. Highest estimate of GCV and PCV was recorded for Cu, which indicate plentiful variability of Cu content for genetic improvement. Moderate estimate of GCV and PCV value were recorded for Mn, Ash, Zn, Fe, and Ca. The difference between GCV and PCV was less for all characters except P, K and Na, which indicate less influence of environment and greater role of genetic architecture on expression of these minerals. Therefore simple selection will be effective in genetic improvement of these minerals. High heritability coupled with high genetic advance were observed for Cu, Mn, Zn and Fe which indicate preponderance of additive genetic effect in control of these minerals and suggested the great chance of genetic improvement of these minerals based on phenotypic performance. Thus the variability found in the present study material could be utilized successfully in different breeding programs for the genetic improvement of existing high yielding varieties through backcross breeding and for the development of desirable genotypes through hybridization.

Genotypic Correlation among Different Minerals

The Table 3 has shown the correlation among different minerals (P, Fe, Mn, Cu, Zn, Na, K, Ca, and Mg) and their ash content in different rice genotypes analyzed. It has been found that there is a significant positive correlation in between ash content and Na. The P content was found to be positively correlated with K and Mg and negatively correlated with Zn. In rice, most of the seed P is found in the form of a mixed K–Mg salt of phytic acid in the aleurone layer and germ (Bryant *et al*., 2005), so one possible explanation of the positive P–Mg–K intercorrelations might be that their levels are all driven by phytate levels in the grain. There is a positive correlation observed between Fe with Zn. Significantly positive correlations were also recognized between Fe and Zn by many workers (Abilgos *et al.*, 2002; Zeng *et al.* 2005; Cheng *et al.*, 2006; Jiang *et al*., 2007) which holds good for the present investigation also. These results suggested that high Fe content might be accompanied with high Zn contents of rice. Mn was found negatively correlated with Cu .The Cu was found negatively correlated with Na and Ca.

The composition of all the minerals varied significantly among the rice cultivars used in the study. The mean mineral content values in brown rice of the cultivars were as follows: P>K>Na>Mg>Ca>Zn>Fe>Mn>Cu. There are reports on slightly different order of mean mineral content values in rice. Jiang *et al.* (2008) found an order of mean mineral content values for eight minerals in brown rice as K>Mg>Ca>Na>Zn>Fe>Mn>Cu.

In recent years, Jiang *et al.* (2007) observed that a significant correlations among the contents of some mineral elements in milled rice. Therefore, the indirect selection could be used for simultaneously improving the mineral elements contents of milled rice. A high genotypic variation has been observed among different parameters of genotypes studied in present investigation. However, the nutritional composition of rice also differs with nature of the soil, environmental conditions and fertilizers applied (Amissah *et al.,* 2003). Studies showed that agricultural practices could influence the nutrient composition of the rice grain, such as iron and zinc contents were influenced by nitrogen application and soil nature (Senadhira *et al.,* 1998). Thus, further investigation is necessary to analyze the mineral element content in milled rice of different genotypes grown in various environments.

It is implied that the genotypic variations provided opportunities to select materials with dense contents of mineral elements (Yang *et al.,* 1998; Gregorio *et al.,* 2002). The first step toward breeding rice cultivars with an enhanced elemental composition (or ionome) is to understand the genetic diversity in germplasm collections available to breeders (Shannon *et al.,* 2015).

Conclusions

Significant genetic variations for grain concentration of all 9 mineral elements were observed, but not a single germplasm was found superior over the others for the all nine mineral content studied. In this case, breeder can go for independent selection of genotype for parental line for a particular mineral for rice breeding programme.

Highest estimate of GCV and PCV was recorded for Cu, which indicate plentiful variability of Cu content for genetic improvement. High heritability coupled with high genetic advance were observed for Cu, Mn, Zn and Fe which indicate preponderance of additive genetic effect in control of these minerals and suggested the great chance of genetic improvement of these minerals based on phenotypic performance. Thus the variability among different land races found in the present investigation could be rich resource for incorporation into rice breeding programme.

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Assessment of Variability in Rice (*Oryza sativa* L.) Germplasm using Agro-Morphological and Quality Traits

Anjali Toppo*, NK Rastogi, AK Sarawgi and Sumitra Upendi
Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur-492012, Chhattisgarh

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The present study was carried out to characterize 47 rice germplasm accessions based on 58 agro-morphological and quality traits. Most of the studied traits showed a wide variation among the germplasm accessions except leaf auricle, leaf collar, leaf ligule, leaf shape of ligule and male sterility. All 47 accessions were found to be distinct on the basis of 53 agro-morphological and quality traits. Unique accessions for different morphological traits were found in Cross. 116, Gadakhuta, CGR: 7144, Kali muchh, Khira sar, Safri, Surmatia, IC-116076, Jhilli paragi, Jhingo, Maiphal jira III, Banki, Bangle, CGR: 7142, Ramti and Gedrei. Desirable accessions identified for the yield ancillary and quality traits were Bangle, Bangoli-1 (II), Ramti, Bankal (II), CGR: 7144, CGR: 7142, Kakadiha, Jhuna, Kanthdudgi and IC-132754. The accessions like Bangle, Banki and Kala jira had both high yield as-well-as better quality traits like kernel length and head rice recovery percentage. These germplasm accessions of rice can be used as phenotypically divergent sources for traits of interest in breeding programmes.

Key Words: Agro-morphological Traits, Characterization, Germplasm, Rice, Variability

Introduction

In any crop, germplasm is an important source of genetic variability. Characterization of germplasm is of great importance for current and future genetic improvement of the crop. Rice breeding strategy involves the collection of variable germplasm and selection of superior genotypes from the germplasm for utilizing them as a promising variety or in hybridization programme to develop a superior variety. Agro-morphological characterization of germplasm accessions is fundamental to provide information for plant breeding programme and is a tool for selecting varieties or lines based on agronomical, morphological, genetic or physiological characters (Ndour, 1998). The demand of germplasm is dynamic. One does not know what tomorrow's need may be and how far germplasm would fulfill them. The available diversity in the germplasm serves as an insurance against unknown future needs. The more the diversity is conserved and made available for future use, the better chance of fulfilling the future demand. Therefore, in the present study an attempt was made to study genetic variability in the indigenous rice germplasm accessions.

Materials and Methods

Forty seven rice (*Oryza sativa* L.) germplasm accessions including five checks were grown in randomized block design at Research-cum-Instructional Farm, IGKV, Raipur during *Kharif* 2015 (Table 1). Each entry was sown in single row at spacing of 20 cm between rows and 15 cm between plants. Crop was raised following recommended package of practices. Observations were recorded on five randomly chosen plants of each genotype per replication for quantitative traits. The qualitative traits were visually assessed according to the National Test Guidelines for DUS test in rice, which was developed by Indian Institute of Rice Research, Hyderabad (Shobha Rani *et al*., 2006). The observation of various characteristics was recorded at different stages of growth with appropriate procedures as per the DUS test guidelines of PPV & FR Act, 2001.

The traits studied were Coleoptile colour, Basal leaf: sheath colour, Leaf: intensity of green colour, Leaf: anthocyanin colouration, Leaf sheath: anthocyanin colouration, Leaf sheath: intensity of anthocyanin colouration, Leaf: pubescence of blade surface, Leaf: auricles, Leaf: anthocyanin colouration of auricles, Leaf: Collar, Leaf: anthocyanin colouration of collar, Leaf: ligule, Leaf: shape of ligule, Leaf: colour of ligule, Culm: attitude, Days to 50% flowering (days), Flag leaf: attitude of blade (early observation), Spikelet: density of pubescence of lemma, Male sterility, Lemma: anthocyanin colouration of keel, Lemma: anthocyanin

**Author for Correspondence: Email-anjali.toppo205@gmail.com*

Table 1. List of the 47 rice germplasm accessions

S.No.	Collector's No.	IC No.	Accessions name	Source
1	CGR:1814	IC-132751	Anjan	Mahasamund
2	CGR:1816	IC-132753	Anjan	Raigarh
3	CGR:1817	IC-132754	Anjan	Raipur
4	CGR:1818	IC-132755	Anjan	Raipur
5	CGR:1819	IC-132756	Bhata anjan	Mahasamund
6	CGR:1829	IC-132767	Anjaniya	Bemetara
7	CGR:1834	IC-132773	Anjaniya	Raipur
8	CGR:1835	IC-132881	Bangle	Raipur
9	CGR:1836	IC-132842	Bangoli-1	Raipur
10	CGR:1837	IC-132883	Bangoli-1 (II)	Raipur
11	CGR:1845	IC-132891	Bankal (II)	Dewas
12	CGR:1846	IC-132892	Banki	Bastar
13	CGR:6323	IC-125558	Kanak chudi	Bastar
14	CGR:6366	IC-125601	Cross. 116	Raigarh
15	CGR:6416	IC-125648	Deshi safri	Rajnandgaon
16	CGR:6644	IC-125878	Gada khuta	Bastar
17	CGR:6711	IC-125945	Gedrei	Raigarh
18	CGR:7133	IC-114277	Jhaler genda	Raigarh
19	CGR:7139	IC-114281	Jhili	Sarguja
20	CGR:7142	NA	Jhilli	Durg
21	CGR:7144	NA	Jhilli	Raipur
22	CGR:7159	IC-114289	Son jhilli	Raigarh
23	CGR:7168	IC-114295	Jhilli paragi	Raigarh
24	CGR:7176	IC-114303	Jhingo	Sarguja
25	CGR:7187	IC-114309	Jhumaki	Bastar
26	CGR:7189	IC-114311	Jhuna	Sarguja
27	CGR:7209	IC-114325	Kala jira	Raigarh
28	CGR:7210	NA	Kanak jira	Durg
29	CGR:7211	IC-114326	Maiphal jira III	Bastar
30	CGR:7306	IC-114362	Kakadiha	Raipur
31	CGR:7367	IC-114403	Kali muchh	Muraina
32	CGR:7472	IC-114470	Kanthdudgi	Raigarh
33	CGR:7565	IC-114505	Kera ghul	Raigarh
34	CGR:7593	IC-114518	Ketaki 11	Sarguja
35	CGR:7629	IC-114539	Khira sar	Sarguja
36	CGR:7634	IC-114543	Khira sar	Sarguja
37	CGR:9186	NA	Ramti	Bastar
38	CGR:9281	IC-115592	Safri	Raipur
39	CGR:9622	IC-11511	Sulthu	Mandla
40	CGR:9671	NA	Surmatia	Raipur
41	CGR:9896	IC-116003	Baronda off type V	Bastar
42	CGR:10007	IC-116076	–	–
43	Check 1		Maheshwari	Raipur (IGKV)
44	Check 2		Jaldubi	Raipur (IGKV)
45	Check 3		Rajeshwari	Raipur (IGKV)
46	Check 4		Indira aerobic 1	Raipur (IGKV)
47	Check 5		Samleshwari	Raipur (IGKV)

colouration of area below apex, Lemma: anthocyanin colouration of apex, Spikelet: colour of stigma, Stem thickness, Stem: length (excluding panicle), Stem: anthocyanin colouration of nodes, Stem: intensity of anthocyanin colouration of nodes, Stem: anthocyanin colouration of internodes, Panicle: length of main axis, Flag leaf: attitude of blade (late observation), Panicle: curvature of main axis, Panicle: number per plant, Spikelet: colour of tip of lemma, Lemma and palea: colour, Panicle: awns, Panicle: presence of secondary

branching, Panicle: secondary branching, Panicle: attitude of branches, Panicle: exertion, Leaf: senescence, Sterile lemma: colour, Grain: phenol reaction of lemma, Grain: weight of 1000 fully developed grains, Grain: length, Grain: width, Decorticated grain: length, Decorticated grain: width, Decorticated grain: shape, Decorticated grain: colour, Endosperm: content of amylose, Decorticated grain: aroma, grain yield per plant, kernel length, kernel length breadth ratio, kernel length after cooking, cooked kernel length breadth ratio, head rice recovery percentage and elongation ratio. Frequency distribution was computed to categorize the accession into different classes. Simple statistics (means, ranges) was calculated to have an idea of the level of variation.

Results and Discussion

To establish distinctness among rice germplasm accessions, 58 qualitative and quantitative characters were studied. Qualitative characters are considered as morphological markers in the identification of landraces of rice, because they are less influenced by environmental changes (Raut, 2003). Frequency distribution for agro-morphological characters in 47 rice germplasm accessions is presented in Table 2.

Morphological Characterization

Qualitative characters are important for plant description (Kurlovich, 1998) and mainly influenced by the consumers preference, socio-economic scenario and natural selection (Hien *et al.,* 2007). Most of the morphological characters showed variation in different accessions except Leaf: auricle, Leaf: collar, Leaf: ligule, Leaf : shape of ligule and male sterility. A majority of accessions were found to possess Coleoptile: colour (43% colourless), Basal leaf: sheath colour (60% green), Leaf: intensity of green colour (62% medium green), Leaf: anthocyanin colouration (60% absent), Leaf sheath: anthocyanin colouration (53% absent), Leaf sheath: intensity of anthocyanin colouration (50% strong), Leaf: pubescence of blade surface (51% strong), Leaf: anthocyanin colouration of auricles (85% colourless), Leaf: anthocyanin colouration of collar (85% absent), Leaf: colour of ligule (89% white), Culm: attitude (55% semi-erect), Flag leaf: attitude of blade early observation (55% erect), Spikelet: density of pubescence of lemma (47% medium), Lemma: anthocyanin colouration of keel (51% absent/very weak), Lemma: anthocyanin colouration of area below apex (73% absent), Lemma: anthocyanin colouration of apex (74% absent), Spikelet: colour of stigma (72% white), Stem: thickness (68% medium), Stem: length (36% long), Stem: anthocyanin colouration of nodes (83% absent), Stem: intensity of anthocyanin colouration of nodes (100% medium), Stem: anthocyanin colouration of internodes (68% absent), Flag leaf: attitude of blade late observation (55% semi-erect), Panicle: curvature of main axis (60% semi-straight), Panicle: number per plant (32% few), Spikelet: colour of tip of lemma (58% white), Lemma and palea: colour (36% straw and brown furrows on straw), Panicle: awns (87% absent), Panicle: presence of secondary branching (91% present), Panicle: secondary branching (58% weak), Panicle: attitude of branches (55% erect), Panicle: exertion (70% well exerted), Leaf: senescence (87% medium), Sterile lemma: colour (90% straw), Grain: phenol reaction of lemma (62% absent), Grain: weight of 1000 fully developed grains (41% low), Grain: length (57% short), Grain: width (53% medium), Decorticated grain: length (45% medium), Decorticated grain: width (57% medium), Decorticated grain: shape (51% long bold), Decorticated grain: colour (55% white), Endosperm: content of amylose (70% high) and Decorticated grain: aroma (94% absent). Similar type of work was also reported by Bisne and Sarawgi (2008), Das and Ghosh (2011), Moukoumbi *et al.* (2011). Parikh *et al.* (2012), Subba Rao *et al.* (2013), Sarawgi *et al*., (2014), Sinha *et al*. (2015), Kumar *et al*. (2016) and Singh *et al*. (2016). Based on the morphological descriptors 47 accessions were classified based on 51 characters.

In the present study some of the unique accessions with distinct features were recorded (Table 3).Unique accessions like Cross. 116, Gadakhuta and CGR: 7144 for purple line basal leaf sheath colour; Cross. 116 and Jaldubi for medium intensity of anthocyanin colouration of leaf sheath; Kali muchh, Khira sar, Jaldubi and Samleshwari for very strong pubescence of leaf blade surface; Safri, Surmatia and IC- 116076 for open culm attitude; Jhilli paragi, Jhingo and Maiphal jira III for very strong spikelet density of pubescence of lemma; Banki for lemma anthocyanin colouration of keel, lemma anthocyanin colouration of area below apex and lemma anthocyanin colouration of apex; Bangle for weak lemma anthocyanin colouration of apex; CGR: 7142 for red spikelet: colour of tip of lemma; IC-116076 for gold and gold furrows on straw background of lemma and palea colour; Banki for reddish to light purple lemma and palea colour; Ramti for purple furrows on straw

Table 2. Frequency distribution of agro-morphological and quality characters of forty seven germplasm accessions of rice

S.No.	Characteristics	States	No. of accessions	Frequency (%)
1.	Coleoptile: Colour	Colourless	20	43
		Green	15	25
		Purple	12	32
2	Basal leaf: Sheath colour	Green	28	60
		Light purple	7	15
		Purple lines	3	6
		Uniform purple	9	19
3.	Leaf: Intensity of green colour	Light	5	10
		Medium	29	62
		Dark	13	28
4.	Leaf: Anthocyanin colouration	Absent	28	60
		Present	19	40
5.	Leaf Sheath: anthocyanin colouration	Absent	25	53
		Present	22	47
6.	Leaf sheath: Intensity of anthocyanin colouration	Very weak	0	0
		Weak	6	27
		Medium	2	9
		Strong	11	50
		Very strong	0	14
7.	Leaf; pubescence of blade surface	Absent	0	0
		Weak	8	17
		Medium	11	23
		Strong	24	51
		Very strong	4	9
8.	Leaf: Auricles	Absent	0	0
		Present	47	100
9.	Leaf: Anthocyanin colouration of auricles	Colourless	40	85
		Light purple	0	0
		Purple	7	15
10.	Leaf: collar	Absent	0	0
		Present	47	100
11.	Leaf: Anthocyanin colouration of collar	Absent	40	85
		Present	7	15
12.	Leaf: Ligule	Absent	0	0
		Present	47	100
13.	Leaf: Shape of Ligule	Truncate	0	0
		Acute	0	0
		Split	47	100
14.	Leaf: Colour of Ligule	White	42	89
		Light purple	0	0
		Purple	5	11
15.	Culm: Attitude	Erect	17	36
		Semi-erect	26	55
		Open	3	7
		Spreading	1	2
16.	Time of heading (50% plants with panicles)	Very early	0	0
		Early	0	0
		Medium	35	74
		Late	12	26
		Very late	0	0
17.	Flag leaf: attitude of blade (early observation)	Erect	26	55
		Semi-erect	21	45
		Horizontal	0	0
		Drooping	0	0
18.	Spikelet: Density of pubescence of lemma	Absent	0	0
		Weak	11	24
		Medium	22	47
		Strong	11	23
		Very strong	3	6

S.No.	Characteristics	States	No. of accessions	Frequency (%)
19.	Lemma: Anthocyanin colouration of keel	Absent or very weak	24	51
		Weak	8	17
		Medium	8	17
		Strong	6	13
		Very strong	1	2
20.	Lemma: Anthocyanin colouration of area below apex	Absent	34	73
		Weak	8	17
		Medium	2	4
		Strong	2	4
		Very strong	1	2
21.	Lemma: Anthocyanin colouration of apex	Absent	34	73
		Weak	8	17
		Medium	2	4
		Strong	2	4
		Very strong	1	2
22.	Spikelet: colour of stigma	White	34	72
		Light green	0	0
		Yellow	0	0
		Light purple	0	0
		Purple	13	28
23.	Stem: length	Very short	4	8
		Short	0	0
		Medium	12	26
		Long	17	36
		Very long	14	30
24.	Stem: Anthocyanin colouration of nodes	Absent	39	83
		Present	8	17
25.	Stem: Intensity of anthocyanin colouration of nodes	Weak	0	0
		Medium	8	100
		Strong	0	0
26.	Stem: Intensity of anthocyanin colouration of internodes	Absent	32	68
		Present	15	32
27.	Panicle: length of main axis	Very short	0	0
		Short	3	6
		Medium	24	51
		Long	14	30
		Very long	6	13
28.	Flag leaf: Attitude of blades (late observation)	Erect	12	26
		Semi-erect	26	55
		Horizontal	9	19
		Deflexed	0	0
29.	Panicle: Curvature of main axis	Straight	17	36
		Semi-Straight	28	60
		Deflexed	1	2
		Dropping	1	2
30.	Panicle: number per plant	Few	68	32
		Medium	32	15
		Many	0	0
31.	Spikelet: colour of tip of lemma	White	27	58
		Yellowish	2	4
		Brown	3	6
		Red	1	2
		Purple	14	30
		Black	0	0

Table 2 Contd.

S.No.	Characteristics	States	No. of accessions	Frequency (%)
32.	Lemma and palea: colour	Straw	17	36
		Gold and gold furrows on straw background	1	2
		Brown spots on straw	7	15
		Brown furrows on straw	17	36
		Brown (tawny)	3	7
		Reddish to light purple	1	2
		Purple spots/ furrows on straw	1	2
		Purple	0	0
		Black	0	0
33.	Panicle: Awns	Absent	41	87
		Present	6	13
34.	Panicle: Presence of secondary branching	Absent	4	9
		Present	43	91
35.	Panicle: secondary branching	Weak	25	58
		Strong	12	28
		Clustered	6	14
36.	Panicle: attitude of branches	Erect	26	55
		Erect to semi erect	7	15
		Semi-erect	12	26
		Semi erect to spreading	2	4
		Spreading	0	0
37.	Panicle: Exertion	Partly exerted	0	0
		Mostly exerted	14	30
		Well exerted	33	70
38.	Sterile lemma: colour	Straw	42	89
		Gold	4	9
		Red	0	0
		Purple	1	2
39.	Grain: Weight of 1000 fully developed grains	Very low	3	6
		Low	19	41
		Medium	16	34
		High	8	17
		Very high	1	2
40.	Grain: Length	Very short	0	0
		Short	27	57
		Medium	20	43
		Long	0	0
		Very long	0	0
41.	Grain: Width	Very narrow	0	0
		Narrow	17	36
		Medium	25	53
		Broad	5	11
		Very broad	0	0
42.	Decorticated grain: length	Short	12	25
		Medium	21	45
		Long	13	28
		Extra long	1	2
43.	Decorticated grain: width	Narrow	4	9
		Medium	27	57
		Broad	16	34
44.	Decorticated grain: shape (in lateral view)	Short slender	1	2
		Short bold	14	30
		Medium slender	1	2
		Long bold	24	51
		Long slender	7	15
		Extra Long slender	0	0

Table 2 Contd.

S.No.	Characteristics	States	No. of accessions	Frequency (%)
45.	Decorticated grain: colour	White	26	55
		Light brown	15	32
		Variegated brown	0	0
		Dark brown	4	9
		Light red	0	0
		Red	2	4
		Variegated purple	0	0
		Purple	0	0
		Dark purple	0	0
46.	Endosperm: content of amylose	Very low	0	0
		Low	3	6
		Medium	11	24
		High	33	70
		Very high	0	0
47.	Decorticated grain: Aroma	Absent	44	94
		Present	3	6

Table 3. Unique accessions for different morphological traits

S.No.	Morphological characters	Colour pattern/ type	Unique accessions
1	Basal leaf sheath colour	Purple lines	Cross. 116, Gada khuta, CGR:7144
2	Leaf sheath intensity of anthocyanin colouration	Medium	Cross. 116, Jaldubi
3	Leaf pubescence of blade surface	Very strong	Kali muchh, Khira sar, Jaldubi, Samleshwari
4	Culm attitute	Open	Safri, Surmatia, IC-116076
5	Spikelet density of pubescence of lemma	Very strong	Jhilli paragi, Jhingo, Maiphal jira
6	Lemma anthocyanin colouration of keel	Very strong	Banki
7	Lemma anthocyanin colouration of area below apex	Very strong	Banki
8	Lemma anthocyanin colouration of apex	Very strong	Banki
		Weak	Bangle
9	Panicle: Curvature of main axis	Deflexed	Rajeshwari
		Drooping	Samleshwari
10	Spikelet: colour of tip of lemma	Red	CGR: 7142
11	Lemma and palea colour	Gold and gold furrows on straw background	IC-116076
		Reddish to light purple	Banki
		Purple furrows on straw	Ramti
12	Decorticated grain length	Extra long	Maheshwari
13	Decorticated grain shape	Medium slender	Ramti
		Short slender	Surmatia
14	Decorticated grain colour	Red	Gada khuta, Gedrei

of lemma and palea colour; Maheshwari for extra long decorticated grain length; Ramti for medium slender decorticated grain shape; Surmatia for short slender decorticated grain shape; and Gada khuta, Gedrei for red colour decorticated grain may be utilized in hybridization programme to provide morphological markers in transgressive segregants towards development of new rice varieties which is essentially required for novelty.

Agronomical Characterization

Rice accessions were evaluated for agronomical traits *viz.,* days to 50% flowering, Panicle: length of main axis, Panicle: number per plant, Time of maturity, Grain: weight of 1000 fully developed grains, Grain: length, Grain: width and grain yield per plant from five randomly selected plants of each entry.

Days to 50% Flowering: It had mean value of 106.84 days and range of 92-122 days. All the accessions fall

in the range of medium to late group. Samleshwari (92 days) had minimum days to 50% flowering followed by Bangle (95 days).

Panicle Length: It exhibited reasonable amount of variation with range values of 19.70-32.52 cm. The average panicle length was 26.15 cm. Most of the accessions fall under the range of 21-25 cm panicle length. The maximum panicle length was observed in Indira aerobic 1 (32.52 cm) followed by Bangoli-1 (II) (32.21 cm). Although it contributes positively yet maximum panicle length is not the only factor responsible for higher grain yield (Abbasi *et al.,* 1995). So, panicle length alone does not determine the high grain yield as traits such as grain size, grain shape, higher number of tillers/plant, longer panicles and greater number of grains/panicle ultimately contribute to higher grain yield (Akram *et al.,* 1994).

Number of Panicles Per Plant: It is another yield attributing trait (Abbasi *et al.,* 1995). A great variability with high range (6.32-14.78) and mean value of 9.84 was exhibited for number of panicles/plant. Ramti had maximum number of panicles (14.78).

Days to Maturity: It exhibited high range (120-150 days) with a mean of 135.21 days Samleshwari had shortest maturity period (120 days). Most of the accessions fall under medium followed by late duration.

Thousand Grain Weight: It is also a yield attributing trait (Abbasi *et al.,* 1995). Most of the accessions were in the range of 21-25 g. Accessions with very high (>30 g) and very low (<15) grain weight were also observed. Rajeshwari (30.91 g) had maximum 1000 grain weight followed by Maheshwari (29.96 g) and Bangle (29.23 g).

Grain Length: Grain length is an important quality parameter. Rice grain can be classified as very long, long, medium, short and very short. It exhibited high range (6.03-10.00 mm) with a mean of 8.12 mm. Accession CGR:7144 (10.00 mm) was found with maximum grain length followed by Maheshwari (9.98 mm) and Kakadiha (9.92 mm).

Grain Width: It exhibited range (2.27-3.37 mm) with mean of 2.71 mm. Most of the accessions fall under medium followed by narrow grain width. Cross. 116 was observed with maximum grain width (3.37 mm) while Bankal (II) had narrow grain width (2.27 mm).

Grain Yield Per Plant: It varied from 20.51 to 34.55 g with a mean value of 28.14 g. Rajeshwari (34.55 g) was observed with maximum grain yield per plant followed by Bangle (34.40 g) and Banki (33.93 g).

After evaluation of 47 accessions for important quantitative characters, on the basis of mean values, desirable accessions were identified for the yield and its component traits (Table 4). Accessions found desirable for different traits were Bangle for days to 50% flowering (earliness) and grain yield per plant; Bangoli-1 (II) for panicle length; Ramti for panicle number per plant; Bangle for 1000 grain weight; CGR: 7144 for grain length and Bankal (II) for grain width. These germplasm accessions for different agronomical characters in phenotypically divergent sources would help in prebreeding and breeding programs.

Quality Characterization

Rice accessions were evaluated for quality traits *viz.,* kernel length, kernel length breadth ratio, kernel length after cooking, cooked kernel length breadth ratio, head rice recovery percentage, elongation ratio and amylose content.

Kernel Length: It showed variation from 3.70 to 6.77 mm with a mean value of 5.19 mm. Bankal II was

Table 4. Desirable rice accessions for yield ancillary traits

S. No.	Days to 50% flowering (earliness)	Panicle length (cm)	Panicle no. per plant	1000 grain weight (g)	Grain length (mm)	Grain width (mm)	Grain yield per plant (g)
1	Samleshwari (92.00)	Indira aerobic 1 (32.52)	Ramti (14.78)	Rajeshwari (30.91)	CGR:7144 (10.00)	Bankal (II) (2.27)	Rajeshwari (34.55)
2	Bangle (95.00)	Bangoli-1 (II) (31.23)	Indira aerobic 1 (13.44)	Maheshwari (29.96)	Maheshwari (9.98)	Safri (2.30)	Bangle (34.40)
3	Bangoli-1 (98.00)	Safri (31.20)	Safri (13.34)	Bangle (29.23)	Kakadiha (9.92)	Jhilli paragi (2.32)	Banki (33.93)
4	IC-132751 (99.00)	IC-132773 (30.40)	Sulthu (12.78)	Kala jira (29.03)	Bangoli-1 (II) (9.53)	Surmatia (2.32)	Kala jira (33.87)
5	IC-132753 (99.00)	Bhata anjan (30.37)	Jhumaki (12.66)	Cross. 116 (28.98)	Kera ghul (9.52)	Bangoli-1 (II) (2.37)	Maheshwari (33.53)

Table 5. Desirable rice accessions for quality traits

S. No.	Kernel length (mm)	Kernel length breadth ratio	Kernel length after cooking (mm)	Cooked kernel length breadth ratio	Elongation ratio	Head rice recovery %	Amylose content (%)
1	Bankal (II) (6.77)	Bankal (II) (3.03)	Rajeshwari (10.10)	Kakadiha (3.22)	IC-132754 (2.91)	Jhuna (58.35)	Kanthdudgi (20.35)
2	Bangle (6.67)	Kali muchh (2.99)	CGR:7142 (10.00)	Baronda off type V (3.01)	IC-132767 (2.84)	Jhingo (57.66)	Rajeshwari (21.19)
3	Bangoli-1 (II) (6.57)	Bangoli-1 (II) (2.94)	CGR:7144 (9.63)	Ketaki 11 (2.92)	Bhata anjan (2.79)	CGR:7142 (56.18)	Khira sar (21.42)
4	Maheshwari (6.44)	Jhilli paragi (2.91)	Baronda off type V (9.63)	Kanak chudi (2.92)	IC-132751 (2.79)	Kali muchh (54.28)	Jhingo (21.75)
5	Banki (6.43)	Kanak chudi (2.86)	Kanak chudi (9.43)	IC-116076 (2.90)	IC-132755 (2.76)	Kala jira (54.20)	Baronda off type V (22.51)

observed for maximum kernel length(6.77 mm) followed by Bangle (6.67 mm) and Bangoli-1 (II) (6.57 mm).

Kernel Length Breadth Ratio: It ranged from 1.65 to 3.03 with a mean value of 2.39. Bankal II (3.03) was observed for maximum kernel length breadth ratio followed by Kali muchh (2.99), Bangoli-1 (II) (2.94) and Jhilli paragi (2.91).

Kernel Length after Cooking: It showed variation from 6.03 to 10.10 mm with a mean value of 8.15 mm. Rajeshwari (10.10 mm) was observed for maximum kernel length after cooking followed by CGR: 7142 (10.00 mm).

Cooked Kernel Length Breadth Ratio: It ranged from 2.03 to 3.22 with a mean value of 2.53. The maximum cooked kernel length breadth ratio was found in Kakadiha (3.22) followed by Baronda off type V (3.01).

Elongation Ratio: It varied from 1.31 to 2.91 with a mean value of 1.93. IC-132754 (2.91) had maximum elongation ratio followed by IC-132767 (2.84).

Head Rice Recovery Percentage: It varied from 32.66 to 58.35 % with a mean value of 43.70 per cent. The maximum head rice recovery percentage was found in Jhuna (58.35%) followed by Jhingo (57.66%).

Amylose Content: It ranged from 14.88 to 30.58% with a mean value of 26.19 per cent. The intermediate amylose content being desirable was recorded in Kanthdudgi (20.35%) followed by Rajeshwari (21.19%), Khira sar (21.42%), Jhingo (21.75%) and Baronda off type V (22.51%).

After evaluation of 47 accessions for important quality traits, on the basis of mean values, desirable accessions were identified for the quality (Table 5). Accessions found desirable for important quality traits were Bankal (II) for kernel length and kernel length breadth ratio; CGR: 7142 for kernel length after cooking; Kakadiha for cooked kernel length breadth ratio; IC-132754 for elongation ratio; Jhuna for head rice recovery percentage; and Kanthdudgi for amyolse content.

The accessions like Bangle, Banki and Kala jira having high yield were also better in quality traits like kernel length and head rice recovery percentage.

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Weed Floral Diversity of Medicinal Value in Terraces of Horticulture Crop Fields in Bharsar, Uttarakhand, India

Anand Singh Bisht*
Department of Basic Sciences & Humanities, VCSG Uttarakhand University of Horticulture and Forestry, Bharsar, Pauri Garhwal-246123, Uttarakhand, India

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An ethnobotanical survey was conducted in order to identify the medicinal weed flora of horticulture crop fields in University Campus, Bharsar, Pauri Garhwal (located at an elevation, of 1950 m in northwest Garhwal Himalaya of Uttarakhand) and to find out the possibilities of utilizing these weeds. The information about the traditional potential uses of species was collected with the help of reference literature of different medicine systems. The study revealed that 117 species of weeds belonging to 98 genera and 43 families in crop fields, possessed medicinal properties. The study suggested a tremendous scope of utilising these weeds to promote additional income to the inhabitants.

Key Words: Biodiversity, Ethnobotany, Garhwal Himalaya, Medicinal plants, Traditional use

Introduction

The Himalaya represents one of the most important mega-centres of the biodiversity, sharing over fifty percent of the vegetational wealth of the Indian subcontinent. In the recent past there has been a deep concern and awareness for the conservation of the fragile Himalayan ecosystem. The diversity, copiousness as well as uniqueness of the plant components in various habitats have retained sound and maintained the aesthetic environment and the serenity of the Himalaya. However, in the recent past couple of years, excessive exploitation of vegetation, unplanned landuse, natural disasters and several developmental processes accelerated deterioration of threatened biodiversity and harmony of the Himalaya ecosystem (Atkinson, 1982; Burkill, 1965; Bisht, 2005).

Garhwal Himalaya possesses luxuriant and varied vegetation within the Himalaya region. Almost every plant has economic value as nutrition, aesthetic or medicine. In fact, a large percentage of crude drugs in the Indian market come from this Himalayan area (Badoni, 1989). According to cumulative evidence, the Garhwal Himalaya has more than 3,500 species of flowering plants, confined to most of which are in forest and alpine meadows. In India out of an estimated 15000-16000 flowering plant species, about 1,500 (10%) have already come under the various categories of threatened plants. The same number of species is used in Indian traditional system of medicine, that is, 600 species with more than 8,000 herbal remedies in Ayurvedic, 500 species in Unani, and 550 species in phyto-pharmaceutical industries. Nearly thirty species from the Garhwal Himalaya have been listed in various categories under threat in the India Red Data Books of which 24 species are from high altitude alpine regions (Rao, 1994; Nautiyal *et al*., 1996; Dhar *et al*., 2002). Several dedicated workers took interest in this region for the collection conservation of medicinal and aromatic plants in past even before 19th century. The ethno-botanical account of Garhwal Himalaya reveals that majority of traders used to collect wild medicinal plants from alpine and sub-alpine zone especially before the onset of seed setting through untrained and unskilled labours and exploited to the plains from higher altitude and export them (Negi *et al.*, 1999). This has led to the unscientific extraction of entire plants. In addition, the over-exploitation changed the environmental conditions and original habitats that have led to gradual loss of plants. In many of the species the exploitation pressure has gone to the extent that these are at the verge of extinction and therefore has been declared as threatened, rare, vulnerable, or endangered depending on the frequency in the nature (Joshi *et al*., 1997).

Plants are rich source of many natural products. From ancient time man has used several plants in attempt to cure diseases and relieve pain. Comparatively few drug plants are cultivated. Most of the supply of

*Author for Correspondence: Email- drbishtas@gmail.com

drugs is obtained from the wild plants. The medicinal value of drug plants is due to the presence of certain chemical substances in plants. In this paper 117 species of weed with medicinal value have been documented based on study undertaken in Bharsar, Pauri Garhwal, Uttarakhand.

Material and Methods

Study Area

The present study was carried out in the temperate regions of Bharsar area (Uttarakhand University of Horticulture and Forestry, covering about 175 hectare areas). Bharsar is situated at about 57 Km from the district Headquarters, Pauri Garhwal on the Pauri-Thalisain-Ram Nagar National Highway 121. The meaning of Bharsar in local dialect is 'Flourished with natural wealth'. Since the ancient time, it is famous for vast biodiversity of temperate vegetation. Owing to favourable environment for horticulture education, Uttarakhand University of Horticulture and Forestry has been established recently (28th April, 2011) here. The district Pauri Garhwal is most fascinating segments of the Himalaya, stretches from the Ram Ganga River that separates Pauri-Kumaon border in the East and to the Ganga demarcating the western border.

Soil

Soil texture, colour and nature represent wide range of variations, depending upon geology, altitude, slope, climate, vegetation and biological and soil chemistry of particular site. In general, the soil is deep clay-loam, slightly acidic and rich in potassium, medium in phosphorous and nitrogen contents, with the exception of some cultivated fields.

Climate

In general, the climate of the Bharsar represents mild summer, higher precipitation and prolonged cold winter season. The climatic factors such as precipitation, temperature, relative humidity and wind, in association with elevation, slope aspects, drainage, vegetation, etc. are responsible for the micro-climate of this area. Generally, days of Bharsar are fairly warm followed by cool nights. The area receives adequate sunshine hours whereas the growing period is shorter due to long winter. The area also receives heavy precipitation during monsoon and occasional snow fall during winter season.

Survey

The present investigation was a result of extensive and intensive field surveys, conducted during November 2013 to April 2015. The specimens were collected by usual methods of collection, preservation and maintenance of specimen in the herbarium with field notes. The collected specimens were identified with the help of recent and relevant floras *i.e* Naithani (1985), Gaur (1999). The specimens deposited at HNB Garhwal University Herbarium (GUH), Srinagar. Information on medicinal properties and qualities of various plant species have been gathered through personnel interview with the local inhabitants and also concern with different literatures. Usually the information collected from the local *vaidyas* or medicinal practitioners; however occasionally the information was also recovered by housewives, rural old folk, and grazers of long experience.

Result and Discussion

The study revealed that out of 169 problematic weeds, 117 weeds were of medicinal importance and used against many diseases. Medicinally important weeds of the study site comprises total 117 species respectively of 43 families, 113 species of dicotyledons (39 families) and 4 species of monocotyledons (4 families) collected during the study period. Out of 43 families, Asteraceae contributed maximum share 17.95 % (21 species), followed by Lamiaceae 9.41 % (11 species), Rosaceae 7.70 % (9 species), and other families make 64.94 % of total flora in study area during study period.

All these weeds are arranged alphabetically by their botanical name, family name; local name and mode of usage (summarized in Table 1). These weeds grow along with the crop plants and are regarded as nuisance for crops, but are the boon to the pharmaceutical industries as these weeds yield chemicals used in formulation of various important drugs. These are also used by *vaidyas* for preparing various herbal formulations (Samant *et al*., 1998, 2001).

Due to lack of awareness about medicinal importance of these weeds they are discarded by the farmers. These weeds can become an additional source of income for the farmers, if they are made aware of the medicinal importance.

The study area is rich in biodiversity corresponds to the climate and topography of temperate vegetation ranging from 1500-2200 m altitude, respectively. Different factors have influenced (lower or exceeded) the normal limit of vegetation type and flowering seasons.

Table 1. Enumeration of Medicinal Weed Flora and Their Traditional Uses

S.No.	Botanical name	Local/ vernacular name	Family	Uses
1	*Achyranthes bidentata* Bl.	Chicheree, Latjira	Amaranthceae	Root infusion taken in malarial fever. Leaf extract supposed to facilitate delivery, used in dropsy and bronchitis.
2.	*Agrimonia pilosa* Ledebour	Lesukuria	Rosaceae	Plant decoction given in cough and diarrhoea, root paste with mustard oil applied round the belly in suppressed urination.
3.	*Ainsliaea latifolia* (D.Don). Schultz.	Kauru	Asteraceae	Decoction of roots given in colic.
4.	*Ajuga bracteosa* Wall. ex Benth.	Neelkanthi	Lamiaceae	Leaf extract used in malarial fever, bitter plant extract is used as a tonic, astringent and febrifuge.
5.	*Anaphalis contorta* (D.Don) Hk.	Bugla	Asteraceae	Paste of heads and leaves applied on cuts wounds.
6.	*Anaphalis adnata* Wallich	Bugla	Asteraceae	Paste of head and leaves applied on cuts, wounds and boils.
7.	*Anemone obtusiloba* D.Don.	Kanchphool, Kakrya	Ranunculaceae	Roots and leaf paste applied externally on ringworm and eczema in folk medicine.
8.	*Anemone rivularis* Buch-Ham.	Mirchilee	Ranunculaceae	Paste of leaves applied externally on forehead in headache. Leaf juice applied on wound, sores, and earache in local therapy.
9	*Artemisia capillaris* Thunb.	Jhirun	Asteraceae	Decoction of leaves taken as a bitter tonic for worms and colic, twigs used as brooms.
10.	*Artemisia roxburghiana* Wall. ex Besser	Kunjaa	Asteraceae	Plant extract antipyretic, tonic and also rubbed on skin allergy.
11.	*Asparagus racemosus* Willd.	Satavari	Liliaceae	Root aphrodisiac, antiseptic, refrigerant often used with fresh water or milk.
12.	*Aster peduncularis* Wall. ex Nees.	Phulyan	Asteraceae	Extract of plant useful to dissolve renal-calculi and root powder as stomachic.
13.	*Astragalus leucocephalus* Graham ex Benth.	Rudravanti	Fabaceae	Roots are used as blood purified and in skin diseases; plant infusion as tonic, leaves used as fodder.
14.	*Barleria cristata* L.	Saundi, Kala-bansa	Acanthaceae	Root decoction used against bronchitis and pneumonia, leaves and root paste applied on wound-swelling, root chips added to local beverages, seeds regarded as antidote to snake bite.
15.	*Begonia picta* Smith	Pattharchatta	Begoniaceae	Decoction of plant in boiled water given in colic and dyspepsia.
16.	*Berberis aristata* DC.	Kingore	Berberidaceae	Juice from bark of stem or root often known as 'Rasaut' often dropped in ophthalmia. Infusion of root given in fever. Fruits edible, bark yields yellow dye.
17.	*Berberis asiatica* Roxb. ex DC.	Kilmora	Berberidaceae	Roots inflammation and stomachache.
18.	*Bergenia ciliata* (Har.) Sternb.	Silpari, Pasanbhed	Saxifragaceae	The leaves and root given to the patient of kidney stone.
19.	*Bidens pilosa* L.	Kumra	Asteraceae	Plant extract with honey used in cough and bronchitis.
20.	*Bistorta amplexicaul* D.Don.	Kutrya	Polygonaceae	Decoction of plant said to cause abortion if taken orally. Leaf paste applied on wounds and extract to relive dysentery
21.	*Boenninghausenia albiflora* (Hk.) Reichb. ex Meisn.	Pissumar, Upanya Ghass	Rutaceae	Leaf paste applied on cuts and wounds, root powder used as antiseptic and juice given in vomiting and dysentery.
22.	*Bupleurum hamiltonii* Balakrishnan	Singu	Apiaceae	Roots used in stomach and liver disorders and plant browsed by cattle.
23.	*Callicarpa macrophylla* Vahl.	Daiya	Verbenaceae	Fruits useful in oral aphthae, leaves after heating applied externally on rheumatic pain

Contd.

S.No.	Botanical name	Local/ vernacular name	Family	Uses
24.	*Chenopodium album* L.	Bathua	Chenopodaceae	Leaves used as pot–vegetable; breads prepared from the grinned grains.
25.	*Clematis barbellata* Edgew	Kanguli, Lagulia	Ranunculaceae	Leaves supposed to be poisonous to cattle, leaf paste externally applied for skin ailments.
26.	*Clematis montana* Buch.-Ham. ex DC	Kujju	Ranunculaceae	Leaf extract given to cure diabetes and urinary troubles.
27.	*Clinopodium umbrosum* (M. Bieb.) C. Koch	Birchee	Lamiaceae	Plant extracts used as an astringent, carminative and as blood purifier, leaves infusion used in gastric troubles and flowers as a source of bee-forage.
28.	*Coccinia grandis* (L.) Voigt	Kaduri	Cucurbitaceae	Leaves and root juice given in diabetes, leaves also supposed to be antiseptic; fruit juice given in gonorrhea.
29.	*Corydalis cornuta* Royle	Indra-Jata	Fumariaceae	Aqueous paste of roots taken to reduce body swelling and inflammations root juice given in fever.
30.	*Cotoneaster microphyllus* Wall. ex Lindley	Bugarchilla	Rosaceae	Leaf extract and fruits given in diarrhoea, root paste applied on cuts and wounds.
31.	*Crotalaria albida* Heyne ex Roth	Chunchuni	Fabaceae	Roasted seed powder taken as blood purifier and roots chewed in constipation.
32.	*Crotalaria medicaginea* Lam.	Ghunghunia	Fabaceae	Leaf juice applied in scabies and urticaria.
33.	*Cucumis hardwickii* Royle.	Elaroo	Cucurbitaceae	Decoction of root barks given and fevers; seeds given in suppressed urination.
34.	*Cyathula tomentosa* (Roth) Moq. in DC.	Lichkura.	Amaranthceae	Leaf extract has emetic properties and given in snakebite.
35	*Cyperus rotundus* L.	Motha	Cyperaceae	Dried underground parts used in perfumes and plant extract used as diaphoretic and astringent.
36.	*Dicliptera bupleuroides* Nees	Kulartore	Acanthaceae	Leaf paste applied on wounds to check bleeding, leaf juice useful in cough and gastro-enteritis.
37.	*Elephantopus scaber* L.	Adhomukha	Asteraceae	Root extract used in intermittent fever and to stop vomiting and leaves as tonic of blood diseases.
38.	*Emilia sonchifolia* (L.) DC.	Hirankuri	Asteraceae	Leaf juice used in eye inflammation and night blindness.
39.	*Erythrina arborescens* Roxb.	Pangara	Fabaceae	Bark used in skin diseases; leaf extract given in suppressed menses, and also for intestinal worms.
40.	*Eupatorium adenophorum* Sprengel	Kharna, Bakura	Asteraceae	Crushed leaves applied on wounds.
41.	*Eurya acuminata* DC.	Deura	Theaceae	Wood used as fuel and for agricultural implements. Green leaves and young twigs lopped for fodder.
42.	*Fagopyrum dibotrys* Wall. ex Meisn.	Banogal, Kanalya	Polygonaceae	Leaf paste rubbed on insect bite.
43.	*Fragaria nubicola* Lindley ex Lacaita	Gand-kaphal	Rosaceae	Leaf juice dropped for relieving earache and fruits also used in local beverages.
44.	*Galium aparine* L.	Khuskusa	Rubiaceae	Extract of leaves used as astringent and plant paste applied on skin diseases.
45.	*Galium asperifolum* Wall.	Liswa kuri	Rubiaceae	Plants paste is use fuel in skin ailments.
46.	*Galium elegans* Wall.	Manjeethee	Rubiaceae	Plant extract given in colic, dyspepsia and as well as in jaundice.
47.	*Geranium nepalense* Sweet	Kaphlya	Geraniaceae	Plant infusion used in fever and renal disorders; roots paste applied externally on itching and eczema or root in tanning industry.
48.	*Geranium wallichianum* D.Don	Ratanjot	Geraniaceae	Root juice used in diarrhoea and ophthalmic.

Contd.

S.No.	Botanical name	Local/ vernacular name	Family	Uses
49.	*Gerbera gossypina* (Royle) G. Beauv.	Kapasee	Asteraceae	Leaf juice applied on wounds and cuts and paste plastered on bone fracture.
50.	*Gnaphalium hypoleucum* DC.	Buglya	Asteraceae	Plant extract applied on cuts and wounds
51.	*Gypsophila cerastioides* D.Don.	Bakarchee	Caryophyllaceae	Poultice of plant applied on boils and wounds.
52.	*Hedera nepalensis* K.Koch.	Laguli	Araliaceae	Leaves and fruit paste applied on ulcers and leaf juice given in dyspepsia.
53.	*Hypericum oblongifolium* Choisy	Chitroi, Chaya	Hypericaceae	Roots yield yellow dye, decoction of leaves and stem given to facilitate delivery
54.	*Hypericum uralum* L.	Bhyoul	Hypericaceae	Paste of leaves applied on cuts to check bleeding. Infusion of leaf given in malarial fever. Seed powder against food poisoning and as abortifacient.
55.	*Impatiens thomsonii* Hk.	Balsam	Balsaminaceae	Seed edible powder of roasted seed with honey given to relieve cough and cold.
56.	*Indigofera heterantha* Wall. ex Brandis	Sakina	Fabaceae	Leaf juice taken in diarrhoea, dysentery and cough.
57.	*Inula cappa* (Buch.-Ham. ex D.Don.) DC.	Athhu, Tamagari	Asteraceae	Roots given in suppressed urination.
58.	*Leucas lanata* Benth.	Bis-kapra	Lamiaceae	Plant infusion given with honey in the treatment of whooping cough and young shoots cooked as vegetable.
59.	*Micromeria biflora* (Buch.-Ham. ex D.Don) Benth.	Gorakhopan, Ban-ajwain	Lamiaceae	Flavour of crushed leaves inhaled in cold and sinusitis, extract of leaves with milk given in gastro-enteritis.
60.	*Mukia maderaspatana* L.	Ban kakari	Cucurbitaceae	Fruits cooked as vegetable given in malarial fever and urinary disorders; seed paste with warm water given to relieve in vomiting.
61.	*Nepeta ciliaris* Wall. ex Benth.	Nueet	Lamiaceae	Decoction of leaves and seeds taken in fever. Leaves also yield essential oil.
62.	*Origanum vulgare* L.	Bantulsi	Lamiaceae	Plant extract used in bronchitis, colic and diarrhea.
63.	*Oxalis corniculata* L.	Bhilmori, Khati-Buti	Oxalidaceae	Leaves taken as salad or cooked as vegetable and leaf juice dropped in cataract and conjunctivitis.
64.	*Parnassia nubicola* Wall. ex Royle	Phutkya	Saxifragaceae	Plant extract taken to stimulate vomiting in case of food poisoning, paste from rootstock applied externally as an antidote of snakebite
65.	*Phyllanthus amarus* Schum. & Thonn.	Bumianwala	Euphorbiaceae	Herb as an astringent stomachache diuretic and febrifuge; leaves said to bear antibacterial properties.
66.	*Pimpinella diversifolia* DC.	Teroi	Apiaceae	Plant extract given in digestive disorders and as well as in cold and cough.
67.	*Piptanthus nepalensis* (Hk.) D.Don	Chembera	Fabaceae	Green pods chewed raw, ripe seed coocked as vegetables and extract used as galactagogue.
68	*Plantago depressa* Willd.	Luhurya	Plantaginaceae	Paste from leaves and seeds applied on cuts wounds and piles; plant art or tied around the belly of infant for good health.
69.	*Plantago erosa* Wall.	Lahuriya	Plantaginaceae	Leaves are used as anti-inflammatory agent.
70.	*Pogostemon benghalense* (Burm.f.) Kuntze	Kala-Basingu	Lamiaceae	Leaf extract in water given in colic and fever, flower important source of bee-forage and plant is a good soil binder.
71.	*Polygonum plebeium* R.Br.	Dondya	Polygonaceae	Root extract applied on head to avoid baldness.
72.	*Potentilla gerardiana* Lindl. ex Lehm.	Baradanti	Rosaceae	Root paste applied on wounds.
73.	*Potentilla nepalensis* Hook.	Baradanti	Rosaceae	Root paste applied on wounds; substitute of *P. fulgence*

Contd.

S.No.	Botanical name	Local/ vernacular name	Family	Uses
74.	*Primula denticulata* Smith	Jalkutra	Primulaceae	Aqueous paste of flowers used in the treatment of diabetes and urinary ailments and root paste applied to kill lice.
75.	*Prinsepia utilis* Royle	Bhainkal	Rosaceae	Root bark used in diarrhoea, flowers useful in apiculture as bee forage and sometimes plant used as biofence.
76.	*Prunella vulgaris* L.	Ust-khadus	Lamiaceae	Extract of the herb used in gastric and breathing problems.
77.	*Quirivella frutescens* (L.) M.R. and S.M. Almeida	Bel-kami	Apocynaceae	Leaf extract supposed to be used in febrifuge and paste applied in leucoderma.
78.	*Rannunculus hirtellus* Royle	Piryali	Ranunculaceae	Plant paste externally used on deteriorated wound.
79.	*Reinwardtia indica* Dumortier	Phiunli.	Linaceae	Petals chewed as tongue wash, considered sacred.
80.	*Rorippa indica* (L.) Hiern.	Piria	Brassicaceae	Plant juice given in diarrhoea and paste applied on sprains.
81.	*Rosa brunonii* Lindley.	Kunja, Kujju	Rosaceae	Flower paste applied on skin ailments.
82.	*Roscoea purpurea* J.E.Smith	Kakoli	Zingiberaceae	Dried powder of leaves used in wound and plant extract as a tonic.
83.	*Rubia manjith* Roxb. ex Fleming	Majethi	Rubiaceae	Dye commercially known as Manjit, extracted from the root and stem, roots medicinal, as tonic and astringent, stem used as an antidote to snake bite and flower extract in bacillary dysentery.
84.	*Rubus ellipticus* Smith	Hinssar, Hisolu	Rosaceae	Fruits and root extract used in local beverages as intoxicating ingredient.
85.	*Rubus foliosus* D.Don.	Kala hissar	Rosaceae	Young twigs and fruits edible.
86.	*Rumex nepalensis* Spreng.	Almora	Polygonaceae	The sap of leaves and stem is applied on cuts for its astringent powder.
87.	*Rumex hastatus* D.Don.	Almoru	Polygonaceae	Leaf extract applied on cuts and wounds to check bleeding and also believed to relive from of nettle sting inflammation.
88.	*Salvia lanata* Roxb.	Ghanyajhar	Lamiaceae	Leaf infusion given in colic and diarrhea, flower paste used in cold and cough.
89.	*Saussurea heteromalla* (D.Don.) Hand.-Mazz.	Murang	Asteraceae	Leaf paste with mustard oil massaged on leucoderma and wounds and root extract taken in fever and colic.
90.	*Saxifraga diversifolia* Wallich ex Seringe in DC.	Silyans	Saxifragaceae	Root extract used as vermifuge.
91.	*Scrophularia himalensis* Royle ex Benth.	Sikula	Scrophulariaceae	Leaves mixed with stored grains as an insecticide.
92.	*Scutellaria scandens* Buch.-Ham ex D.Don.	Kutlaphul	Lamiaceae	Aqueous extract of leaves and flowers given in dysentery and vomiting.
93.	*Siegesbeckia orientalis* L.	Liskura	Asteraceae	Decoction of plant with boiled rice waters taken in diarrhoea and bowl complaints.
94.	*Smilax aspera* L.	Kukurdara	Smilacaceae	Roots diuretic and diaphoretic. Root paste with mustard oil massaged on rheumatic-arthritis.
95.	*Solanum pseudo-capsicum* L.	Jangli-mirch	Solanaceae	Seeds used in the treatment of boils and gonorrhoea, and tonic and for abdominal pain.
96.	*Solidago virgaurea* L.	Pinja-phool	Asteraceae	Juice of leaves given in kidney troubles, decoction of whole herb used for treatment of asthma, rheumatism and wounds and root chewed in throat irritation.
97.	*Sonchus asper* (L.) Hill.	Pili-dudhi	Asteraceae	The plant used as a tonic to purify blood and in hepatitis and leaf paste applied on wounds.
98.	*Sonchus brachyotus* DC.	Karatu	Asteraceae	Roots used as folk medicine against cough and bronchitis; young shoots and leaves cooked as vegetable during famine.

Contd.

S.No.	Botanical name	Local/ vernacular name	Family	Uses
99.	*Stellaria media* (L.) Vill.	Badyalu	Caryophyllaceae	Plant paste externally applied on burns, boils, and wounds.
100.	*Swertia cordata* (D.Don.) C.B. Clarke	Chirata	Gentianaceae	Plant used as substitute for 'Chirayita'.
101.	*Tagetes minuta* L.	Jangli genda	Asteraceae	Anti-microbial, antibiotic, anti-spasmodic, anti-parasitic, antiseptic, sedative.
102.	*Taraxacum officinale* Weber	Kanphuliya	Asteraceae	Root extract used in the treatment of migraine, hepatitis, and headache.
103.	*Teucrium quadrifarium* Buch.-Ham. ex D.Don.	Bilmga	Lamiaceae	Root chewed for sore throat, infusion of leaves used as abortifacient.
104.	*Thalictrum foliolosum* DC.	Pili Jari	Ranunculaceae	Root used in ophthalmia and also in colic and fever.
105.	*Thalictrum secundum* Edgew.	Mamari	Ranunculaceae	Root juice taken to relieve stomach disorders in folk medicine.
106.	*Thlaspi arvense* L.	Maula	Brassicaceae	Poultice of leaves applied on cuts and wound.
107	*Trifolium repens* L.	Tpatiya	Fabaceae	Leaf paste used as an astringent; plant provides good fodder.
108.	*Triumfetta rhomboidea* Jacq.	Liswa kura	Tilliaceae	Root juice applied on the cuts; hot infection of fruits and leaves given to facilitate delivery.
109.	*Urena lobata* L.	Chatkura	Malvaceae	Stem yields a coarse fiber, flower expectorant, root paste applied on body pain and rheumatism.
110.	*Urtica dioica* L.	Kandali	Urticaceae	Rheumatism and several skin ailments; leaf extract to avoid baldness.
111.	*Valeriana hardwickii* Wall.	Somaya	Valerianaceae	Root decoction use in urinary disorders; paste applied externally in joint pains. Dried roots used as an incense and insecticide.
112	*Valeriana jatamansii* Jones	Indian Valerian	Valerianaceae	Roots used as an aphrodisiac and in mental disorders, as well as in local beverage to promote aroma. Dried roots also used as an incense and insecticide.
113.	*Verbascum thapsus* L.	Akulubir	Scrophulariaceae	Plants extract taken in bronchitis and asthma; seeds used as narcotic; plants extract also used in fish poisoning flowers rarely used as dye.
114.	*Vernonia cinerea* (L.) Less.	Kalgira	Asteraceae	Leaf extract used in dysentery and seeds in cough and cold.
115.	*Viola biflora* J. Smith	Banafsa	Violaceae	The whole plant either in the form of extract or powder taken as diaphoretic, useful in skin and blood diseases, flowers and leaves boiled with tea, supposed to be or good for fever and cough.
116.	*Viola pilosa* Bl.	Banafsa	Violaceae	Fresh flower boiled with tea to relieve cough and cold. Flowers eaten raw: leaf paste applied on headache and jaundice.
117.	*Viola tricolor* Wall.	Banafsa	Violaceae	Decoction useful in malarial fever, bronchitis and asthma, root used as an emetic, flower demulcent, sometimes eaten raw and leaf juice applied on cuts and wounds.

Natural vegetation in vicinity of towns and villages in the sub-tropical belt has been subjected to more biotic disturbances as compared to the villages at high elevations. There is abundance of grasses and annuals during monsoon, whereas perennials, shrubs and trees mostly bloom during spring and summer (Bisht *et al.*, 1988; Bisht and Sharma, 2014).

The most significant observation on vegetation in the study area was the presence of numerous medicinal plant species, the fact is generally ignored by scientists. Each

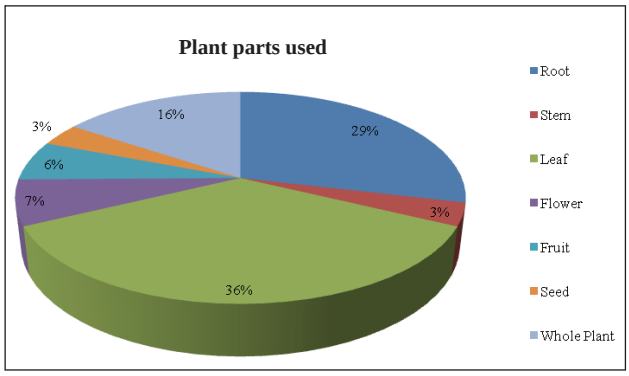

Fig. 1. Percentage of useful parts of plants

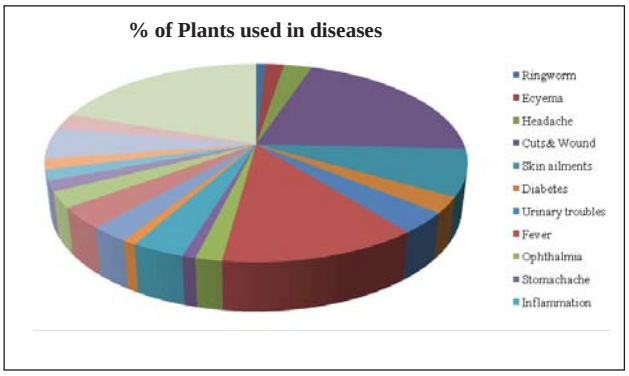

Fig. 2. Percentage of plants parts used in different diseases

plant species has its own value in the form of fodder, and vegetable, flowers as bee forage, resin, tannin, gum, dye, ornamentation, psychomedicine and medicines, etc. Total 117 weed species were also purely medicinal and used in the form of leaves, stem, bark, root, flowers, fruits, seeds, and whole plant (Fig. 1). These plant species are used against dropsy, bronchitis, cut and wounds (total 24 plants are used 20.51%), insect and snake bite, relieve from suffering of nettle sting, malarial and other fever (15 plants are used 12.82%), facilitate delivery, body pain, rheumatism, fever, cold and cough, gonorrhoea, colic and dyspepsia, diarrhea, digestive and respiratory disorders, diabetes and urinary ailments, relieving earache, body swelling and contusions, psycho-medicines, treatments of migraines, hepatitis and headache, dysentery, and 23 plants (19.66%) are used in other diseases by villagers and *Vaidhyas* (Fig 2). *Achyranthus bidentata, Agrimonia pilosa, Anaphalis contorta, A. triplinervis, Aster peduncularis, Anemone vitifolia, Argemone ochroleuca, Asparagus recemosus, Berberis aristata, Barleria cristata, Begonia picta, Bupleurum hamiltonii, Clematis buchananiana, Coccinia grandis, Coelogyne cristata, Cyathula tomentosa, Gerbera gossypina, Gnaphalium hypoleucum, Hedychium spicatum, Inula cappa, Jasminum humile, Leucus lanata, Saussurea heteromalla, Senecio graciliflorus, Siegesbeckia orientalis, Solidago virgaurea, Sonchus asper, Swertia cordata, Taraxacum officinale,* etc. were the medicinally important species; highest contribution of the family Astraceae (21 species) was associated with the horticultural fields.

Out of 117 medicinal weeds some weeds e.g. *Berberis* spp., *Valariaana jatamansii* are presently of high commercial value and used in many pharmaceuticals. Genus *Berberis* is well known for its active compound 'Berberine', which has anti-diabetic, anti-microbial, anti-cancer, anti-lipidemic and anti-oxidant properties (Potdar *et al*., 2012). Due to presence of active principle in roots and rhizomes of *Valeriana* (valepotriates, dihydrovaltrate, antioxidant activity) the plant is very valued for the commercial purpose (Bhatt *et al*., 2012). Except of these two species, *Bergenia ciliate*, *Phyllanthus amarus*, *Rubia manjith*, *Roscoea purpurea* and *Swertia cordata*, have highly market value and also income generating sources for local peoples.

The extinction of these weed flora of medicinal plants, importance from their natural habitat of present study area is a matter of great concern but it has not attracted the attention of naturalists and environmentalists. This is probably because the medicinal wealth of this area is little known and remote locality and changing atmospheric conditions and lack of knowledge, infectious nature of some dominating weeds, e.g. *Eupatorium adenophorum* are among the other factors responsible for the extinction of these important medicinal plant species. These weeds can become an additional source of income for the farmers who generally discard them during weeding. If they are made aware of the medicinal importance of these crop weeds, it can add monetary benefit.

The study illustrated that medicinal weeds in horticulture crop fields, have a tremendous scope of utilizing these weeds, especially to promote additional income to the local peoples.

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SHORT COMMUNICATION

Text-mining for Identifying Abiotic Stress Candidate Genes to Screen Bread Wheat (*Triticum aestivum*) Germplasm

Monica Jamla, Ambika Baldev Gaikwad, Sherry Rachel Jacob and Sunil Archak
ICAR-National Bureau of Plant Genetic Resources, New Delhi-110012, India

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An exhaustive text-mining of flowering plants' nucleotide data for the genes known to be associated with abiotic stress tolerance shortlisted 132 putative candidate genes. Primers were designed for orthologous amplification of the gene sequences in two wheat varieties and based on the banding pattern, 24 loci were tested in 13 heat and drought tolerant wheat genotypes along with a susceptible control for their utility in germplasm screening.

Key Words: Abiotic Stress, Bioinformatics, Candidate gene, Text-mining, Wheat

Wheat is the second most produced food-grain worldwide (FAOSTAT, 2016). However, it has been predicted that every ºC of temperature increase will lead to reduction of the global wheat production by 6% (Asseng *et al*., 2015). Consequently, researchers around the world have been trying to develop wheat germplasm lines with tolerance to abiotic stress (Bansal *et al*., 2013). Gene-specific markers have been shown to be highly useful in trait-specific germplasm screening (Singh *et al*., 2015; Archak *et al*., 2016). Abiotic stress is a complex trait and involves signal trafficking of different classes of proteins (Agarwal and Jha, 2010). However, huge amount of sequence data is available in the public domain (Benson *et al*., 2015) which facilitates the application of *in silico* techniques to identify putative genes involved in abiotic stress response pathway in plants. Computational tools (Moreau and Tranchevent, 2012) including simple supervised text-mining (Zhu *et al*., 2013) have been employed in the discovery of candidate genes.

Present study was taken up to text-mine open source gene database to identify candidate genes from plants putatively involved in abiotic stress response, amplify the genes in wheat and test for suitability in screening germplasm. Nucleotide database of the Genbank (www.ncbi.nih.nim.gov.in) was searched using keywords "abiotic stress" and "flowering plants" in December of 2011. The text-mining was supervised to choose only those genes that were (i) published in journals; (ii) with complete coding sequences; and (iii) reported in two or more species. Hypothetical, predicted, putative, partial, unpublished, directly submitted, precursor, exon-only, duplicates of same gene with different sizes and genomic scaffolds were therefore avoided. Sequences from sources like clones, less studied cultivars and naturally interspecific hybrids were also not downloaded from database. The text-mining resulted in 132 putative abiotic stress tolerance genes belonging to 37 plant species. Among the candidates shortlisted, 18 genes were from wheat. The stress-pathway candidate genes included enzymes (e.g. Oxidase and Mitogen activated protein kinase kinase), membrane proteins (e.g. Aquaporins and Copper chaperones), DNA binding proteins (e.g. Dehydration responsive element binding protein and Osmotic stress tolerance protein), ubiquitous proteins (e.g. Defensins and Profilins), and organellar proteins (e.g. chloroplastic Ferritin and mitochondrial ATP-synthase).

Primer 3.0 software tool (fokker.wi.mit.edu/primer3) was used to design heterologous primers for all the 132 genes. Amplification was tested in two wheat genotypes – heat resistant Raj-3765 (IC0532594) and heat susceptible PBW-343 (IC0532751). DNA extraction, PCR amplification and electrophoresis were carried out as described earlier (Archak *et al*., 2003). Amplification patterns are shown in Fig. 1A. Based on clear and single band amplification, 24 STS loci were shortlisted to screen 13 genotypes known to be heat and drought tolerant along with Agra Local, the susceptible

**Author for Correspondence: Email- sunil.archak@icar.gov.in*

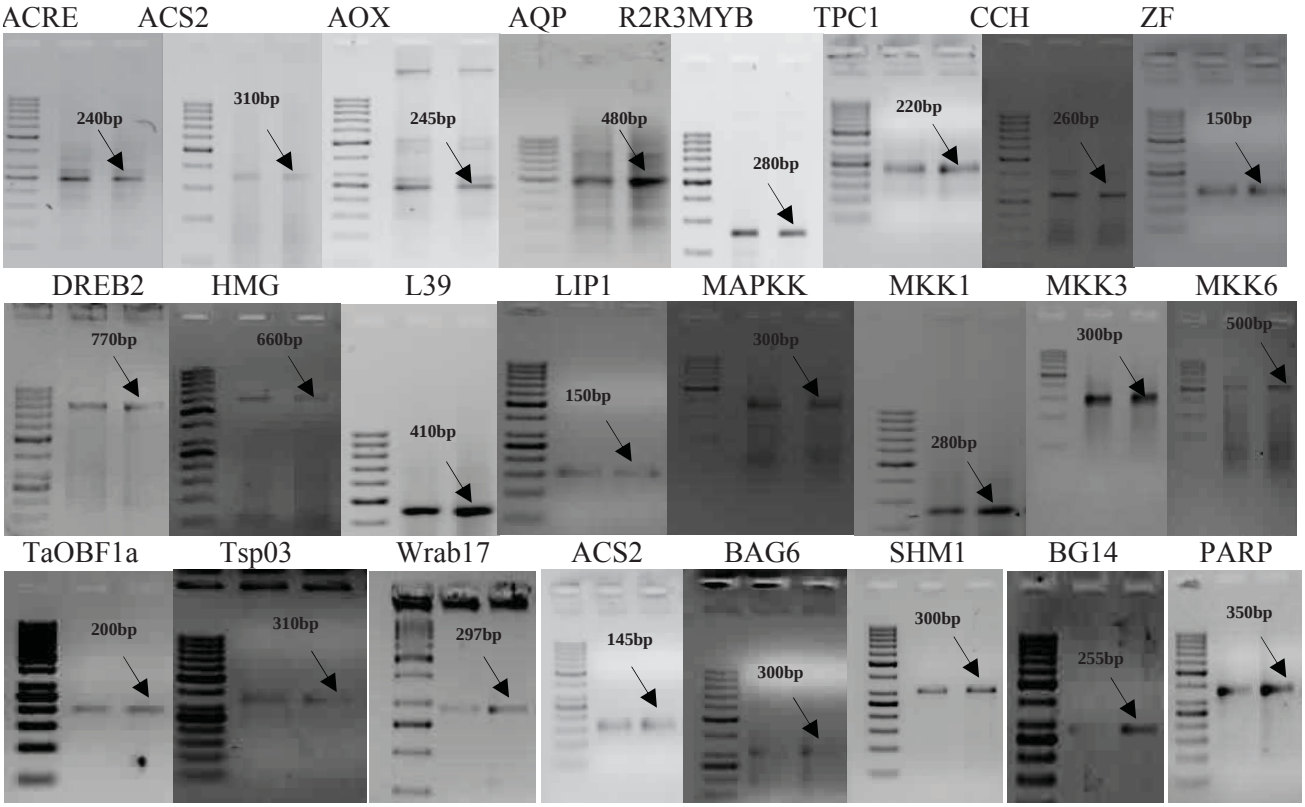

Figure 1A: Amplification profile of 24 STS loci.
Gene names are mentioned on the top of each gel picture. Lane: 1: 50/100 bp ladder, 2: Raj3765, 3: PBW343.

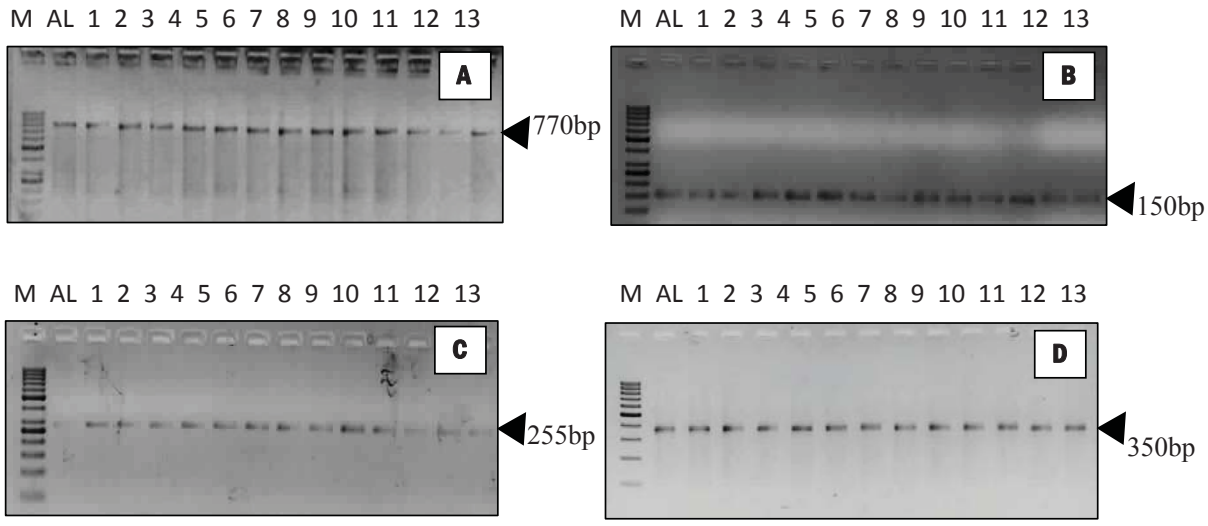

Figure 1B: Amplification profile of four candidate genes in 14 wheat accessions
Candidate genes: (A) LIP1 (B) TaOBF1a (C) Wrab17 (D) SHM1. Lanes: M: 50bp ladder, AL: Agra Local, 1: AKAW-3717, 2: HTW 6, 3: HTW 11, 4: WCF8-HT13, 5: Hindi 62, 6: KRL 99, 7: KRL 3-4, 8: Kharchia Local, 9: Kharchia 65, 10: WCF 12-7, 11: WCF 12-61, 12: WCF 12-19, 13: WCF 12-208.

control (Table 1). DNA extraction, PCR amplification and electrophoresis were carried out as described earlier (Archak *et al.*, 2003). It was observed that amplicons did not exhibit discernible length polymorphism (Fig 1B). Amplicons of BG14 (Non-specific lipid transfer protein), SHM1 (Serine hydroxyl methyltransferase 1), LIP1 (GDSL-lipase protein), TaOBF1a (Basic leucine zipper protein) and Wrab17 (Late embryogenesis

Table 1. Details of wheat genotypes employed in marker screening

S.No.	Accesion No.	Name	Biological Status	Unique feature
1	IC582907	AKAW-3717	Genetic Stock	Early heat and drought tolerance
2	IC29007A	HTW 6	Others	Terminal heat tolerance
3	IC35117	HTW 11	Others	Terminal heat tolerance
4	IC443622	WCF8-HT13	Genetic Stock	Drought and lodging resistance; WUE
5	IC296681	Hindi 62	Others	Heat and drought tolerance
6	IC546936	KRL 99	Genetic Stock	Salinity and sodicity tolerance
7	IC408331	KRL 3-4	Genetic Stock	Salt tolerance greater than Kharchia 65
8	IC296742	Kharchia Local	Others	Salt tolerance
9	IC335540	Kharchia 65	Released cultivar	Salt tolerance
10	IC594376	WCF12-7	Genetic Stock	Drought tolerance
11	IC594377	WCF12-61	Genetic Stock	Drought tolerance
12	IC594378	WCF12-19	Genetic Stock	Drought tolerance
13	IC594379	WCF12-208	Genetic Stock	Drought tolerance
14	IC138332	Agra Local	Landrace	Susceptible control

abundant protein) were gel-extracted using QIAquick columns and were sequenced (single pass) to find out the existence of sequence polymorphism. The chromatogram analysis was done using Finch TV (www.geospiza.com/Products/finchtv.shtml) and sequences were aligned using BIOEDIT (www.mbio.ncsu.edu/bioedit/bioedit.html). No sequence polymorphism was observed.

Present study could list 132 candidate genes involved in various pathways linked to response to heat and drought in plants. Primers were designed and successful amplification of these candidate genes in wheat was demonstrated. Neither fragment length nor sequence polymorphism was observed in selected 24 loci. Considering the indispensable nature of each of the gene shortlisted, this result was not unexpected. Based on the limited data generated by the study, it was concluded that the candidate genes could only be shortlisted based on experiments to detect differential expression. However, the study opens up possibility of employing candidate genes for validating germplasm accessions identified as tolerant to heat or moisture stress in field experiments.

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SHORT COMMUNICATION

'Te.pattang' [*Haematocarpus validus* (Miers) Bakh. f. ex Forman] – The Lesser-Known Promising Fruit of Garo Hills, Meghalaya

KC Momin[1], AN Sangma[1], CP Suresh[1], YS Singh[1], A Ojha[2] and SR Rao[2]*
[1]*Department of Horticulture, North Eastern Hill University, Tura Campus, Chandmari-794002, Meghalaya, India*
[2]*Department of Biotechnology Bioinformatics, North Eastern Hill University, Shillong Campus, Shillong-793022, Meghalaya, India*

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Haematocarpus validus, commonly known as blood fruit, is a promising fruit of the Menispermaceae family and is found in the hilly tracts of Garo hills region of Meghalaya. The fruits are highly valued by the locals as a medicine and ripe fruits consumed fresh. It is a dioecious evergreen perennial woody climber which is found growing wild in West, East and North Garo hills. It is one of the rare plants and its germplasm needs to be collected and conserved for its potential horticultural value. The present paper deals with the phenological and genomic information on blood fruit.

Key Words: Antioxidant, Fruit diversity, Genetic Information, Morphology, Resource Utilization

Meghalaya is popularly known as the cradle of plant species amongst the botanists. It is home to several plants and diverse animal groups. This is an important part of the Indo-Myanmar global biodiversity hot-spot (one of the 34 global biodiversity hot-spots of the world). The Garo Hills region of Meghalaya has a rich diversity of underutilized plant species. Many of these species have a great horticultural value. Amongst various species of wild plants available here, blood fruit [*Haematocarpus validus* (Miers) Bakh. f. ex Forman], locally known as '*Te.pattang*' is a promising, anti-oxidant rich and medicinally important fruit. In the Garo Hills region, it is a rare plant species and natural populations are disappearing at an alarming rate. This is due to illegal exploitation, deforestation, soil degradation and loss of biodiversity. It therefore needs special attention from the conservation point of view. It is naturally found growing in the dry land in the hilly regions in India, Bangladesh, Sri Lanka, Indonesia and Thailand (Khatun *et al*., 2014). The fruit is rich in iron and it is highly valued by the local people for treating anaemia and other blood related disorders. The plant takes around seven years to mature and flower if grown from seeds and around four years when it is vegetatively propagated from cuttings. This species has a well established local market and a bunch of fruits costs around Rs.100 per bunch (10-15 fruits in a bunch). The moisture content of the fruit is 90.12% of fresh weight. It has a pH of 2.77, TSS of 21% and the total sugar content of the fruit of 11.07 % (Rahim *et al*., 2015).

Blood fruit is native to South East Asia and is mainly distributed in India (Khatun *et al.*, 2014; Kar *et al*., 2013), Bangladesh (Rahim *et al*., 2015; Khatun *et al*., 2014), Indonesia (Khatun *et al.*, 2014), Singapore (Khatun *et al*., 2014) and Sri Lanka (Singh *et al*., 2014). In India, the species is found growing wild in Andaman & Nicobar Islands (Singh *et al.*, 2014; Khatun *et al.*, 2014), Assam (Khatun *et al.*, 2014), Mizoram (Kar *et al.*, 2013) and Meghalaya (Jeeva, 2009; Khatun *et al.*, 2014). The plant is found growing wild in the hilly tracts of West, North and East Garo Hills region of Meghalaya, where it grows under harsh conditions. The climate of the East Garo Hills district is hot and humid during the summer followed by cool and dry weather during the winter. The West Garo Hills district experiences a fairly high temperature for most part of the year with an average rainfall of 330 cms. The district has mostly dense tropical mixed forest and a small patch of temperate forest in the higher parts of Tura range. The climatic condition of North Garo Hills is sub-tropical with adequate rainfall. In all the three districts the temperature ranges from 5°-36°C. Despite its multifaceted importance, the population is declining in its natural stands. Neither *in-*

**Author for Correspondence: Email- sureshcp2112@gmail.com*

vivo (sanctuaries, national parks, gene banks, etc.) nor *in vitro* (plant tissue cultures, cryopreservation, etc.) efforts have been made for its conservation and recovery. Not a single report is available dealing with either of these aspects for *Haematocarpus validus*. Attempts were made to identify few plants in three different districts of Garo hills where it was commonly found; the growing areas have been presented in Table 1.

Haematocarpus validus is a large woody climber which spread on tall trees. Leaves are simple, alternate, non-peltate, elliptic and 3 veined. The bark is light grayish brown and rough. The branches are stout and the wood consists of consecutive layers of thin radiating plates. The inflorescences are cauliflorous, axillary, extra-axillary, terminal panicle or racemes. It is dioecious. The male flowers have 12-15 sepals, imbricate in 3 series, usually inner series is larger. Of the 6 petals, 3 of the inner series are auriculate at the base. The 6 stamens are free, with the enlarged connectives projecting inwards. Calyx and the corolla of the female flowers are similar to the male flowers. There are 6 minute staminodes, and 6 carpels with reflexed styles. Fruits are drupes, ellipsoid, narrow near the base (Fig. 1). There is a style scar near the base and a smooth exocarp. Seeds are curved, non-endospermic, with a short radicle, and thick and long cotyledons. Seeds may be dispersed by barochory (gravitational dispersal), zoochory (dispersal by birds or animals), anthropochory (dispersal by humans).

Under Garo hills condition, the vine comes into flowering from October to December and fruits are available in the local markets from last week of March till June. Fruits are dark red, full of copious blood red juice when ripe and have a densely fibrous mesocarp. Preliminary investigations revealed that the average fruit weight is around 21.14g, fruit length 3.67cm, fruit girth 22.24mm, having a TSS of 12.7 %. Fruits are single seeded, weighing 5.52g, having a seed length 2.61cm, seed girth of 12.35mm, rind thickness of 2.83mm and rind weight of 8.17g.

Even though *Haematocarpus validus* is a less-known promising edible fruit, yet it has a lot of potential uses. Fruits of *H. validus* are slightly acidic, sweet when fully ripe and are eaten raw. The fruits have high anthocyanin content which gives true blood red colour which can be used as a colouring agent and as a natural dye for food products (Singh *et al*., 2014). Fruit extracts can also be used in colouring soft drinks and desserts (Rahim *et al*., 2015). Moreover, use of natural dye from this fruit will be very much helpful in avoiding health risk in human. The local people of Garo hills also use this fruit for preparing wines.

Ripe fruits are a good source of iron, anti-oxidants and Vitamin C and are used by the locals for treatment of anaemia and other blood disorders. Fruits have a vitamin C content of 13.15 mg/100gm, carotenoids 1170 µg and β-carotene 9.0 µg. Ripe fruits are sliced and soaked in a glass of water overnight and taken as medicine the next morning.

Sequence information of important nucleic acid organellar genes play an essential role in the evolution and phlyogentic status of any organism. However, there are only few reports available for the genetic characterization of *Haematocarpus vaildus.* The 1048 bp, 26S ribosomal RNA gene (partial sequence) has been reported by Hoot *et al.* (2015). Similarly the conserved maturase K (*mat*K) with the nucleotide sequence of 1617 bp has also been sequenced by Wefferling *et al.*

Table 1. Identification of growing areas in Garo hills, Meghalaya

District	Collection locality	Latitude	Longitude	Altitude
East Garo Hills, Meghalaya	Kusimkolgre-B	N23°30'58.0''	E090°35'58.0''	281 m
	Kusimkolgre-B	N25°31'00.1''	E090°36'00.0''	278 m
	Kusimkolgre-B	N25°30'54.6''	E090°35'48.3''	259 m
	Kusimkolgre-A	N25°30'57.2''	E090°35'56.8''	258 m
North Garo Hills, Meghalaya	Resu Bakrapara	N25°54'751''	E090°36'091''	158 m
	Resu Bakrapara	N25°54'816''	E090°35'978''	162 m
	Resu Bakrapara	N25°54'912''	E090°35'827''	191 m
	Resu Songma	N25°54'458''	E090°36'456''	083 m
West Garo Hills, Meghalaya	Balsrigittim	N25°31'601''	E090°13'623''	297 m
	Allotgre	N25°31'807''	E090°12'532''	435 m
	Chitoktak	N25°31'501''	E090°13'797''	339 m
	Stadium	N25°32'124''	E090°12'469''	433 m

a. Fruit bearing plants **b. Ripe fruits**

c. Female flowers **d. Longitudinal section of fruit**

Fig.1. *Haematocarpus validus*

(2013). The NADH dehydrogenase subunit F (*ndh*F) chloroplast gene of 2022 bp nucleotides has also been sequenced and was reported by Wang *et al.* (2012). Similarly ATPase beta subunit (*atp*B) a conserved region of chloroplast of *Haematocarpus vaildus* has been sequenced for 1407 bp long nucleotide and was reported by Wang *et al.* (2012). tRNA-Leu (*trn*L) and *rbc*L gene of *Haematocarpus vaildus* have been also sequenced and published by Wang *et al.* (2012). Such critically important genomic information will enable us to assess the quantum and range of genetic variability within the species and help to select the appropriate genotypes for conservation purpose.

With the growing concern and commitment to hill area development and poverty alleviation, there has been an increasing interest in untapped and underutilized wild bio-resources that contribute to the household food and livelihood security. The value and importance of the wild edible plants and fruits of *Haematocarpus validus* in particular, is least worked out. This plant is a rich source of anti-oxidants, vitamins, minerals, good source of natural dye and has a good medicinal value. An emphasis needs to be given to identify more areas to explore the potential pockets for cultivation which can bring in more economic benefits to the local communities if harnessed properly.

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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXXIII[rd] meeting held on December 7[th], 2015 at the ICAR-National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 30 germplasm lines out of 68 proposals considered. The information on registered germplasm is published with the purpose to disseminate the information to respective breeders for utilization of these genetic stocks in their crop improvement programmes. Upon request, the developer(s)/author(s) is/are obliged to distribute the material for crop improvement programme of National Agricultural Research System.

1. Mainagali (IC0390780; INGR15037), Rice (*Oryza sativa* L.) Germplasm with Long Sterile Glume

AK Sarawgi*, GR Sahu, RK Rao and Jitendra Tiwari
Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur-492012, Chhattisgarh, India
*(*Email: sarawgi1@yahoo.co.in, hodgpbigkv@gmail.com*)

Chhattisgarh has a wide variability of rice germplasm. Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur maintains a huge collection of 23,250 rice germplasm accessions. The registered germplasm Mainagali (IC0390780, INGR15037) with long sterile glume was collected from Dharmjaigarh Block of Raigarh District of Chhattisgarh.

Morpho-agronomic characteristics: The lemma palea colour of registered germplasm is brown and kernel colour is white with long slender grains. Its spikelets look like flying birds.

Associated characters and cultivation practices: In this accession spikelets are found with long sterile glumes. Length of sterile glume is nearer to lemma length. Long sterile glumes prevent infestation of insect pests in spikelets. This accession is planted normally in mid land condition of Chhattisgarh Plains.

Morphological descriptions and mean agronomic traits are presented below

Characteristics	Mainagali (IC0390780, INGR15037)
Basal leaf sheath colour (BLSC)	Green
Leaf blade colour (LBC)	Green
Collar colour (CC)	Green
Auricle colour (AC)	Light Green
Culm internode colour (CmlC)	Green
Apiculous colour (ApC)	Light Green
Stigma colour (SgC)	White
Awning (An)	Absent
Days to maturity (DM)	132.5
Plant height (PH) cm	161.7
Tiller No. (Til No.)	5.5
Lemma palea colour (LmPC)	Brown
Seed coat colour (ScC)	White
100 grain weight (TW) gm	3.31
Grain length (GRL) mm	9.0
Grain breadth (GRB) mm	2.9
Grain ratio (L/B)	3.1
Grain type	Long Slender

Note: Quantitative data given based on the mean of 4 years.

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**Compiled and edited by: Anjali Kak and RK Tyagi, Division of Germplasm Conservation, ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi–110012.*

2. Nariyal Phool (IC0390772; INGR15038), a Rice (*Oryza sativa* L.) Germplasm with Clustered Spikelets in the Range of 2-10

AK Sarawgi*, GR Sahu, RK Rao and Jitendra Tiwari
Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur-492012, Chhattisgarh, India
*(*Email: sarawgi1@yahoo.co.in, hodgpbigkv@gmail.com*)

Chhattisgarh is blessed with a wide variability of rice germplasm accessions. IGKV, Raipur has a huge collection of 23,250 rice germplasm accessions. The registered germplasm Nariyal Phool **(**IC0390772, INGR15038) with clustered spikelets was collected from Saraipali block of Mahasamund district of Chhattisgarh.

Morpho- agronomic characteristics: The lemma palea colour of the germplasm is gold and gold furrows on straw and kernel colour is white and translucent. Due to clustering habit, spikelets look like the flower of coconut, so it is called Nariyal Phool by local inhabitants.

Associated characters and cultivated practices: In this accession clustering of spikelet recorded in broad range i.e. 2 to 10 grains amongst all clustered accessions available in IGKV rice germplasm. Whereas, clustering of 3 grains was found in large frequency (35.4%) followed by 4 grains (20%). A minimum frequency of clustering observed was 10 grains (2.55%). This germplasm accession is cultivated in low land condition of Chhattisgarh Plains.

Morphological description and mean agronomic traits are presented below

Characteristics	Nariyal Phool (IC 0390772, INGR 15038)
Basal leaf sheath colour (BLSC)	Green
Leaf blade colour (LBC)	Green
Collar colour (CC)	Green
Auricle colour (AC)	Light Green
Culm internode colour (CmlC)	Green
Apiculous colour (ApC)	Light Green
Stigma colour (SgC)	White
Awning (An)	Absent
Days to maturity (DM)	145.8
Plant height (PH) cm	138.6
Tiller No. (Til No.)	10.7
Lemma palea colour (LmPC)	Gold and gold furrows on straw
Seed coat colour (ScC)	White
100 grain weight (TW) gm	1.91
Grain length (GRL) mm	8.4
Grain breadth (GRB) mm	2.4
Grain L/B ratio	3.5
Grain type	Medium Slender

Note: Quantitative data given based on the mean of 4 years.

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3. KBRL77-1 (IC0616061; INGR15039), a Wheat (*Triticum aestivum*) Germplasm with Karnal Bunt Resistance

Indu Sharma*, Ritu Bala, NS Bains, RC Sharma, Satish Kumar, MS Saharan and Vinod Tiwari
ICAR-Indian Institute of Wheat & Barley Research (IIWBR), Karnal-132001, Haryana, India
*(*Email: ramindu2000@yahoo.co.in*)

Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. KBRL 57, a Karnal bunt (KB) free wheat stock was developed from a cross between Aldan and H567.71, both lines are resistant to the disease (Bala *et al.,* 2015). This stock was used as a donor to introgress the KB resistance into PBW 343, the famous wheat cultivar of India. The introgression was done using conventional backcrossing method along with artificial inoculations with KB fungus. KBRL 77-1 is one such line developed through this introgression.

Morpho-agronomic characteristics: The parental lines PBW 343 and KBRL 57 and the germplasm KBRL 77-1 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980).The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in table 1a & 1b.

Associated characters and cultivation practices: The germplasm KBRL 77-1 is highly resistant to Karnal bunt disease of wheat. KBRL 77-1 is also high yielding and agronomically desirable. With limited sources of resistance to KB, KBRL 77-1 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

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Table 1a. KB infection and yield data of KBRL 77-1 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/meter	Grains per spike	1000-grains weight
KBRL 77-1	KBRL 57/*6PBW 343	92	146	114	63	46
KBRL 57	Donor Parent	97	149	123	54	46
PBW 343	Recipient parent	93	142	134	55	43

Table 1b. Agronomic characteristics of KBRL 77-1 and the parents

Name	Pedigree	KB infection (%)				Yield (q/ha)			
		2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 77-1	KBRL 57/*6PBW 343	0.8	0.4	0.5	0.5	51.6	44.9	52.3	49.6
KBRL 57	Donor Parent	0.0	0.0	0.3	0.1	41.3	39.2	41.3	40.6
PBW 343	Recipient parent	15.3	11.4	19.7	15.5	43.5	39.8	44.2	42.5

4. KBRL 78-2 (IC0616062; INGR15040), a Wheat (*Triticum aestivum*) Germplasm with Karnal Bunt Resistance and High 1000 Grain Weight

Indu Sharma*, Ritu Bala, NS Bains, RC Sharma, Satish Kumar, MS Saharan and Vinod Tiwari
ICAR-Indian Institute of Wheat & Barley Research (IIWBR), Karnal-132001, Haryana, India
*(*Email: ramindu2000@yahoo.co.in*)

Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. The basic studies on KB at PAU, Ludhiana have revealed a few diverse sources of resistance (Sharma *et al.*, 2005) which were incorporated in to a high yielding wheat variety WH 542 (Kaur *et al.*, 2011) using backcross approach and simultaneous screening for the disease resistant lines. Further genetic analysis in derivatives from the crosses of donors with WH 542 indicated that the donors are diverse for resistance to KB which was found to be governed by 2-3 additive genes (Bala *et al.*, 2011). KBRL 78-2 is one such line developed utilizing Aldan as a donor parent.

Morpho-agronomic characteristics: The parental lines WH 542 and Aldan and the germplasm KBRL 78-2 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980). The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in Table 1a & 1b.

Table 1a. KB infection and yield data of KBRL 78-2 and the parents

		KB infection (%)				Yield (q/ha)			
Name	Pedigree	2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 78-2	ALDAN/*6WH 542	1.7	1.7	2.0	**1.8**	51.2	49.6	46.8	**49.2**
ALDAN	Donor Parent	3.2	0.8	1.6	**1.9**	35.0	34.0	32.5	**33.8**
WH 542	Recipient parent	42.1	37.9	46.4	**42.1**	47.3	44.7	45.3	**45.8**

Table 1b. Agronomic characteristics of KBRL 78-2 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/ meter	Grains per spike	1000-grains weight
KBRL 78-2	ALDAN/*6WH 542	94	148	114	63	51
ALDAN	Donor Parent	101	150	103	45	49
WH 542	Recipient parent	92	142	129	67	39

Associated characters and cultivation practices: The germplasm KBRL 78-2 is highly resistant to Karnal bunt disease of wheat. Also this line carries good agronomic characteristics and high 1000 grains weight of 51 g. With limited sources of resistance to KB, KBRL 78-2 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

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5. KBRL 79-2 (IC0616063; INGR15041), a Wheat (*Triticum aestivum*) Germplasm with Karnal Bunt Resistance and High Number of Tillers/m

Indu Sharma*, Ritu Bala, NS Bains, RC Sharma, Satish Kumar, MS Saharan and Vinod Tiwari
ICAR-Indian Institute of Wheat & Barley Research (IIWBR), Karnal-132001, Haryana, India
*(*Email: ramindu2000@yahoo.co.in*)

Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. The basic studies on KB at PAU, Ludhiana have revealed a few diverse sources of resistance (Sharma *et al.*, 2005) which were incorporated in to a high yielding wheat variety WH 542 (Kaur *et al.*, 2011) using backcross approach and simultaneous screening for the disease resistant lines. Further genetic analysis in derivatives from the crosses of donors with WH 542 indicated that the donors are diverse for resistance to KB which was found to be governed by 2-3 additive genes (Bala *et al.*, 2011). KBRL 79-2 is one such line developed utilizing CMH 77.308 as a donor parent.

Morpho-agronomic characteristics: The parental lines WH 542 and CMH 77.308 and the germplasm KBRL 79-2 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980). The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in table 1a & 1b.

Table 1a. KB infection and yield data of KBRL 79-2 and the parents

Name	Pedigree	KB infection (%)				Yield (q/ha)			
		2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 79-2	CMH 77.308/*6 WH 542	2.5	2.3	1.9	2.2	49.7	51.3	52.6	51.2
CMH 77.308	Donor Parent	1.9	3.2	2.4	2.5	32.0	36.0	38.0	35.3
WH 542	Recipient parent	42.1	37.9	46.4	42.1	47.3	44.7	45.3	45.8

Table 1b. Agronomic characteristics of KBRL 79-2 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/ meter	Grains per spike	1000-grains weight
KBRL 79-2	CMH 77.308/*6WH 542	97	137	146	57	53
CMH 77.308	Donor Parent	103	149	92	43	46
WH 542	Recipient parent	92	142	129	67	39

Associated characters and cultivation practices: The germplasm KBRL 79-2 is highly resistant to Karnal bunt disease of wheat. Also this line carries good agronomic characteristics and high number of tillers per meter. With limited sources of resistance to KB, KBRL 79-2 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

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6. KBRL 80-3 (IC0616064; INGR15042), a Wheat (*Triticum aestivum*) Germplasm with Karnal Bunt Resistance and High Number of Grains/Spike

Indu Sharma*, Ritu Bala, NS Bains, RC Sharma, Satish Kumar, MS Saharan and Vinod Tiwari
ICAR-Indian Institute of Wheat & Barley Research (IIWBR), Karnal-132001, Haryana, India
*(*Email: ramindu2000@yahoo.co.in*)

Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. The basic studies on KB at PAU, Ludhiana have revealed a few diverse sources of resistance (Sharma *et al.*, 2005) which were incorporated in to a high yielding wheat variety WH 542 (Kaur *et al.*, 2011) using backcross approach and simultaneous screening for the disease resistant lines. Further genetic analysis in derivatives from the crosses of donors with WH 542 indicated that the donors are diverse for resistance to KB which was found to be governed by 2-3 additive genes (Bala *et al.*, 2011). KBRL 80-3 is one such line developed utilizing H 567.71 as a donor parent.

Morpho-agronomic characteristics: The parental lines WH 542 and H 567.71 and the germplasm KBRL 80-3 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980). The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in Table 1a & 1b.

Table 1a.KB infection and yield data of KBRL 80-3 and the parents

Name	Pedigree	KB infection (%)				Yield (q/ha)			
		2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 80-3	H 567.71/*6WH 542	1.3	2.6	1.4	1.8	42.6	45.2	46.8	44.9
H 567.71	Donor Parent	3.0	1.9	2.8	2.6	36.2	32.1	31.6	33.3
WH 542	Recipient parent	42.1	37.9	46.4	42.1	47.3	44.7	45.3	45.8

Table 1b. Agronomic characteristics of KBRL 80-3 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/meter	Grains per spike	1000-grains weight
KBRL 80-3	H 567.71/*6WH 542	96	147	123	70	50
H 567.71	Donor Parent	105	146	104	46	45
WH 542	Recipient parent	92	142	129	67	39

Associated characters and cultivation practices: The germplasm KBRL 80-3 is highly resistant to Karnal bunt disease of wheat. Also this line carries good agronomic characteristics and high number of grains per spike. With limited sources of resistance to KB, KBRL 80-3 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

References

Anonymous (2015) Progress report of All India Coordinated Wheat & Barley Improvement Project 2014-15, Vol. III, Crop Protection. (Eds.): M S Saharan, Sudheer Kumar, R Selvakumar, Subhash Katare, Poonam Jasrotia and Indu Sharma. Indian Institute of Wheat & Barley Research, Karnal. India. pp. 76-80.

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7. KBRL 81-1 (IC0616065; INGR15043), a Wheat (*Triticum aestivum)* Germplasm with Karnal Bunt Resistance

Indu Sharma*, Ritu Bala, NS Bains, RC Sharma, Satish Kumar, MS Saharan and Vinod Tiwari
ICAR-Indian Institute of Wheat & Barley Research (IIWBR), Karnal-132001, Haryana, India
*(*Email: ramindu2000@yahoo.co.in*)

Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. The basic studies on KB at PAU, Ludhiana have revealed a few diverse sources of resistance (Sharma *et al.*, 2005) which were incorporated in to a high yielding wheat variety WH 542 (Kaur *et al.,* 2011) using backcross approach and simultaneous screening for the disease resistant lines. Further genetic analysis in the derivatives from the crosses of donors with WH 542 indicated that the donors are diverse for resistance to KB which was found to be governed by 2-3 additive genes (Bala *et al.,* 2011). KBRL 81-1 is one such line developed utilizing HD 29 as a donor parent.

Morpho-agronomic characteristics: The parental lines WH 542 and HD 29 and the germplasm KBRL 81-1 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980). The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in Table 1a & 1b.

Table 1a. KB infection and yield data of KBRL 81-1 and the parents

Name	Pedigree	KB infection (%)				Yield (q/ha)			
		2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 81-1	HD 29/*6WH 542	3.4	2.9	4.7	3.6	54.3	44.8	49.2	49.4
HD 29	Donor Parent	4.1	2.8	3.9	3.6	31.0	34.8	38.1	34.6
WH 542	Recipient parent	42.1	37.9	46.4	42.1	47.3	44.7	45.3	45.8

Table 1b. Agronomic characteristics of KBRL 81-1 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/meter	Grains per spike	1000-grains weight
KBRL 81-1	HD 29/*6WH 542	89	148	116	58	45
HD 29	Donor Parent	96	145	106	48	42
WH 542	Recipient parent	92	142	129	67	39

Associated characters and cultivation practices: The germplasm KBRL 81-1 is highly resistant to Karnal bunt disease of wheat. Also this line carries good agronomic characteristics. With limited sources of resistance to KB, KBRL 81-1 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

References

Anonymous (2015) Progress report of All India Coordinated Wheat & Barley Improvement Project 2014-15, Vol. III, Crop Protection. (Eds.): M S Saharan, Sudheer Kumar, R Selvakumar, Subhash Katare, Poonam Jasrotia and Indu Sharma. Indian Institute of Wheat & Barley Research, Karnal. India. pp. 76-80.

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8. KBRL82-2 (IC0616066; INGR15044), a Wheat (*Triticum aestivum*) Germplasm with Karnal Bunt Resistance and High Number of Tillers/m

Indu Sharma*, Ritu Bala, NS Bains, RC Sharma, Satish Kumar, MS Saharan and Vinod Tiwari
ICAR-Indian Institute of Wheat & Barley Research (IIWBR), Karnal-132001, Haryana, India
*(*Email: ramindu2000@yahoo.co.in*)

Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. The basic studies on KB at PAU, Ludhiana have revealed a few diverse sources of resistance (Sharma *et al.*, 2005) which were incorporated in to a high yielding wheat variety WH 542 (Kaur *et al.,* 2011) using backcross approach and simultaneous screening for the disease resistant lines. Further genetic analysis in the derivatives from the crosses of donors with WH 542 indicated that the donors are diverse for resistance to KB which was found to be governed by 2-3 additive genes (Bala *et al.*, 2011). KBRL 82-2 is one such line developed utilizing HP 1531 as a donor parent.

Morpho-agronomic characteristics: The parental lines WH 542 and HP 1531 and the germplasm KBRL 82-2 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980). The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in Table 1a & 1b.

Table 1a. KB infection and yield data of KBRL 82-2 and the parents

Name	Pedigree	KB infection (%)				Yield (q/ha)			
		2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 82-2	HP 1531/*6WH 542	2.1	3.6	4.5	3.4	52.7	47.6	49.9	50.1
HP 1531	Donor Parent	2.8	1.7	3.1	2.5	29.1	34.5	33.7	32.4
WH 542	Recipient parent	42.1	37.9	46.4	42.1	47.3	44.7	45.3	45.8

Table 1b. Agronomic characteristics of KBRL 82-2 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/meter	Grains per spike	1000-grains weight
KBRL 82-2	HP 1531/*6WH 542	91	139	143	54	47
HP 1531	Donor Parent	107	147	107	49	49
WH 542	Recipient parent	92	142	129	67	39

Associated characters and cultivation practices: The germplasm KBRL 82-2 is highly resistant to Karnal bunt disease of wheat. Also this line carries good agronomic characteristics including high number of tillers per meter. With limited sources of resistance to KB, KBRL 82-2 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

References

Anonymous (2015) Progress report of All India Coordinated Wheat & Barley Improvement Project 2014-15, Vol. III, Crop Protection. (Eds.): M S Saharan, Sudheer Kumar, R Selvakumar, Subhash Katare, Poonam Jasrotia and Indu Sharma. Indian Institute of Wheat & Barley Research, Karnal. India. pp. 76-80.

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9. KBRL 83-3 (IC0616067; INGR15045), a Wheat (*Triticum aestivum*) Germplasm with Karnal Bunt Resistance and High 1000 Grains Weight

Indu Sharma*, Ritu Bala, NS Bains, RC Sharma, Satish Kumar, MS Saharan and Vinod Tiwari
ICAR-Indian Institute of Wheat & Barley Research (IIWBR), Karnal-132001, Haryana, India
*(*Email: ramindu2000@yahoo.co.in*)

Karnal bunt (KB) disease of wheat is importance due to its implications on international wheat grain market. The wheat grains infested with this disease cannot be exported outside the country due to quarantine regulations. Thus incorporation of resistance to this disease became a primary objective, if wheat is to be exported. Resistance breeding has emerged as the only viable option for controlling the KB problem. However, very few sources of resistance to this disease are known. The basic studies on KB at PAU, Ludhiana have revealed a few diverse sources of resistance (Sharma *et al.*, 2005) which were incorporated in to a high yielding wheat variety WH 542 (Kaur *et al.,* 2011) using backcross approach and simultaneous screening for the disease resistant lines. Further genetic analysis in the derivatives from the crosses of donors with WH 542 indicated that the donors are diverse for resistance to KB which was found to be governed by 2-3 additive genes (Bala *et al.,* 2011). KBRL 83-3 is one such line developed utilizing W 485 as a donor parent.

Morpho-agronomic characteristics: The parental lines WH 542 and W 485 and the germplasm KBRL 83-3 were tested for yield and other morpho-agronomic characteristics during three years from 2012-13 to 2014-15 (Anonymous 2015). Also these lines were inoculated artificially every year with spores of *Nevossia indica* using the syringe method as proposed by Aujla *et al.* (1980). The data on various traits recorded along with yield (q/ha) and Karnal bunt infection is given in table 1a & 1b.

Table 1a. KB infection and yield data of KBRL 83-3 and the parents

Name	Pedigree	KB infection (%)				Yield (q/ha)			
		2012-13	2013-14	2014-15	Av.	2012-13	2013-14	2014-15	Average
KBRL 83-3	W 485/*6WH 542	3.6	1.5	2.7	2.6	51.3	51.6	49.3	50.7
W 485	Donor Parent	2.4	3.4	3.3	3.0	36.1	37.0	35.6	36.2
WH 542	Recipient parent	42.1	37.9	46.4	42.1	47.3	44.7	45.3	45.8

Table 1b. Agronomic characteristics of KBRL 83-3 and the parents

Name	Pedigree	Plant height (cm)	Days to maturity	Number of tiller/meter	Grains per spike	1000-grains weight
KBRL 83-3	W 485/*6WH 542	89	149	142	54	49
W 485	Donor Parent	99	149	116	45	49
WH 542	Recipient parent	92	142	129	67	39

Associated characters and cultivation practices: The germplasm KBRL 83-3 is highly resistant to Karnal bunt disease of wheat. Also this line carries good agronomic characteristics including high 1000 grains weight. With limited sources of resistance to KB, KBRL 83-3 can be used in wheat breeding programs across the country for incorporation resistance to this disease.

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10. PAU16055 (IC0616571; INGR15046), a Wheat (*Triticum aestivum* L.) Germplasm with Leaf Rust and Stripe Rust Resistance Genes Lr57 and Yr40

Parveen Chhuneja*, Satinder Kaur and HS Dhaliwal
School of Agricultural Bio-technology, Punjab Agricultural University (PAU) Ludhiana-141027, Punjab, India
*(*Email: pchhuneja@pau.edu*)

An *Aegilops geniculata* ($U^gU^gM^gM^g$) accession PAU3547 was crossed with a leaf rust and stripe rust susceptible *T. aestivum* cv. WL711 and disomic substitution lines with 5M chromosome of *Ae. geniculata* substituted for 5D of wheat {DS5D(5M)} were developed through restricted backcrossing and selfing. These substitution lines were resistant to leaf rust and stripe rust and have been registered as INGR03018. For the reduction of the linkage drag, one of the substitution lines was crossed with a Chinese Spring stock carrying inhibitor for *Ph1* locus (CSPh^I) and resulting F_1 was crossed to WL711. Leaf rust and stripe rust resistant introgression lines (ILs) were developed by induced homoeologous chromosome pairing between wheat chromosome 5D and $5M^g$ of *Aegilops geniculata* (UM). Characterization of rust resistant homozygous ILs with Genomic *in situ* hybridization (GISH) method using *Aegilops comosa* (M) DNA as probe identified an IL PAU16055 (syn. T598) having small introgression on the short arm of wheat chromosome 5D. The IL PAU16055 showed complete resistance to the most prevalent pathotypes of leaf rust and stripe rust in India. Molecular mapping using physically mapped RFLP probes revealed that the alien introgression in PAU16055 conferring resistance to leaf rust and stripe rust comprised less than 25% of the short arm of wheat chromosome 5D (Kuraparthy *et al.,* 2007).

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11. PAU16057 (IC0616573; INGR15047), a Wheat (*Triticum aestivum* L.) Germplasm with New leaf Rust and Stripe Rust Resistance Genes

Parveen Chhuneja*, Satinder Kaur, Kuldeep Singh and HS Dhaliwal
School of Agricultural Bio-technology, Punjab Agricultural University (PAU) Ludhiana-141027, Punjab
*(*Email: pchhuneja@pau.edu*)

Aegilops umbellulata acc. 3732 was found to be an excellent source of resistance to major wheat diseases including leaf rust and stripe rust. An amphiploid *Ae. umbellulata* acc. 3732 and *Triticum durum* cv. 'WH890' was crossed with Chinese Spring Ph^I to induce homoeologous pairing between *Ae. umbellulata* and wheat chromosomes. The F_1 was crossed to the susceptible *Triticum aestivum* cv. 'WL711' and leaf rust and stripe rust resistant plants were selected among the backcross progenies. Homozygous lines were selected and screened against six *Puccinia triticna* and four *Puccinia striiformis* f. sp. *tritici* pathotypes at the seedling stage and a mixture of prevalent pathotypes of both rust pathogens at the adult plant stage. Depending on the rust reactions and allelism tests, the introgression lines with new seedling leaf rust and stripe rust resistance genes were identified. Introgression line PAU16057 carries two new genes - one for leaf rust resistance and one for stripe rust resistance introgressed into wheat from *Ae. umbellulata* (Chhuneja *et al.,* 2008). This introgression with no apparent linkage drag is being used in the wheat breeding programme. A marker *Lr57-Yr40_caps16* is the closest linked marker which is being used for marker assisted selection of these genes. Leaf rust and stripe rust resistance genes in PAU16057 have been designated as *Lr76* and *Yr70*, respectively (Bansal *et al.,* 2016).

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12. PAU16058 (IC0616574; INGR15048), a Wheat (*Triticum aestivum* L.) Germplasm with New Leaf Rust and Stripe Rust Resistance Genes

Parveen Chhuneja*, Satinder Kaur, Kuldeep Singh and HS Dhaliwa
School of Agricultural Bio-technology, Punjab Agricultural University (PAU), Ludhiana-141027, Punjab
*(*Email: pchhuneja@pau.edu*)

Aegilops peregrina (syn *Aegilops variabilis*) 2n=4x=28, a tetraploid non progenitor species of wheat with UUSS genome. It has been found to be a useful source for resistance to stripe rust and leaf rust, making this species an important source to transfer useful genes. *Ae. peregrina* acc. pau 3519, was crossed with Chinese Spring stock, CS (Ph^1), carrying an inhibitor of Ph^I locus for the induction of homoeologous pairing. The resultant F_1 plants were crossed with rust susceptible *T. aestivum* cv. WL711(NN), which has *kr* (crossability) alleles. All BC_1 plants were screened at the seedling stage and adult plant stage against leaf rust and stripe rust. The plants resistant to both the rusts were backcrossed to WL711 (NN) to recover the recurrent genotype. Some selected BC_2F_1plants were selfed to BC_2F_4introgression lines. Homozygous wheat-*Ae. peregrina* ILs *viz.* PAU16058 with 2n=42 chromosomes was selected for a donor stock for transfer of leaf rust and stripe rust resistance to elite wheat backgrounds.Molecular mapping using F_2 population between PAU16058 and WL711 mapped stripe rust resistance gene *YrP* at a distance of 6.7cM from three co-localized markers (*Xgwm234, 5DS_276,* and *5DS_159*) while leaf rust resistance gene *LrP* was mapped at distance of 1.1cM from *YrP* towards distal end of chromosome 5D.

13. PAU16059 (IC0617118; INGR15049), a Wheat (*Triticum aestivum* L.) Germplasm with New Leaf Rust and Stripe Rust Resistance Genes

Kuldeep Singh, Parveen Chhuneja*, Satinder Kaur and HS Dhaliwal
School of Agricultural Bio-technology, Punjab Agricultural University (PAU) Ludhiana-141027, Punjab
*(*Email: pchhuneja@pau.edu*)

The diploid 'A' genome progenitor gene pool of wheat, comprising three closely related species *T. monococcum*, *T. boeoticum* and*T. urartu*, harbours useful genes for many economically important traits including resistance to different diseases. *T. monococcum* accession. PAU14087 and *T. Boeoticum* accession PAU5088 are highly resistant to leaf rust and stripe rust and RIL population generated from these two accessions segregated for resistance to leaf rust and stripe rust. One of the RILs designated as RIL101 wascrossed to susceptible *T. durum* parent, N59 and F_1 further crossed and backcrossed with hexaploidwheat cultivar WL711 led to the development of leaf rust and stripe rust resistant introgression lines (Singh *et al.,* 2007). Segregating populations from these introgression lines have been evaluated in field and glass house for leaf rust and stripe rust resistance and one gene for leaf rust and two genes for stripe rust resistance have been identified. The leaf rust resistance gene from *T. monococcum LrTm* has been mapped on wheat chromosome 6A. Two stripe rust resistance genes one each from *T. monococcum* and *T. boeoticum* were mapped on chromosome 2A and 5A in the RIL population derived from *T. boeoticum/T. monococcum* cross (Chhuneja *et al.,* 2008). One of the QTL designated as *QYrTm.pau-2A* maps in the 3.6 cM region between the SSR markers *Xwmc407* and *Xwmc170.* Other QTL on chromosome 5A designated as *QYrTm-5A* mapped in 8.9 cM region between the markers *Xbarc151* and *Xcfd12* on the long arm. The introgression lines with leaf rust and stripe rust resistance are bing used to transfer these genes to elite wheat backgrounds.

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14. PAU16060 (IC0616575; INGR15050), a Wheat (*Triticum aestivum* L.) Germplasm with New Leaf Rust and Stripe Rust Resistance Genes

Parveen Chhuneja*, Satinder Kaur, Kuldeep Singh and HS Dhaliwal
School of Agricultural Bio-technology, Punjab Agricultural University (PAU) Ludhiana-141027, Punjab
**(Email: pchhuneja@pau.edu)*

A leaf rust and stripe rust resistant accession of diploid non-progenitor species with CC genome, namely *Aegilops caudata* L. acc. PAU#3556, was crossed with *Triticum durum* cv. WH868 and an amphiploid was synthesized which was further crossed with a Chinese Spring stock, CS (Ph^1), carrying an inhibitor for *Ph1* locus, for the induction of homoeologous pairing. The F_1 plants were crossed with a leaf rust and stripe rust susceptible cultivar WL711 for transferring leaf and stripe rust resistance genes to bread wheat. Homozygous F_8 introgression line PAU16060 with 2n=42, was developed with high level of resistance to both leaf rust and stripe rust. It was crossed with wheat cv. PBW343 and BC-RIL population developed. The population segregated for single seedling leaf rust resistance gene and an adult plant stripe rust resistance genes. The genetic mapping using SSRs located leaf rust resistance on short arm of wheat chromosome 5D (Riar *et al.*, 2012). Further genetic analysis using markers from wheat survey sequence (IWGSC 2014) mapped stripe rust resistance locus, temporarily designated as *YrAc*, at the distal most end of 5DS linked with a group of four co-located SSRs and two RGA-STS markers at a distance of 5.3cM. Leaf rust resistance *LrAc* mapped at a distance of 9.0cM from the *YrAc* and at 2.8cM from RGA-STS marker *Ta5DS_2737450* (Toor *et al*., 2016). PAU16060 and derived BC-RILs are being used for transfer of these genes to elite wheat backgrounds using marker assisted selection.

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15. PAU16062 (IC0616577; INGR15051), a Wheat (*Triticum aestivum* L.) Germplasm with New Leaf Rust and Stripe Rust Resistance Genes

Parveen Chhuneja*, Satinder Kaur and HS Dhaliwal
School of Agricultural Bio-technology, Punjab Agricultural University (PAU) Ludhiana-141027, Punjab
**(Email: pchhuneja@pau.edu)*

An *Aegilops geniculata* accession 3547 was crossed with a susceptible *T. aestivum* cv. WL711 and disomic substitution lines with 5M chromosome of *Ae. geniculata* substituted for 5D of wheat {DS5D(5M)} were developed through restricted backcrossing and selfing. These substitution lines were resistant to leaf rust and stripe rust and have been registered as INGR03018. For the reduction of the linkage drag, one of the substitution lines was crossed with a Chinese Spring stock carrying inhibitor for *Ph1* locus ($CSPh^I$) and F_1 was crossed to WL711. Leaf rust and stripe rust resistant introgression lines were developed by induced homoeologous chromosome pairing between wheat chromosome 5D and $5M^g$ of *Aegilops geniculata* (UM). Characterization of rust resistant homozygous introgression lines using genomic *in situ* hybridization with *Aegilops comosa* (M) DNA as probe identified an introgression line T756 (PAU16062) with cytologically undetectable introgression. The introgression line PAU16062 showed complete resistance to the most prevalent pathotypes of leaf rust and stripe rust in India. Molecular mapping revealed that cryptic alien introgression conferring resistance to leaf rust and stripe rust comprised less than 5% of the short arm of wheat chromosome 5D. Genetic mapping with an F_2 population of PAU16062 demonstrated the monogenic and dominant inheritance

of resistance to both diseases. Two diagnostic RFLP markers, previously mapped on chromosome arm 5DS, co-segregated with the rust resistance in the F_2 population. The unique map location of the resistant introgression on chromosome 5DS suggested that the leaf rust and stripe rust resistance genes were new and were designated *Lr57* and *Yr40*(Kuraparthy *et al*., 2007). A STS marker *Lr57-Yr40_caps16* has been found to co-segregate with these genes and is being used for marker assisted transfer of *Lr57* and *Yr40* to elite wheat backgrounds.

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16. PBW703 (IC0616578; INGR15052), a Wheat (*Triticum aestivum* L.) Gene Pyramided Line Carrying Leaf Rust Resistance Genes *Lr*24 and *Lr*28 and Stripe Rust Resistance Genes *Yr*10 and *Yr*15

NS Bains*, P Chhuneja, A Sharma, S Kaur, P Srivastava, GS Mavi and VS Sohu

Dept. of Plant Breeding and Genetics, Punjab Agricultural University (PAU), Ludhiana-141004, Punjab

*(*Email: nsbains@rediffmail.com;navtejsingh@pau.edu*)

High productivity and wide adaptation rendered wheat variety PBW 343 an excellent target for incorporation of rust resistance genes through marker assisted selection (MAS). PBW 343, (one of the 'Attila' sibs from CIMMYT, Mexico) was released by Punjab Agricultural University in 1995 for timely sown, irrigated conditions of North Western Plains Zone (NWPZ). After a reign of more than a decade as a mega variety grown on more than 7 million hectares, PBW 343 succumbed to highly virulent stripe rust race, 78S84, which led to its exit from cultivation in this zone. Earlier it had succumbed to new leaf rust strains belonging to 'race 77 complex'. MAS generated near isogenic lines in PBW 343 background with leaf rust resistance genes *Lr*24 and *Lr*28 had been developed previously (Chhuneja *et al.,* 2005) and a high yielding version named as BWL 9250 was identified for further crosses. BWL9250 was crossed and backcrossed to two different genetic stocks, Avocet 6*/*Yr10* and Avocet 6*/*Yr15* individually for incorporation of the highly effective stripe rust resistance genes *Yr*10 and *Yr*15. Both individual backcross selected progenies (BC_2F_1) were subjected to MAS and identified positive plants were involved in convergent crosses to pyramid the four genes viz., *Lr*24-*Lr*28-*Yr*10-*Yr*15. Genes *Lr*24, *Lr*28 are present on chromosomes 3DL and 4AL respectively while *Yr*10 and *Yr*15 are present on 1BS and have accessions of *Agropyron elongatum* (Syn. *Thinopyrum ponticum*), *Triticum speltoides*, *Triticum spelta* and *Triticum dicoccoides* respectively as their original sources (McIntosh *et al.,* 1995). Markers *Xwmc313*, *scs-73$_{719}$-1(SCAR)*, *Xbarc* 8 and *Xpsp*3000 (http://maswheat.ucdavis.edu, http://wheat.pw.usda.gov/cgi-bin/graingenes) were employed for marker assisted selectionof genes *Lr*28, *Lr*24, *Yr*15 and *Yr*10 respectively. A large set of lines was carried to homozygosity with extensive use of off-season location in Lahaul-Spiti (HP) and molecular marker assays for the rust resistance genes. Two outstanding derivatives PBW 698 and PBW 703 were nominated for all India coordinated wheat trials under irrigated regime for timely sown and late sown conditions respectively. PBW 703 was confirmed to be positive for all the four genes with least detriment to the recipient parent attributes and was thus chosen for registration as a stock.

Morpho-agronomic characteristics: PBW 703 is 100 cm tall, with 116 tillers per metre row length and 17 spikelets per spike. It took 99 days to flower (50%) and yielded 52.9 q/ha under timely sown conditions. In contrast to PBW 343, PBW 703 has red glume colour (tightly linked to *Yr*10 gene). PBW 703 was evaluated in NIVT (National Initial Varietal Trial) in 2012-13 at eight locations under late-sown, irrigated conditions. It was promoted to AVT (Advanced Varietal Trial) carried out at 17 locations in NWPZ during 2013-14, whose summary of results is given below:

AVT I -late sown, irrigated conditions	PBW 703	WH 1021	HD 3059	PBW590	PBW343	C.D.
Yield (Q/ha)	46.9	40.3	48.6	40.0	-	0.8
Average coeff. of stripe rust infection	1.3	19.9	4.7	31.5	58.9	-
Average coeff. of leaf rust infection	0.0	11.0	0.2	5.0	8.1	-

Associated characters and cultivation practices: PBW 703 showed complete resistance to two widely prevalent stripe rust races 78S84 and 46S119 and two major leaf rust races 77-5 and 104-4 at seedling as well as adult plant stage. PBW 703 is agronomically competitive, carries four effective rust resistance genes and can be of great significance as a parental line in wheat breeding programmes of the country.

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17. DWR 30 (IC0616068; INGR15053), a Barley (*Hordeum vulgare L.*) Germplasm with High Beta Glucan Content in Grain

Dinesh Kumar*, RPS Verma, Sneh Narwal, Jogendra Singh, Rekha Malik, AS Kharub and Indu Sharma
ICAR-Indian Institute of Wheat & Barley Research (IIWBR), Karnal-132001, Haryana
**(Email: dkbiochem69@gmail.com)*

With the changing lifestyles and increasing urbanization, the diseases like coronary heart disease, diabetes *etc*. are on the rise in India. One of the ways suggested to control these diseases is changes in the dietary habits. Besides this in past few years it has been shown that inclusion of nutraceuticals such as soluble dietary fibres can help in controlling the blood cholesterol and glucose levels besides providing benefits to gut health. Cereals, specifically, the barley and oats possess higher amounts (3-7%) of one such dietary fibre called beta glucan. The mixed linkage (1-3; 1-4) beta glucans have been shown to lower postprandial blood glucose and lower the LDL cholesterol and thus help in reducing the risk of heart diseases and type-2 diabetes (Sullivan *et al*., 2013) and is approved in many countries as health benefitting soluble fibre. Screening of germplasm lines and varieties for higher grain beta glucan lines was started at the ICAR-IIWBR, Karnal and the germplasm line DWR30 (hulled barley) has been identified with higher beta glucan content (>6.0 % dwb). The genotype can serve as a good material for basic scientific studies regarding biochemical and genetic factors controlling beta glucan content in the barley grains being grown under sub-tropical climates of India where grain filling period is too short as compared to temperate climates. Further the genotype can also be used for food barley improvement programme, wherein barleys with higher beta glucan content can be very useful from health point of view.

After initial screening at ICAR-IIWBR, Karnal, DWR 30 was evaluated at seven locations (Karnal, Hisar, Ludhiana, Faizabad, Kanpur, Rewa and Bajaura) during 2012-13 and at eight locations (Karnal, Durgapura, Hisar, Ludhiana, Faizabad, Kanpur, Rewa and Bajaura) during 2013-14 for different grain quality traits and average values are given in Table 1 and Table 2.

Table 1. Mean performance (mean of seven locations) of genotypes with high beta glucan content during *rabi* 2012-13

Genotype	Beta Glucan (% dwb)	Protein (% dwb)	Bold grain (%)	Thin grain (%)	1000 grain wt (g)
DWR30	6.9	12.1	74.2	2.5	49.3
DWRUB73 (c)	5.8	13.0	74.8	3.6	49.5
RD2668 (c)	5.7	11.9	62.2	5.4	40.5
BHS352 (c)*	6.5	12.8	14.2	48.2	29.7
HBL276 (c)*	6.0	14.0	20.7	44.1	29.4

Source: AICW&BIP – Barley Network (2012-13)*Husk less barley

Table 2. Mean performance (mean of eight locations) of genotypes with high beta glucan content during *rabi* 2013-14

Genotype	Beta Glucan (% dwb)	Protein (% dwb)	Bold grain (%)	Thin grain (%)	1000 grain wt (g)
DWR30	7.4	12.3	65.0	6.0	48.3
DWRUB73 (c)	5.7	12.7	83.0	4.9	49.8
RD2668 (c)	6.0	12.3	62.9	7.9	41.1
BHS352 (c)*	6.4	14.3	14.1	57.9	32.3
HBL276 (c)*	5.4	15.3	6.6	62.5	25.9

Source: AICW&BIP – Barley Network (2013-14) *Husk less barley

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18. BK 1127 (IC06160298; INGR15054), a Barley (*Hordeum vulgare L.*) Germplasm with High Thousand Grain Weight and Protein Content

Dinesh Kumar[1]*, RPS Verma[2], Sneh Narwal[1], Jogendra Singh[1], Vishnu Kumar, AK Khippal, AS Kharub[1] and Indu Sharma[1]

[1]*ICAR-Indian Institute of Wheat & Barley Research (IIWBR), Karnal-132001, Haryana, India*

[2]*International Center for Agricultural Research in the Dry Areas, Morocco*

**(Email: dkbiochem69@gmail.com)*

Grain number and thousand-grain weight (TGW) are considered to be the most important grain yield components in case of cereal crops including barley. Thousand grain weight is considered as an important parameter in case of two-row barleys as higher thousand grain weight is important contributing factor in addition to the higher tillering capacity for yield compensation as compared to six rowed varieties. Furthermore, the TGW trait is widely used as a standard indicator for grain development and quality and presently is limiting factor for six row barley in India. At ICAR-IIWBR, Karnal, BK 1127, has been identified having high mean thousand grain weight (mean value > 50.0 g) during two crop seasons over different diverse locations. This genotype can serve as useful material for genetics studies and developing improved barley cultivars for higher thousand grain weight in barley.

There is renewed interest in the barley grain since last few years due to its health benefits and it is expected that in coming years the consumption of food barley may increase (Baik and Ullrich, 2008). Therefore, the genotypes of barley are also being screened for higher protein content without compromising the grain boldness. Genotype BK 1127 has higher protein content (mean value of > 14.0% dwb) also. BK 1127 by combining the higher protein and high thousand grain weight, can prove useful source of nutritional traits for the future food barley improvement programme in the country.

After initial screening at ICAR-IIWBR, Karnal, BK 1127 was evaluated at seven locations (Karnal, Hisar, Ludhiana, Faizabad, Kanpur, Rewa and Bajaura) during 2012-13 and at eight locations (Karnal, Durgapura, Hisar, Ludhiana, Faizabad, Kanpur, Rewa and Bajaura) during 2013-14 for grain quality traits, including the bold seeded checks of two row barley and mean values of different traits are presented in Table 1 and 2.

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Table 1. Mean performance (mean of seven locations) of genotypes with high thousand grain weight during *rabi* 2012-13

Genotype	1000 grain wt (g)	Protein (% dwb)	Bold grain (>2.5mm) (%)	Thin grain (<2.2 mm) (%)
BK 1127	53.6	14.6	94.8	1.0
DWR 91 ©	35.1	12.3	69.6	7.3
DWRUB 52 ©	44.3	11.6	82.5	2.4

Source: AICW&BIP – Barley Network (2012-13)

Table 2. Mean performance (mean of eight locations) of genotypes with high thousand grain weight during *rabi* 2013-14

Genotype	1000 grain wt (g)	Protein (% dwb)	Bold grain (>2.5mm) (%)	Thin grain (<2.2 mm)(%)
BK 1127	59.8	14.4	86.9	1.3
DWR 28 (c)	50.8	12.8	91.1	2.0
DWRUB 52 (c)	46.3	10.2	85.6	3.1
DWRB 92 (c)	50.2	13.5	84.5	5.3
BH 902 (c)*	42.1	11.1	85.6	5.3

Source: AICW&BIP – Barley Network (2013-14) *Six rowed barley

19. SRP#75 (IC0616375; INGR15055), a Self-Compatible Obligate Sexual Guinea Grass (*Panicum maxicum* Jacq.) Line

P Kaushal*, KK Dwivedi, A Radhakrishna, DR Malaviya and AK Roy
ICAR-Indian Grassland and Fodder Research Institute, Jhansi-284003, Uttar Pradesh, India
*(*Email pkaushal70@gmail.com*)

Guinea grass (*Panicum maximum* Jacq.) is a high yielding perennial multicut forage grass, widely grown in tropical and sub-tropical countries. Tetraploid cytotypes (2n=4x=32) with obligate apomictic mode of reproduction are most predominant (Savidan 1981, Jain *et al.,* 2003). Breeding through hybridization approach is restricted in these grasses owing to apomixis, and thus a large part of potential variability goes untapped (Savidan 2000). Identification and utilization of sexual lines in otherwise apomictic crops has great potential in generating desirable variability for genetical and breeding studies. However, availability of obligate sexual lines in guinea grass is highly limited both nationally and internationally. Moreover, most of the obligate sexual lines are generally weak and self-incompatible, and do not set seed on self-pollination. To our knowledge, no sexual line in guinea grass is registered in India. It thus becomes imperative to identify and utilize sexual lines in guinea grass. Additionally, obligate sexual line with self compatible and vigourous morphology would be added advantage in their selection as one of the parents.

A segregating population (represented by more than 85 progenies) was generated from a cross between an exotic self-incompatible sexual line (SPM92) and an obligate apomictic variety (Riversdale), and was characterized for mode of reproduction (sexual, apomictic or facultative) utilizing methyl salicylate mediated cleared whole ovule mounts observed under differential interference contrast microscope following Kaushal *et al.* (2008). Self-compatibility was tested by subjecting panicles to forced self pollination in pollination bags. Amongst the progenies, a rare self-compatible obligate sexual plant viz., SRP#75 was identified. This plant (SRP#75) generated all sexual embryo-sacs (ES), with no multiple ES and less aborted ES (19%), was self-compatible, vigourous, perennial, multicut and vegetatively propagated, thus making it highly suitable to be utilized as female parent in hybridization programme in guinea grass genetics and breeding experiments.

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20. L-4704 (IC0616579; INGR15056), a Lentil (*Lens culinaris* subsp. *culinaris*) Germplasm with High Grain Iron and Zinc

HK Dikshit*, Dharmender Singh, Muraleedhar Aski, Jyoti Kumari, Harish Kumar and Akanksha Singh
Division of Genetics, ICAR-Indian Agricultural Research Institute, Pusa Campus-110012, New Delhi, India
*(*Email:harshgeneticsiari@gmail.com;hk_dikshit@rediffmail.com*)

The cultivated lentil is an ancient crop originated somewhere in the 'Fertile Crescent'. All Lens species are self-pollinated annual diploids with 2n = 2x = 14 chromosomes having haploid genome size of 4063 Mbp (Arumuganathan and Earle, 1991). It is cultivated in as many as 52 countries across the world with an area and production of 4.08 million ha and 4.36 million t, respectively (FAO, 2013). Its wide-spread cultivation owes to its ability to produce a high quality protein in drought-prone marginal environments. In India, lentil is cultivated on 1.48 million ha area with production and productivity of 0.98 mt and 660 kg ha^{-1}, respectively. Micronutrient malnutrition affects more than two billion people worldwide. Particularly vulnerable are women and preschool children in south Asia, Africa and Latin America. Micronutrient malnutrition has been addressed through food fortification, dietary supplementation and biofortification of staple crops, but to date such programs have had limited success. Sustainable solutions to malnutrition in general, including micronutrient malnutrition, calls for better linking food systems with the dietary needs of people. The biofortification approach holds great promise for improving the nutritional, health, and socioeconomic status of people around the world. Lentils are rich in minerals: Se (500–2500 μg kg^{-1}), Fe (60–80 mg kg^{-1}), Zn (44–54 mg kg^{-1}), and with very low concentration of phytic acid (6–8 mg g^{-1}) and high in ascorbic acid. (Casey Johnson *et al*., 2013). L 4704 is unique because of it is rich in Iron and Zinc, 136.91 mg/kg and 71.69 mg/kg of seed respectively. It was developed at Division of Genetics, IARI, and New Delhi by pedigree method of selection from cross between L 4149 × L 4076 parents.

Morpho-agromonic characters: Morpho-agromonic characters of line L 4704 are its height ranges 40-44 cm with erect plant type with days to 50% flowering ranges from 70-74. It reaches to physiological maturity around 130 to 135 days. The 100 seed weight of L 4704 is 2.5 grams. Seed testa colour is brown and pattern of seed testa is dotted in nature along with orange red cotyledon. The harvest index ranges between 31-33 %. Number of pods per plant rages between 160-165 with a single plant yield of 6.0 to 6.5 gms. Multilocation data on yield in NHZ (1098 kg/ha), NWPZ (1063kg/ha) and in NEPZ (1072 kg/ha) and 100 seed weight (gm) NHZ (3.1 gm) NWPZ (2.9 gm) and NEPZ (3.4 gm) (ACRIP on MULLaRP *Rabi* report – 2010). Uniqueness of this line for having high grin Fe 136.91 mg/kg seed and Zn 71.69 mg/kg seed (reference).

Associated characters and cultivated practices: This line is moderately resistant to resistant root knot nematode (*Meloidogyne inconita*) and nematode M *javanica*. Land should be prepared by one ploughing and two harrowing. Lentil is grown in *rabi* season. Sowing time in October – November in *rabi*. Seed rate is 35-40 kg/ha. Spacing is 30 x 10 cm. Seeds are treated fungicide, insecticide and with rhizobium culture before sowing. Sowing is done by drilling or broadcasting method. One weeding and two hoeing are done for control of weeds. Manuring: 3 to 5 tons FYM and DAP 100 kg/ha. Generally, lentil is grown as unirrigated crop in the residual soil moisture but irrigation at pod development stage helps in getting more yield.

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21. Chilli Queen Sima (IC0615423; INGR15057), a Chilli (*Capsicum annum)* Germplasm with Tall Plant and High Capsaicin Content. SHU (Scoville Heat Unit) Red Fruit 274500 and Green Fruit 259500

Sumanta Misra*
Pandapara, Jalpaiguri-735132, West Bengal, India
*(*Email: sumantamisra@ymail.com*)

22. CS 1100-1-2-2-3 (IC0511389; INGR15058), an Indian mustard (*Brassica juncea* (L.) Czern. Germplasm with Suitable for Salt Affected Soils of Indo-Gangetic Plains

PC Sharma, Jogendra Singh and DK Sharma*
ICAR-Central Soil Salinity Research Institute (CSSRI), Karnal-132001, Haryana, India
* (*Email: director.cssri@icar.gov.in*)

Globally, 932.2 million hectare area is affected with salinity and sodicity stresses (Metternicht and Zinck, 2003), out of which, an area of nearly 6.73 million hectare is affected by these stresses in India (Singh *et al.*, 2014). Indian mustard[*Brassica juncea* (L.) Czern and Coss] is an important oil-seed crop in the world and is grown in more than 50 countries across the globe, which often experiences saline stress as it is grown extensively in the arid and semi-arid regions of the world. Salinity stresses contribute to yield losses and this low economic yield is related to the crop's susceptibility. There is a greater need to improve crop plants for salinity tolerance. Hence, it becomes necessary to develop salt tolerant genotypes in Indian mustard. One of the approaches is the characterization of the available germplasm for identification of tolerant genotypes that provides an initial germplasm base for breeding salt-tolerant crops.

Consistent breeding efforts at ICAR-Central Soil Salinity Research Institute (ICAR-CSSRI), Karnal resulted in the development of an improved salt tolerant genotype CS 1100-1-2-2-3 by crossing two salt tolerant genotypes CS 52 and CS 609-B10 (CS 52: a highly salt tolerant variety; CS 609-B10: a high yielding (Seed and oil) salt tolerant genotype, both developed at ICAR-Central Soil Salinity Research Institute, Karnal). Pedigree method was followed for selection and evaluation of germplasm in salt affected soils for high seed yield and tolerance to soil salinity conditions.

Morpho-agronomic characteristics: On the basis of three year (2012-13 to 2014-15) trials conducted for saline/alkaline conditions in AICRP on Rapeseed and Mustard, CS 1100-1-2-2-3 provided mean seed yield of 2090 kg/ha which was 23% higher than yields of two checks i.e. CS 54 (1707 kg/ha) and Kranti (1704 kg/ha). It also provided 26-28% higher oil yield (798 kg/ha) than CS 54 (620.5 kg/ha) and Kranti (633.5 kg/ha). This strain matures, on an average, in 138 days and takes 59 days to flower. The strain attains the height of approximately 175 cm; main shoot length (89) and 1000 seed weight (5g) (Table 1).

Associated characters and cultivated practices: CS 1100-1-2-2-3also showed resistance to Alternaria blight under natural conditions compared to check Rohini and salt tolerant variety CS 54. Alterneria blight severity in pods was at par with checks. Further, it also showed much lesser incidence of white rust, powdery mildew, downy mildew and sclerotinia rot compared to check Rohini. Under artificial conditions also, similar performance was recorded. Against mustard aphid, data of 24 trails showed lesser average aphid infestation index (AAI)

Table 1. Multi-location performance on important traits like yield and yield components [Locations: Salinity [Agra (ECiw 12 dS/m) Karnal (ECe 10.7 dS/m), Hisar (ECe 10.6 dS/m)]; Alkalinity: Karnal (pH 9.3) and Lucknow (pH 9.4)]

Parameters	Year of testing	Proposed genotype CS 1100-1-2-2-3	Check 1 CS 54 (NC)	Check 2 Kranti (NC)
Mean Seed Yield (Kg/ha)	2012-13	2168	1923	1841
	2013-14	2053	1649	1770
	2014-15	2049	1550	1502
	Mean	2090	1707	1704
Per cent increase (+) or decrease (-) over checks	2012-13		+12.74	+17.76
	2013-14		+24.50	+15.99
	2014-15		+32.19	+36.42
	Mean		+23.14	+23.39
Mean Oil Yield (Kg/ha)	2012-13	- #	- #	- #
	2013-14	789	639	683
	2014-15	807	602	584
	Mean	798	620.5	633.5
Per cent increase (+) or decrease (-) over checks	2012-13		-	-
	2013-14		+23.47	+15.52
	2014-15		+34.05	+38.18
	Mean		+28.76	+26.85
Plant height (cm)	2012-13	170	164	176
	2013-14	170	172	175
	2014-15	186	170	170
	Mean	175	169	174
Main shoot length (cm)	2012-13	87	90	98
	2013-14	88	87	94
	2014-15	92	87	81
	Mean	89	88	91
1000 Seed weight (g)	2012-13	5	5	4
	2013-14	6	4	5
	2014-15	5	5	4
	Mean	5	5	4

[Source – AICRP on R&M Annual Report 2012-13 (Page PB 73, Table 2.3.30), 2013-14 (Page PB 81, Table 2.3.31) and 2014-15 (Page PB 75, Table 2.3.33)]. # During the year 2012-13, data on Oil Yield were not reported.

compared to checks CS 54, Kranti, Rohini and Varuna. CS 1100-1-2-2-3 responded favorably to the additional doses of fertilizer (N: P: K). Further 100% Recommended dose of fertilizer was found suitable for this genotype. Looking to its seed and oil yields and disease resistance, CS 1100-1-2-2-3is being proposed for identification for salt affected soils conditions (saline and alkaline) of *Rabi* season in the states of Haryana, Punjab and Uttar Pradesh.

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23. JEX/A 785 (IC0616582; INGR15059), a Potato (*Solanum tuberosum L.)* Germplasm Suitable for Cold Chipping and Resistance to Cold Induced Sweeting

Raj Kumar*[1], RS Marwaha[1], SK Pandey[2] and BP Singh[2]
[1]*CPRI-Central Potato Research Station, Jalandhar, Punjab-144003, India*
[2]*ICAR-Central Potato Research Institute (CPRI), Shimla, Himachal Pradesh, India*
*(*Email: rajcprs@hotmail.com; rajcprs@rediffmail.com; rajcprs@gmail.com)*

Potato is a semi-perishable commodity and has to be consumed within a short period of time, or is required to be shifted to the cold store for round the year availability. Unfortunately, during cold storage potato undergoes an undesirable phenomenon known as cold-induced sweetening where the rate of conversion of starch to reducing sugars is accelerated (van Es and Hartmans, 1987). It also results in lowering the quality of processed products due to an unwanted brown colouration in potato chips and crisps (Edwards *et al*., 2002). The source for cold chipping and resistance to cold induced sweetening are hard to find. In search of sources for cold chipping and resistance to cold induce sweetening primitive cultivated Andigena group (148 accessions) germplasm were evaluated from 2006-2008 (Marwaha *et al.,* 2008). This resulted in identifying JEX/A 785 as a useful source for resistance to cold induced sweetening and cold chipping. JEX/A-785 produced good chip colour after reconditioning at 20°C for 4 weeks of potatoes cold stored for 6 months and was identified as most suitable for cold chipping. This unique and rare trait of JEX/A 785 of producing light coloured acceptable chip colour after withdrawal of tuber material from cold store was also verified in 2009 at Jalandhar and Shimla. This accession can be used as parents for the development of indigenous cold chipping varieties. JEX/A 785 also possess resistance to cold induced sweetening as it even just after withdrawal from cold store contained lower levels of total sugars (including reducing sugar and sucrose) than the prescribed limit (>1.25% on fresh weight) which imparts sweet taste in table potatoes.

Morpho-agronomic Characteristics

Tubers of JEX/A 785 are round shape, whitish cream skin, small sized with shallow eyes and cream flesh colour. The flower is blue-violet in colour. Plant is tall with red brown as secondary stem colour which is highly scattered throughout. Anthocyanin colouration of rachis is present. Leaflets are ovate in shape. The yield performance of JEX/A 785 is lower than commercial Indian processing varieties Kufri Chipsona-1 and Kufri Chipsona-3.

Associated Characters and Cultivated Practices

This accession is susceptible to late blight and early blight diseases. It can be grown in Indian sub-tropical plains in autumn crop season.

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24. LBRIL-102 (IC0611477; INGR15060), a Wheat (*Triticum aestivum)* Germplasm with Spot Blotch Resistant

Gyanendra Singh*, BS Tyagi, Sonia Sheoran, Ashish Ojha, Virender Singh, Rajita and Indu Sharma
ICAR-Indian Institute of Wheat & Barley Research (IIWBR), Karnal-132001, Haryana, India
**(Email:gysingh@gmail.com)*

Spot blotch or *Helminthosporium* Leaf Blight (HLB) caused by *Bipolaris sorokiniana*, is one of the major biotic constraint to wheat production in Africa, South America, warm wheat growing regions of South Asia and particularly to Indian subcontinent, affecting the livelihood of small scale farmers, who depend on the wheat cultivation (Duveiller *et al.,* 2005). Improvement of host resistance against leaf blight, widening the genetic base of the model genotypes through introduction of new alleles for HLB resistance is one of the major activities at Indian Institute of Wheat and Barley Research, Karnal to meet the challenge. The cross was made between most susceptible Indian genotype Sonalika (II53.388/AN//YT54/N10B/3/LR/4/B4946.A.4.18.2.1Y/Y53//3/Y50) and highly resistant Brazilian genotype BH 1146 (Fronteira/Mentana//Ponta Grossa 1). The 220 recombinant inbred lines (RILs) developed from this cross in F_{9-10} generation, were phenotypically evaluated for spot blotch during crop season 2012-14 under high disease pressure at two hot spot locations (Coochbehar and Kalyani) in eastern India and also at IIWBR, Karnal under field and epiphytotic conditions in polyhouse (3 replications). Phenotypic data was recorded on double digit scale (taking disease reaction of top two leaves, flag and flag-1) at dough stage. The promising line LBRIL102 showed spot blotch resistance (Table 1) consistently across the locations and over the two years (Singh *etal.,* 2014). Disease resistance was improved in LBRIL 102 over its donor parent BH 1146.

Morpho-agronomic characters: The duration of days to heading and days to maturityhas increased but the plant height has significantly reduced as compared to the resistant check BH 1146. The average thousand kernel weight (TKW) of LBRIL 102 was 42.0 g which is on par with the best check BH 1146 having TKW 43.0 g. Disease resistance was improved without compromising the yield.

Associated characters and cultivation practices: Besides HLB, the proposed genotype was also rust resistant in all the environments. Diagnostic markers reported earlier *Xgwm*371 (Kumar *et al.,* 2010) and SSRs-*Xbarc59*, *Xbarc*232were also used to validate the promising line for spot blotch resistant (Singh *et al*., 2014).

Table1. LB score of LBRIL102 as compared to checks at four environments of India

	Karnal		Kalyani		Coochbehar		Polyhouse	
	2012-13	2013-14	2012-13	2013-14	2012-13	2013-14	2012-13	2013-14
LBRIL 102	02	02	02	03	13	13	13	13
SONALIKA (C)	79	79	89	89	89	89	99	99
BH1146 (C)	13	13	24	24	24	13	35	24

(C)-check

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25. HGMS-20 (IC0617407; INGR15061), a Cotton (*Gossypium hirsutum* L.) Germplasm Suitable as Parent to Produce Hybrid Seed with Less Cost

SS Siwach*, RS Sangwan, Omender Sangwan, SR Pundir, Somveer and Ashis Jain
Dept. of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar-125004, Haryana
*(*Email:*cotton@hau.ernet.in)

It is a genetic male sterile line of *Gossypium hirsutum* designated as HGMS 20. Its male sterility is governed by a single recessive gene. This line is a cross between a genetic male sterile (HGMS 1) and GAK 32 a male parent. The female line HGMS 1 has genetic male sterility characteristic along with cream petal and cream pollen colour, normal cup shaped leaves, whereas male parent GAK 32 has cream petal and yellow anthers with petal spot. Repeated backcrossing of heterozygote (male) with the homozygote recessive (female) resulted in the development of HGMS 20 line. This genetic male sterile line has been developed by SS Siwach, RS Sangwan, Omender Sangwan, SR Pundir, Somveer and Ashish Jain from Cotton Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. The progeny of this line produces 50 per cent male fertile and 50 per cent male sterile plants. HGMS 20 has normal, medium broad cup shaped leaves. Its flower has cream petal and yellow anther colour with petal spot inside the petal base. This line also has good fibre quality i.e. 2.5% span length (27.1 mm), fibre strength (22.4 g/tex), micronaire value (4.6) and uniformity ratio (51 %).

26. HGMS-21 (IC0610389; INGR15062), a Cotton (*Gossypium hirsutum L.*) Germplasm Suitable as Parent to Produce Hybrid Seed with Less Cost

SS Siwach*, RS Sangwan, Omender Sangwan, SR Pundir, Somveer and Ashis Jain
Dept. of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar-125004, Haryana
*(*Email: cotton@hau.ernet.in*)

It is a genetic male sterile line of *Gossypium hirsutum* designated as HGMS 21. Its male sterility is governed by a single recessive gene. This line is a cross between a genetic male sterile (HGMS 1) and Super okra a male parent. The female line HGMS 1 has genetic male sterility characteristic along with cream petal and cream pollen colour, normal cup shaped leaves, whereas male parent Super okra has cream petal and yellow anthers with deep leaf lobes. Repeated backcrossing of heterozygote (male) with the homozygote recessive (female) resulted in the development of HGMS 21 line. This genetic male sterile line has been developed by SS Siwach, RS Sangwan, Omender Sangwan, SR Pundir, Somveer and Ashish Jain from Cotton Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. The progeny of this line produces 50 per cent male fertile and 50 per cent male sterile plants. HGMS 21 has okra type leaves. Its flower has yellow petal and cream anther. This line also has good fibre quality i.e. 2.5 % span length (26.1 mm), fibre strength (20.8 g/tex), micronaire value (5.0) and uniformity ratio (51 %).

27. MS SLA 9 & SLB 9 (IC0612149 & IC0612150; INGR15063), a Sorghum (*Sorghum bicolor*) MS Line with Bold Seed and Panicle

Prabhakar*, M Elangovan and IK Das
ICAR-Indian Institute of Millets Research (IIMR), Rajendranagar, Hyderabad-500030, Telangana
*(*Email:prabhakar@millets.res.in*)

Rabi sorghum is grown over a total area of 5.6 million hectares mainly in the states of Maharashtra, Karnataka, Telangana and Andhra Pradesh with average productivity of 819 kgs/ha. Hybrid vigour and its commercial exploitation have paid rich dividends in *kharif* sorghum, but less impact in *rabi* sorghum. In *Rabi,* this could be realized only when the sterile and restorer lines having the seasonal adaptability and desired combining ability are identified and used in the development of *rabi* sorghum hybrids. In order to develop new parental lines with diversity and broaden the genetic base in *rabi* materials, 161 indigenous and 159 exotic lines were used for identifying maintainer and restorer gene reactions on A1 cytoplasm. New MS lines with diverse genetic base were derived.

The male sterile line SLA-9 & SLB-9 was developed at Centre on *Rabi* Sorghum (Indian Institute of Millets Research), Solapur. Male sterile line SLA-9 was developed from a cross between *rabi* MS line 104B and SPV 1538 during *Rabi* 2000. The F2 population was raised in Rabi 2001 and 27 agronomically superior derivatives were advanced. The selections were reduced to 5 lines in F4. Superior cross derivatives were test crossed for identification of lines with maintainer genes and sterile were further advanced to BC5. One agronomically superior male sterile line having good combining ability and *rabi* traits was developed as MS SLA-9 male sterile line. The pedigree of MS SLA-9 & SLB-9: 104 B × SPV 1538 (104B = 296B × Swati, 296B = IS 3922 × Karad local, Swati = SPV86 × M35-1, SPV 1538 = Selection from Phul Mallige, Chandakpur village, Aland taluk, Gulbarga district, Karnataka).

Entry	Days to 50% flower	Plant height (cm)	Grain yield / plant (g)	100 seed weight (g)	Panicle length (cm)	Panicle width (cm)	Branches / panicle	Charcoal Rot (%)
SLB 8	72	185	68	2.8	18	4	46	19.6
SLB 9	71	173	77	4.4	24	6	53	14.3
SLB 10	70	163	63	3.0	16	5	63	27.5
SLB 11	74	196	75	2.7	15	6	69	17.8
SLB 12	73	188	69	2.7	15	4	33	18.2
SLB 19	75	183	81	3.7	24	6	94	16.6
SLB 25	73	172	59	3.3	19	6	61	22.7
SLB 29	69	185	78	3.3	12	6	71	19.4
SLB 36	64	187	66	3.6	16	7	60	27.5
SLB 39	65	180	71	3.0	13	7	65	17.1
SLB 45	69	230	64	4.1	13	6	59	25.4
SLB 46	67	201	70	3.2	15	6	64	26.1
SLB 49	73	205	65	3.0	16	7	70	28.3
104B (C)	76	160	58	3.7	20	5	67	34.2
CD at 5 %	3.88	8.09	5.66	0.25	3.12	1.02	13.65	5.46
C.V.%	5.0	11.2	27.6	17.4	23.5	18.5	23.4	24.9

Morpho-agronomic characteristics: A total of 14 B lines were evaluated in *rabi* seasons of 2006-07 and 2007-08 at Centre on *Rabi* Sorghum (IIMR), Solapur. Theses parental lines were compared with the checks 104B, parental line of commercial rabi hybrid CSH 15R. Performance of 14 B lines indicated that SLB-9 flowered in 71 days compared to check 104B (76 days). Panicle length was more in case of SLB-9 (24 cm). The MS SLA-9 was superior by 32.7% and 42.6% over the check 104B for grain yield and charcoal rot, respectively. Thus, MS SLA-9 & SLB-9 is diverse and superior in grain yield.

Associated characters and cultivation practices: It is bold seeded and also tolerant to drought. It has

superior grain quality (seed shape, color and luster) than the check 104B. The MS line is having good general and specific combining ability for high grain yield. It offers better resistance to charcoal rot and possesses better grain quality. This diverse parental line SLA-9 is suited to *Rabi* season and can be directly used for the development of commercial *rabi* hybrids.

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28. MS SLA 29 & SLB 29 (IC0612157 &IC0612158; INGR15064), a Sorghum (*Sorghum bicolor)* MS Line with Compact Head

Prabhakar*, M Elangovan and IK Das

ICAR-Indian Institute of Millets Research (IIMR), Rajendranagar, Hyderabad-500 030, Telangana

**(Email: prabhakar@millets.res.in)*

Rabi sorghum is grown over a total area of 5.6 million hectares mainly in the states of Maharashtra, Karnataka, Telangana and Andhra Pradesh with average productivity of 819 kgs/ha. Hybrid vigour and its commercial exploitation have paid rich dividends in *kharif* sorghum, but less impact in rabi sorghum. In *Rabi*, this could be realized only when the sterile and restorer lines having the seasonal adaptability and desired combining ability are identified and used in the development of *rabi* sorghum hybrids. In order to develop new parental lines with diversity and broaden the genetic base in *rabi* materials, 161 indigenous and 159 exotic lines were used for identifying maintainer and restorer gene reactions on A1 cytoplasm. New MS lines with diverse genetic base were derived. Male sterile line MS SLA-29 was developed from a cross between *rabi* MS line 104B and Selection from IS 3420-2-1 during *Rabi* 2000. The F2 population was raised in *Rabi* 2001 and 41 agronomically superior derivatives were advanced. The selections were reduced to 7 lines in F4. Superior cross derivatives were test crossed for identification of lines with maintainer genes and sterile were further advanced to BC5. One agronomically superior male sterile line having good combining ability and *rabi* traits was developed as MS SLA-29 male sterile line. The pedigree of MS SLA-29 & SLB-29 is 104B × IS 3420 (104B = 296B × Swati, 296B = IS 3922 × Karad local, Swati = SPV86 × M35-1, IS 3420 = Local landrace from Parbhani, Maharashtra).

Morpho-agronomic characteristics: A total of 14 B lines were evaluated in *rabi* seasons of 2006-07 and 2007-08 at Centre on *Rabi* Sorghum (IIMR), Solapur.

Entry	Days to 50% flower	Plant height (cm)	Grain yield / plant (g)	100 seed weight (g)	Panicle length (cm)	Panicle width (cm)	Branches / panicle	Charcoal Rot (%)
SLB 8	72	185	68	2.8	18	4	46	19.6
SLB 9	71	173	77	4.4	24	6	53	14.3
SLB 10	70	163	63	3.0	16	5	63	27.5
SLB 11	74	196	75	2.7	15	6	69	17.8
SLB 12	73	188	69	2.7	15	4	33	18.2
SLB 19	75	183	81	3.7	24	6	94	16.6
SLB 25	73	172	59	3.3	19	6	61	22.7
SLB 29	69	185	78	3.3	12	6	71	19.4
SLB 36	64	187	66	3.6	16	7	60	27.5
SLB 39	65	180	71	3.0	13	7	65	17.1
SLB 45	69	230	64	4.1	13	6	59	25.4
SLB 46	67	201	70	3.2	15	6	64	26.1
SLB 49	73	205	65	3.0	16	7	70	28.3
104B (C)	76	160	58	3.7	20	5	67	34.2
CD at 5 %	3.88	8.09	5.66	0.25	3.12	1.02	13.65	5.46
C.V.%	5.0	11.2	27.6	17.4	23.5	18.5	23.4	24.9

Theses parental lines were compared with the checks 104B, parental line of commercial *rabi* hybrid CSH 15R. Performance of 14 B lines indicated that SLB-29 flowered in 69 days compared to check 104B (76 days). Panicle length was compact (12 cm) with more branches (71) than 104B (67). The MS SLA-29 was superior by 34.4% and 43.2% over the check 104B for grain yield and charcoal rot, respectively. Thus, MS line SLAS-29 is early with compact head, high yield and more branches. Thus, MS SLA-29 & SLB-29 is early, diverse and superior in grain yield.

Associated characters and cultivated practices: It is bold seeded and also tolerant to drought. It has superior grain quality (seed shape, color and luster) than the check 104B. MS line is diverse, early and superior in grain yield and tolerance to charcoal rot. The MS line is having good general and specific combining ability for high grain yield. It offers better resistance to charcoal rot and possesses better grain quality. This diverse parental line is suited to Rabi season and can be directly used for the development of commercial *rabi* sorghum hybrids.

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29. JCR/PLB 299 (IC0341862; INGR15065), a Kidneybean (*Phaselous vulgaris)* Germplasm with Resistant to Anthracnose (*Colletotrichum lindmuthianum)*

JC Rana[1*], PN Sharma[2], TR Sharma and Anju Pathania[2]
[1]*ICAR-National Bureau of Plant Genetic Resources, Pusa campus, New Delhi–110012, India*
[2]*CSK-HPKV, Palampur, Kangra, Himachal Pradesh–176062, India*
*(*Email:ranajc2003@yahoo.com*)

Common bean (*Phaseolus vulgaris* L.) also known as *rajmash* is one of the most important legumes grown all over the world including India particularly in the hilly regions. The crop is predisposed to the attack of various pathogens like fungal, bacterial and viral during humid environments throughout the growing season. Bean anthracnose is a serious seed born disease and early infection during growing period of susceptible cultivar leads to heavy yield losses. The pathogen possess high degree of pathogenic variability and >100 races of *C. lindemuthianum* have been identified worldwide. Management of this disease can be done by using certified seed, crop rotation, seeds and foliar treatment with fungicides and genetically resistant varieties. Among these, use of genetically resistant varieties is most effective, least expensive and easy to adopt by marginal farmer and resource poor farmers. Germplasm comprising 99 accessions was evaluated at two hot spots i.e. Shimla and Palampur and also under artificial epiphytotic conditions at Palampur against 4 races of *C. lindemuthianum* viz., 03, 515, 598 and 529. Germinated seed dip method of inoculation was used for evaluation of resistance. The disease reaction was recorded after 6 days by using 0-5 point scale. Accession IC0341862 was found resistant to all the four races. Additional features of this accessions include bush type plant growth habit, deep pink flower colour, white seed colour, pod length (11.80 cm), no. of pods (18.00), no. of seeds (6.00) and 100 seed weight (22.04 g).

30. DRMR-541-44 (IC0598624; INGR15066), an Indian Mustard (*Brassica juncea* L.) Germplasm with Drought Tolerant under Rainfed Condition

VV Singh, Dhiraj Singh*, M Singh, PK Rai, B Ram, SP Singh, A Kumar, HS Meena, BK Singh and ML Meena
ICAR-Directorate of Rapeseed-Mustard Research (DRMR), Sewar, Bharatpur-321303, Rajasthan, India
*(*Email:director.drmr@gmail.com*)

DRMR 541-44, an Indian mustard (*Brassica juncea* L.) genotype derived from inter specific hybridization between *Brassica juncea* and *Brassica carinata* was studied during 2010-11 along with 20 germplasm

for morpho-physiological and biochemical characters under irrigated and rainfed condition in RCBD with 3 replications. DRMR 541-44 recorded less decrease in seed yield and more seed yield under rainfed condition as compared to other genotypes. The carbohydrate content decreased under rainfed condition whereas free proline increased significantly. The increase in free proline under stress condition might be attributed to one of the defence mechanism of plant to drought situation. The high seed yield of DRMR 541-44 under rainfed condition could be due to high plant dry weight and carbohydrate accumulation. (DRMR Annual Report, 2011-12).DRMR 541-44 was also tested for physiological basis of drought tolerance with 15 other strains under AICRP (RM) programme-2011-12 at Ludhiana, Bharatpur and Kanpur centers. The different strains were sown in paired rows under irrigated and rainfed conditions in 3 replications under RCBD factorial design. DRMR 541-44 showed < 1 DSI and higher seed yield than the check RH 819 at Bharatpur and Kanpur centers. It also showed < 10% reduction (even less than check RH 819) in RWC under drought condition. (AICRP RM Annual Progress Report, 2012). Thirteen B. *juncea* genotypes/ germplasm were further studied for their different morpho-physiological characters under irrigated and drought condition during 2011-12. There were 2 rows each of 5m long for each genotype. The spacing between rows and within plant was kept 30 and 10cm respectively. The experiment was planned in randomized complete block design with three replications under rain out shelter.

The physiological characters investigated under irrigated and drought situation showed appreciable variation at both the phenotypic and genotypic level. DRMR 541-44 showed higher tolerance index and higher photosynthesis under drought situation along with other genotypes. Water potential measured at flowering stage showed increase potential under drought condition and the proposed strain DRMR 541-44 along with other genotypes recorded high water potential as compared to others genotypes. Seed yield recorded on per plant basis showed significant decrease under drought condition over the irrigated condition. After significant decrease, maximum seed yield was recorded in DRMR 541-44. On the other hand, maximum tolerance index was observed in DRMR 541-44 even higher than the check RH 819. Thus on the basis of photosynthesis, leaf water potential, high water use efficiency, and yield DRMR 541-44 germplasm were identified as promising ones.

(DRMR Annual Report, 2012-13). DRMR 541-44 was evaluated along with check variety RH 819 and other 40 genotypes for assessing drought tolerance through physiological parameters during 2013-14 under AICRP RM physiological trials at Kanpur and Ludhiana. Proposed strain recorded consistently <10% reduction in terms of Relative water content (RWC %), SPAD Chlorophyll, seeds/siliquae and 1000 seed weight when genotype was grown under irrigated (IR) and rain fed (RF) conditions at both the centres (AICRP RM Annual Progress Report 2014). DRMR 541-44 was evaluated along with check variety RB 50 and RH 406 and other 31 genotypes for assessing drought tolerance during 2014-15 under AICRP RM physiological trials. Proposed strain recorded DSI value less than 1 at all the four locations i.e. Kanpur, Hisar, Bharatpur and Ludhiana which indicates its drought tolerance. Further, DRMR 541-44 exhibited less than 10% reduction in harvest index (%) and oil content as compared to checks. Reduction in Relative water content (RWC %) and SPAD Chlorophyll values was also minimum (<20%). (AICRP RM Annual Progress Report 2015).

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Referees for Volume 29 (1, 2 & 3), 2016

The Editors gratefully acknowledge the help rendered by following referees in reviewing the manuscripts published during 2016.

Agrawal, R C
Registrar General
Protection of Plant Varieties and Farmers' Rights Authority, NASC Complex, DPS Marg
Opposite Todapur Village, Pusa Campus
New Delhi-110012

Akhtar, Jameel
Senior Scientist
Division of Plant Quarantine
ICAR-National Bureau of Plant Genetics Resources
Pusa Campus, New Delhi-110012

Anitha, K
Principal Scientist
ICAR- NBPGR Regional Station
Rajendranagar, Hyderabad- 500030
Telangana

Anjani, K
Principal Scientist (Plant Breeding)
ICAR-Indian Institute of Oilseed Research
Rajendra Nagar-500030, Hyderabad
Telangana

Arya, Lalit
Principal Scientist
Division of Genomic Resources
ICAR-National Bureau of Plant Genetics Resources
Pusa Campus, New Delhi-110012

Bag, Manas Kumar
Senior Scientist
Division of Plant Pathology
ICAR-National Rice Research Institute
Cuttack-753006, Odisha

Bains, T S
Sr. Breeder (Pulses)
Punjab Agricultural University
Ludhiana-141004, Punjab

Bhardawaj, Rakesh
Principal Scientist
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Bhatt, K C
Principal Scientist
Division of Plant Exploration and Germplasm Collection
ICAR-National Bureau of Plant Genetic Resources
New Delhi 110012

Biswas, K K
Principal Scientist
Division of Plant Pathology
ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012

Chakrabarty, S K
Principal Scientist
ICAR-NBPGR Regional Station
Rajendra Nagar- 500030, Hyderabad
Telangana

Das, I K
Principal Scientist
ICAR-Indian Institute of Millets Research
Rajendranagar, Hyderabad-500030
Telangana

Yadav, Vijay Kumar
Sr. Rice Breeder and Officer-in-Charge
AICRP on Rice
C.S. Azad University of Agriculture and Technology
Kanpur-208002, Uttar Pradesh

Dubey, S C
Principal Scientist & Head
Division of Plant Quarantine
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Dwivedi, D K
Professor
Department of Plant Molecular Biology and Genetic Engineering
N.D. university of Agriculture and Technology
Kumargunj, Faizabad-224229, Uttar Pradesh

Fougat, Ranbir Singh
Unit Officer and Professor & Head
Anand Agricultural University
Anand-388110, Gujarat

Gangopadhyay, K K
Principal Scientist
Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Gopala Krishnan, S
Principal Scientist
Division of Genetics
Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012

Gotmore, Vinita P
Principal Scientist
Division of Crop Improvement
ICAR-Central Institute for Cotton Research,
Post Bag No. 2, Shankar Nagar P.O.
Nagpur-440010, Maharashtra

Gupta, Rajini
Reader
Department of Botany
Kiromal College
University of Delhi
Delhi-110007

Gupta, S K
Senior Pearl Millet Breeder
International Crops Research Institute for the Semi-Arid Tropics
Patancheru-502324, Telangana

Hossain, Firoz
Senior Scientist
Division of Genetics
ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012

Hussain, Zakir
Principal Scientist
Division of Vegetable Crops
ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012

Jonnakuti, Prakasa Rao
Department of Botany
Andhra University
Visakhapatnam-530003, Andhra Pradesh

Kar, Chandan Saurav
Principal Scientist (Plant Breeding)
Division of Crop Improvement
ICAR-Central Research Institute for Jute and Allied Fibres, Barrackpore,
Kolkata-700120,West Bengal

Karad, Sunil
Associate Professor (Plant Breeding)
Zonal Agriculture Research Station
Sub montane Zone, Kolhapur-416012
Maharashtra

Kumar, Sundeep
Principal Scientist
Division of Genomic Resources
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Kumari, Jyoti
Senior Scientist (Plant Breeding)
Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetics Resources
Pusa Campus, New Delhi-110012

Laha, G S
Principal Scientist
Division of Plant Pathology
ICAR-Indian Institute of Rice Research
Rajendranagar, Hyderabad-500030
Telangana

Malik, S K
Principal Scientist
Tissue Culture and Cryopreservation Unit
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Mathew, Dan
Scientist
Plant Genetic Resources
Jawaharlal Nehru Tropical Botanic Garden and
Research Institute, Palode
Thiruvananthapuram-695562, Kerala

Mitra, Jiban
Principal Scientist & Head
Crop Improvement Division
Central Research Institute for Jute
and Allied Fibres, Barrackpore
Kolkata-700120, West Bengal

Molla, K A
Scientist
Division of Genetics
ICAR-National Rice Research Institute
Cuttack-753006, Orissa

Naik, P S
Project Coordinator
All India Coordinated Research Project on Potato
ICAR-Central Potato Research Institute
Shimla-171001, Himachal Pradesh

Nayar, E R
Retd. Principal Scientist
ICAR-National Bureau of Plant Genetics Resources
Pusa Campus, New Delhi-110012

Nayar, N M
Emeritus Scientist,
Jawaharlal Nehru Tropical Botanic Garden and
Research Institute
Thiruvananthapuram-695586, Kerala

Negi, K S
Principal Scientist
ICAR-NBPGR Regional Station
Bhowali-263132 Uttarakhand

Pandravada, S R
Principal Scientist
ICAR-NBPGR Regional Station
Rajendra Nagar
Hyderabad-500030
Telangana

Pitchaimuthu, M
Principal Scientist (Horticulture)
Division of Vegetable Crops
ICAR-Indian Institute of Horticulture Research
(IIHR), Hessaraghatta lake post, Bengaluru-560089
Karnataka

Pradheep, K
Principal Scientist
Division of Plant Exploration and Germplasm
Collection
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Prasad, T V
Principal Scientist
Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetics Resources
Pusa Campus, New Delhi-110012

Pratap, Aditya
Principal Scientist (Plant Breeding)
Crop Improvement Division
ICAR-Indian Institute of Pulses Research
Kanpur-208017, Uttar Pradesh

Radhamani, J
Principal Scientist
Division of Germplasm Conservation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Pandey, Arun Kumar
Professor
University of Delhi, New Delhi-110007

Pandey, Anjula
Principal Scientist
Division of Plant Exploration and Germplasm
Collection
ICAR- National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Rajkumar, S
Senior Scientist
Division of Genomic Resources
ICAR-National Bureau of Plant Genetics Resources
Pusa Campus, New Delhi-110012

Rameash, K
Senior Scientist
ICAR-Sugarcane Breeding Institute
Coimbatore-641018, Tamil Nadu

Rana, J C
Head, Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetics Resources
Pusa Campus, New Delhi-110012

Rawat, G S
Dean & Scientist-G
Wildlife Institute of India,
Dehradun-248001, Uttarakhand

Santhy, Venoor
Principal Scientist
ICAR-Central Institute for Cotton Research
Nagpur-440010
Maharashtra

Satpathy, P C
Professor & Breeder (Potato)
Orissa University of Agriculture & Technology
Bhubaneswar-751003, Odisha

Sharma, J B
Principal Scientist (Plant Breeding)
Division of Genetics
ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012

Sharma, Neelam
Principal Scientist
Tissue Culture and Cryopreservation Unit
ICAR-National Bureau of Plant Genetics Resources
Pusa Campus, New Delhi-110012

Sharma, R R
Principal Scientist
Division of Food Science & Post Harvest Technology
ICAR-Indian Agricultural Research Institute
Pusa Campus
New Delhi-110012

Singh, Anil Kumar
Professor
Department of Horticulture
Institute of Agriculture Sciences
Banaras Hindu University
Varansi-221005, Uttar Pradesh

Singh, Baleshwar
Principal Scientist
Division of Plant Quarantine
ICAR- National Bureau of Plant Genetics Resources
Pusa Campus, New Delhi-110012

Singh, Dinesh
Principal Scientist
Division of Plant Pathology
ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012

Singh, Dinesh Kumar
Professor
Department of Vegetable Science
G.B. Pant University of Agriculture & Technology
Pantnagar-263145, Uttarakhand

Singh, Naveen
Senior Scientist
Division of Genetics
ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110 012

Singh, Prithipal
Former Reader
Kirori Mal College
University of Delhi
New Delhi-110007

Singh, Rakesh
Principal Scientist
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi -110 012

Sivaraj, N
Principal Scientist
ICAR-NBPGR Regional Station
Rajendra Nagar, Hyderabad-500030
Telangana

Sudhakar, J V
Botanical Assistant
Botanical Survey of India
Southern Regional Centre
TNAU Campus, Lawley Road P.O.
Coimbatore-641003, Tamil Nadu

Sujatha, M
Principal Scientist
Head, Crop Improvement Section
ICAR-Indian Institute of Oilseeds Research
Rajendranagar, Hyderabad-500030
Telangana

Talluri, Rama Srinivas
Principal Scientist
Division of Fruits and Horticultural Technology
ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012

Tiwari, J K
Professor
Department of Botany and Microbiology
Hemvati Nandan Bahuguna Garhwal University
Srinagar, Garhwal-246174, Uttarakhand

Uniyal, P L
Associate Professor
Department of Botany
University of Delhi (North Campus)
Delhi-110007

Sujata V
Principal Scientist
Division of Genetics
ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012

Vasimalla, Celia Chalam
Principal Scientist
Division of Plant Quarantine
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Verma, Manjusha
Principal Scientist
Division of Genomic Resources
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Yadav, Mahesh C
Principal Scientist (Genetics)
Division of Genomic Resources
ICAR-National Bureau of Plant Genetics Resources
Pusa Campus, New Delhi-110012

Yadav, Rashmi
Principal Scientist
Division of Germplasm Evaluation
ICAR-National Bureau of Plant Genetic Resources
Pusa Campus, New Delhi-110012

Yadav, Sangita
Principal Scientist
Division of Seed Science and Technology
ICAR-Indian Agricultural Research Institute
Pusa Campus, New Delhi-110012

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3. WOI (1985) *The Wealth of India - Raw Materials. A Dictionary of Indian Raw Materials and Industrial Products - Raw Material* Vol 1: A (Revised). Publications and Information Directorate, Council of Scientific and Industrial Research, New Delhi, 513 p.
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