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# INDIAN SOCIETY OF PLANT GENETIC RESOURCES

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- To serve and promote the scientific cause and to advance academic interest in the field of plant genetic resources.
- 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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# CONTENTS

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# Conservation and Sustainable Use of Agrobiodiversity

**José Graziano da Silva**
*Director-General, Food and Agriculture Organization of the United Nations*

The Food and Agriculture Organization of the United Nations (FAO) has a longstanding history in pursuing the goal of alleviating poverty and eradicating hunger through the promotion of sustainable agricultural development, and the conservation and sustainable use of biodiversity for food and agriculture. Since its inception, FAO has provided an intergovernmental platform where biodiversity-related policies are discussed and relevant agreements are negotiated and adopted by member countries. The International Plant Protection Convention (IPPC), the adoption of which reaches back into the early 1950s, the 1995 Code of Conduct for Responsible Fisheries and the International Treaty on Plant Genetic Resources for Food and Agriculture (Treaty) adopted in 2001 are examples of such agreements. Beyond policy development and support, FAO assists its Members in operational activities, including in the implementation of global policy instruments. FAO manages a broad range of programmes and activities to enhance sustainable agricultural systems and management practices.

Conservation and sustainable use of agrobiodiversity are global responsibilities, as evidenced by an increasing number of international instruments and organizations that have joined FAO's early efforts. In fact, a new governance landscape has developed over the last decades, during which FAO expanded and strengthened its activities and intensified collaboration with its partners. In this period, FAO has created new instruments, such as the Treaty, and broadened the mandate of its Commission on Genetic Resources for Food and Agriculture (Commission), which since 1995 covers all genetic resources for food and agriculture (i.e. plant, animal, aquatic, forest, micro-organism and invertebrate genetic resources), and addresses all matters related to biodiversity for food and agriculture. FAO has also taken on a key role in the implementation of related work programmes and global initiatives, including under the Convention on Biological Diversity, and has provided guidance and advice to national policymakers as well as to international initiatives and organizations. Most recently, in 2013, FAO, together with UNEP, UNESCO and UNDP joined a collaborative partnership arrangement in support of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES), which will further foster and facilitate better international coordination in the field of biodiversity and ecosystem services.

These developments are evidence of FAO's responsiveness and indicate that governments have recognized the need for global and coordinated action on biodiversity for food and agriculture.

Climate change is one of the reasons for the increasing awareness of policy-makers of the important role of biodiversity for food and agriculture. Biodiversity and genetic resources for food and agriculture are expected to play a key role in the adaptation of agricultural production systems to the impacts of climate change, which is essential to achieve our food security and nutrition objectives, as reflected in the Sustainable Development Goals (SDGs). Genetic resources may contribute greatly to global and national efforts to cope with climate change. They are part of those unique synergies that agriculture offers, according to the IPCC Synthesis Report[1]. We need to build on these synergies to meet the climate change adaptation and mitigation needs of the coming decades.

The two major areas of work of FAO's activities on the conservation and sustainable use of biodiversity for food and agriculture – policy development and technical assistance to countries – complement each other and are mutually supportive. These two aspects are briefly explored below, as well as some of the instruments available to transform policies into practical action and to reflect practical issues in the intergovernmental policy debate.

## FAO's Global Policy Mandate on Agrobiodiversity

Various bodies of FAO contribute in many different ways to FAO's biodiversity agenda for food and agriculture.

1 IPCC, 2014: Climate Change 2014: Synthesis Report. Contribution of Working Groups I, II and III to the Fifth Assessment Report of the Intergovernmental Panel on Climate Change [Core Writing Team, R.K. Pachauri and L.A. Meyer (eds.)]. IPCC, Geneva, Switzerland, 151 pp

These include FAO's committees on agriculture, forestry and fisheries and the IPPC's Commission on Phytosanitary Measures established. However, the Commission on Genetic Resources for Food and Agriculture and the International Treaty on Plant Genetic Resources for Food and Agriculture provide perhaps the main intergovernmental fora addressing, within their respective mandates, the conservation, use and exchange of genetic resources for food and agriculture.

The Commission, established in 1983, has a coordinating role and deals with policy, sectoral and cross-sectoral matters related to the conservation and sustainable use of genetic resources for food and agriculture. Through it, countries reach consensus on policies for the sustainable use and conservation of genetic resources for food and agriculture and the fair and equitable sharing of benefits derived from their use. The Commission guides the preparation of FAO's global country-driven assessments and develops in response policies and action plans. It also guides and monitors the implementation of its policy instruments, which allows FAO to report on a regular basis on the state of the different sectors of genetic resources.

In the past, the Commission's work has largely focused on the contribution of genetic resources to specific sectors, such as crop and livestock production. However, with its current work on a country-driven report on *The State of the World's Biodiversity for Food and Agriculture*, the Commission acknowledges the importance of interactions between the biodiversity of the different sectors: for example, the synergies within mixed systems (e.g. crop–livestock, crop– aquaculture, agroforestry, etc.) or the potential benefits of integrated approaches to the management of biodiversity at the ecosystem or landscape scales, or at the level of policy and institutional development. The report will also address various categories of biodiversity, such as pollinators and soil-dwelling organisms, that are not the main targets of management or harvesting, but nonetheless contribute to the productivity and the sustainability of production systems.

The Governing Body of the Treaty promotes its implementation, through the adoption of plans and programmes, the establishment and maintenance of cooperation with other relevant organizations, fundraising strategies as well as the operation of the Treaty's Benefit-Sharing Fund. The Treaty facilitates access to essential genetic materials for research, breeding and IPCC, 2014: Climate Change 2014: Synthesis Report. Contribution of Working Groups I, II and III to the Fifth Assessment Report of the Intergovernmental Panel on Climate Change [Core Writing Team, R.K. Pachauri and L.A. Meyer (eds.)]. IPCC, Geneva, Switzerland, 151 pp. training for food and agriculture. Those who access the materials must agree to use them for research, breeding and training purposes under specific conditions. On the other hand, the Treaty provides for the sharing of monetary and non-monetary benefits arising from the utilization of the materials. The Treaty recognizes, in addition, through its provisions on Farmers' Rights, the enormous contribution farmers have made to the ongoing development of the world's wealth of plant genetic resources and calls for protecting the traditional knowledge of these farmers, increasing their participation in national decision-making processes and ensuring that they share in the benefits from the use of these resources.

## FAO'S Operational Activities on Agrobiodiversity

FAO's intergovernmental policy activities are complemented by extensive country-level operations related to the conservation and sustainable use of genetic resources for food and agriculture. FAO implements a significant proportion of these through its Technical Cooperation Programmes, while several are funded through its various bilateral, tripartite and multilateral funding systems. Increasingly, a significant amount of FAO's activities are funded through its south-south cooperation mechanism.

In general, FAO provides technical support and policy guidance that result in strengthened human and institutional capacities, and improved policy-enabling environments. Activities relevant to agrobiodiversity span from action against desertification to support of family farming projects or support of governments in the development and implementation of national biodiversity strategies.

The following examples stand for numerous initiatives and programmes supported by FAO and give evidence of the diversity and richness of approaches:

- In 2002, in order to safeguard and support the world's agricultural heritage systems, FAO started an initiative for the dynamic conservation of **Globally Important Agricultural Heritage Systems** (GIAHS). The GIAHS Initiative promotes public understanding, awareness, and national and

international recognition of agricultural heritage systems. With the aim to safeguard the social, cultural, economic and environmental goods and services for family farmers, smallholders, indigenous peoples and local communities, GIAHS fosters an integrated approach combining sustainable agriculture and rural development.

- **Action Against Desertification** (AAD) is an initiative of the African, Caribbean and Pacific Group of States (ACP) to restore drylands and degraded lands in Africa, the Caribbean and the Pacific to tackle the detrimental social, economic and environmental impact of land degradation and desertification. AAD focuses on restoring degraded lands in drylands and fragile ecosystems using plant-based solutions and putting communities at the heart of the action in Burkina Faso, Niger, Nigeria, Senegal, the Gambia, Ethiopia, Fiji and Haiti, regenerating their productivity for the sustainable livelihoods of rural communities.
- The **Benefit-Sharing Fund of the Treaty** invests directly in high-impact projects supporting farmers in developing countries in conserving crop diversity in their fields and assisting farmers and breeders globally in adapting crops to changing needs and demands. The Fund seeks to accelerate the conservation and use of plant genetic resources on a global scale through technology transfer, capacity building, high-impact projects and innovative partnerships involving farmers, plant breeders, civil society and other stakeholders. The Fund's priorities are on-farm management and conservation, food security and innovative partnerships.
- **Agroecology** applies ecological concepts and principles to farming systems, focusing on interactions between plants, animals, humans and the environment for food security and nutrition. Species and genetic diversification of the agroecosystem in time and space is one of its key principles. Since 2014, FAO has played an instrumental role in facilitating dialogue on the role of agroecology in advancing food security and nutrition, and in supporting the development of the agroecology knowledge base.
- FAO plays a leading role in facilitating and coordinating the **International Pollinator Initiative** (IPI). In 2000, recognizing the decline of pollinators and its effect on agricultural production and agro-ecosystem diversity, the Convention on Biological Diversity (CBD) established the International Initiative for the Conservation and Sustainable Use of Pollinators (also known as the International Pollinator Initiative – IPI). Since then, a range of actions have been undertaken, including the establishment of FAO's Global Action on Pollination Services for Sustainable Agriculture. A number of tools and guidance documents have been prepared on issues such as the economic valuation of pollination services, determining the risk of pesticides to wild bees, detecting and evaluating pollination deficits in crops, the socio- economic evaluation of pollinator-friendly practices, and monitoring pollinator communities.
- FAO assists countries in implementing globally agreed action plans, such as the Second **Global Plan of Action for Plant Genetic Resources**. Through guidelines and work on the ground, FAO assists countries in the formulation and implementation of national conservation and sustainable use strategies. Botswana, Egypt, Iran, Jordan, Lebanon, Lesotho, Malawi, Mozambique, Rwanda, Tanzania and Zambia have most recently made use of the guidelines.
- FAO's **Global Soil Partnership** (GSP) was established in December 2012 as a mechanism for enhanced collaboration and synergy among all stakeholders to increase the implementation of sustainable soil management. According to FAO's 2015 report on the Status of the World's Soil Resources, soil organic carbon and soil biodiversity are crucial to increase food availability and the soil's resilience to climate change. The GSP also strives to raise awareness on the role of sustainable soil management in safeguarding biodiversity, highlighting that soils are a key reservoir of global biodiversity.

## Strengthening Partnerships for Agrobiodiversity

As recognized on the new Agenda for Sustainable Development (2030 Agenda), the global challenges that we face can only be overcome if we work together through partnerships. This is certainly true of the conservation and sustainable use of agrobiodiversity.

FAO has a longstanding history of collaborating with governments, organizations and other stakeholders on agrobiodiversity. FAO is a key partner of the work

programme on agricultural biodiversity of the Convention on Biological Diversity and leads three of its cross- cutting initiatives, for (i) soil biodiversity, (ii) biodiversity for food and nutrition, and (iii) pollinators.

FAO also facilitates global and regional partnerships and networks, and hosts various partnership alliances, such as the Global Soil Biodiversity Initiative. For example, FAO's *Global Action on Pollination Services for Sustainable Agriculture* has been created to increase synergies and collaboration among a number of global and regional initiatives, programmes and projects to work towards the common goal of promoting the conservation, restoration and sustainable use of pollinator diversity in agriculture and related ecosystems. Under this partnership, a recent GEF/UNEP/FAO project demonstrated that enhancing pollinator density and richness could improve yields in Africa, Asia, and Latin America, and that ecological intensification through enhancement of pollinators can contribute to food security and nutrition[2,3].

FAO also co-hosts instruments relevant to agrobiodiversity, such as the FAO-WHO International Code of Conduct on Pesticide Management, or the IPPC, which promotes international cooperation on plant protection from harmful pests which may be introduced through international trade.

A new but very important collaborative arrangement in the field of biodiversity is the afore-mentioned Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES), which assesses the state of biodiversity and ecosystem services. FAO, together with UNEP, UNESCO and UNDP have committed themselves to collaborate closely with IPBES.

2 http://www.fao.org/3/a-i1929e.pdf.

3 Garibaldi *et al.* (2016).Mutually beneficial pollinator diversity and crop yield outcomes in small and large farms. Science. 351 (6271) pp.388-391.

## A Global Platform for Mainstreaming Biodiversity

While collaboration is an integral part of the global biodiversity agenda, it is probably fair to say that we all struggle to leave the silos of our disciplines, sectors and organizations. We need to collaborate rather than compete. If we want real transformation and lasting protection of the biodiversity that humanity and its food systems depend on, we have to respond through collaborative efforts that cut across sectors.

The 2030 Agenda is an important step in this regard, as it requires us to do more and to do it together. It embodies a growing recognition that sustainable, biodiversity-friendly and climate-smart agricultural development are of pivotal importance to the global transformation needed to achieve the Sustainable Development Goals (SDGs). Together with the Aichi Biodiversity Targets, the SDGs provide the global framework for action on biodiversity. FAO is committed to their achievement, in the firm belief that agrobiodiversity will be key to this successful transformation.

In this context, at its last session in September of this year, FAO's Committee on Agriculture requested FAO to mainstream biodiversity in agriculture, including livestock, to promote its contribution to ecosystem services and to climate change adaptation and mitigation. The Committee also requested that the issue of mainstreaming biodiversity across agriculture, forestry and fisheries be addressed as a cross-cutting issue at the next meetings of the relevant technical committees. FAO stands ready to support its Members in their efforts to mainstream biodiversity across the agricultural sectors and to conserve and sustainably use agrobiodiversity with a view to achieve the SDGs and the Aichi Targets. In addition, FAO will continue to provide a neutral platform for stakeholders to discuss and agree on concrete action to facilitate the conservation and sustainable use of agrobiodiversity.

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# Changing Paradigms in Managing Agrobiodiversity through Use: An Appraisal

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The scientific and conscious management, use and conservation of agrobiodiversity has undergone several paradigm shifts in the past few centuries. In my own career, I did witness these changes occurring many times. Hence, I take this opportunity to delve upon some of the changes in the past and offer some suggestions that are required for needed action to ensure effective and long-term management of agrobiodiversity.

## Biodiversity under Domestication

In nature, all organisms have been living in harmony for millions of years; humans (nomadic and forest tribes) were greatly dependent on the endless diversity among and within species, along with that of their habitats and ecosystems. When humans transited from nomadic hunter-gatherer to a more settled lifestyle due to adoption of agriculture some 12,000 years ago, they started to look for such bioresources which could provide them food, feed, fodder, fibre and improved livelihood. The intervention of humans by way of domestication and farming affected the pattern of evolution, diverting the selection from 'fitness' to that of 'human preference'. The available diversity of domesticated species, which provides the basis for the quality, range and extent of choices available to the humankind, is an outcome of such evolution influenced by frequent human interventions, especially by the farm women, over the millennia.

In this context, first we must recognize the difference between biodiversity and agrobiodiversity. Crops, wild species, animal breeds, fish, pollinators and several micro-organisms, which are constituents of agrobiodiversity, directly and indirectly help the humans. Had we not judiciously used agrobiodiversity, possibly our food basket would not have been what it is today. Yet we need to diversify it further to meet our increasing demands for food and nutrition.

By 2050, we would need 70% additional food grains. To ensure that, we must re-emphasize the need for using available genetic resources more effectively and efficiently. We have also seen that if these genetic resources were not protected properly by the tribal people living at subsistence level, possibly these resources would not have been saved. We are also aware that the number of species existing on the earth is enormous and research conducted so far is rather limited. We thus need to explore the unexplored having many valuable traits. Unfortunately, in the past we have been researching mainly on those crops which are of direct use to us. So far, the whole world is dependent on 60% of its energy and food requirement just mainly on three crops: wheat, rice and maize.

## Origin and Ownership of Genetic Resources

As a student of genetics and plant breeding, we were taught two commonly held principles for the development of genetic resources and their use. These had been: i) genetic resources were a common heritage of human kind, and ii) they were freely exchanged. How true. If this would have not happened, many of the daily food staples like maize, potato, tomato etc., having their centres of origin in South America, would not have come to India and many crops like sugarcane, pulses, egg plant etc. would have not gone to other countries. We know it very well that rice in the South-East Asia, wheat in West Asia and North Africa, maize in the Central America, and potato in the Latin America and parts of Europe emerged as staple foods that proliferated and subsequently dominated the world food bowl along with millets, pulses, oilseeds, *Saccharum*, cucurbits, citrus,

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forage crops and many other species. Among the non-food crops, cotton, jute and bamboo are worth mentioning that have originated from the Indian sub-continent. Thanks to the great efforts of Vavilov, who had single handedly travelled the whole world when communication was so difficult and collected a large number of seeds and plants that enabled him to understand and suggest the concept of centres of origin of crop plants. Today, we fondly call these as Vavilovian centres of origin.

The collection, evaluation, exchange and utilisation of genetic resources in exotic areas accelerated during the second half of the 20th century. This enabled the whole world in boosting food production while keeping pace with the ever increasing world population. Today, when we look back at the degree of dependence on genetic diversity that came from outside the country, one would be amazed that many of those countries who today have gained/capitalised on agrobiodiversity resources did not have a single plant that originated in their country! This dependence is predicted to increase more in future, given the current trends of climate change, emerging needs for expanding our food basket and changing consumer preferences for more healthy and nutritious foods.

As stated earlier, till the late-twentieth century, genetic resources were exchanged freely, not only amongst farmers, but also between plant breeders and researchers within and outside the country. In the late 1980s, this perception got changed; with biodiversity being regarded as a treasure under the national sovereignty system. The paradigm shift from free flow of genetic resources to a restricted exchange emerged as a reality soon after the Convention on Biological Diversity (CBD) came into force in December 1993. Thus, germplasm exchange became operational under the legal instruments or *sui-generis syst*em as per guidelines of international treaties. The underlying idea was that if genetic resources are used to develop commercial products such as new plant varieties, then the subsequent benefits must be shared with the provider(s) of the genetic resources. Hence, the concept of free exchange of agrobiodiversity, has now been changed to protect the right of those who own the germplasm. Thus, the new legal issues that have now emerged prominently are restricting the flow of germplasm. This is an obvious challenge in the present context which has to be addressed jointly by all of us.

## Humans–The Catalysts of Change

The obvious change in public perception towards genetic resources has been also due to an alarming rise in world population: since for thousands of years, population grew rather slowly, but in the last century it jumped dramatically. Between 1900 and 2000 the increase in world population was three times greater than the entire previous history of humanity– an increase from 1.5 to 6.1 billion in just 100 years. There are more than 7.4 billion humans living on earth today, whereas 200 years ago, this number was even less than 1 billion! It is expected that at this rate, the world would have around 9.7 billion humans by 2050. Hence, the balance in nature has enormously been disturbed. Mahatma Gandhi, the Father of Nation had said that 'nature has provided for everyone's need but not for everyone's greed'.

Unfortunately, the human greed has disturbed the entire equilibrium. Geologists have started predicting that almost 12,000 years of Holocene has come to an end. Why? Because it is the human beings who have adopted a path of complete destruction of life support systems. This new epoch is being said to have begun from 1950, when radioactive elements from nuclear testing were spread all over the globe and characterized by mass extinctions, plastic pollution, and spike in carbon emissions in the atmosphere. It is now said that we are entering into an era called 'Anthropocene', wherein anthropogenic activities have re-shaped the earth's land, oceans, air and biodiversity to an enormous extent. Consequently, biological diversity has significantly reduced, the earth has become warmer and all over the world we are facing greater incidence of natural catastrophic events.

A recent study shows that about 58 per cent of the world's land surface, and 9 out of 14 of the world's terrestrial biomes, have fallen below 'safe threshold' of biodiversity, impacting a wide range of services provided by biodiversity, including crop pollination, waste decomposition, regulation of the global carbon cycle, and socio-cultural services that are critical to human well-being. Another study has shown that over the past 500 years, rate of extinction of vertebrates, is a clear signal of elevated species loss which has markedly accelerated over the past hundreds of years. In fact, these rates are so high that life on Earth is embarking on its sixth greatest extinction event in its 3.5 billion years of history. In the Anthropocene, humanity faces the imperative question of how to transform agriculture enabling it to feed the world, contribute to eradicate poverty, and

contribute to a stable planet. Most importantly, it has been said that averting a dramatic decay of biodiversity and the subsequent loss of ecosystem services is still possible through intensified conservation efforts, but that window of opportunity is rapidly closing. This we should not be allowed to happen and must ensure that this trend is reversed.

## Global Outlook Towards Agrobiodiversity

Global thinking and inter-governmental approach to handle the management of genetic resources to improve food and nutrition security under the changing scenario witnessed many developments since the late 20$^{th}$ century. It started with the United Nations Conference on Human Environment held in Stockholm in 1972, with emphasis on population, agriculture and environment. Later the World Leaders congregated at the United Nation's Conference on Environment and Development (UNCED), also known as the 'Earth Summit' at Rio de Janeiro in 1992. One of the major outcomes of this was the adoption of Convention on Biological Diversity (CBD) in 1993, which directly addressed the ways to protect biological resources being are our life support system, from getting extinct. A major shift caused by the CBD was to place these resources under territorial sovereignty of individual nations where they are found or got originated, with legal rights to the nations to determine their access benefit sharing (ABS) system. For addressing trade related concerns, the World Trade Organization (WTO) was established which helped in enacting the Agreement on Trade Related Aspects of Intellectual Property Rights (TRIPS), including those related to agriculture (UPOV and patents).

Almost a decade later, the discussions surrounding the International Undertaking for Plant Genetic Resources (IUPGR) of the FAO culminated in the adoption of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) in 2001. The overall objectives of the ITPGRFA was to ensure conservation and sustainable use of PGRFA and to have both fair and equitable sharing of benefits derived from their use, in harmony with the CBD, for sustainable agriculture and food security. It also recognised for the first time the farmers' right on GRFA. The central piece of the treaty is the Multilateral System (MS) of facilitated access of PGRFA through a Standard Material Transfer Agreement (SMTA) that are freely accessible for breeders and researchers of member countries. The Treaty covers a series of crops listed in Annex 1, which includes 35 food crops and 29 forages. It also covers *ex situ* collection of those crops held by the CG genebanks. Though these crops, account for about 80 per cent of the world's food calories from plants, they do not represent all the 100 food crops of importance to food security and 18,000 forages of value to food and agriculture. Soybean, groundnut, sugarcane, oil palm etc. are among those crops that are still not included in Annex 1 even after 16 years of the Treaty implementation.

This treaty, while in harmony with the CBD, created an alternative multilateral ABS regime for the agricultural sector in order to facilitate access to, and the international transfer of, those plant genetic resources that are 'the raw material indispensable for crop genetic improvement' and thus important for global food security. More recently (2010), the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilisation (Nagoya Protocol) has been developed as a bilateral mechanism for ABS under CBD. It calls upon nations to develop effective legislative, administrative or policy measures to provide bilaterally those genetic resources that are within its jurisdiction and have been accessed in accordance with prior informed consent and on mutually agreed terms between the two parties.

## India's Response to Changing Paradigms

India has been one of the first countries to develop and enact laws related to biodiversity, in response to the new regimes in international law concerning access, conservation and property rights on genetic resources. Obviously, these processes had not been easy. A formidable task was to maintain a balance between the new and traditional rights. Accordingly, three Acts were passed by the Indian Parliament in the beginning of current century in an attempt to protect the nation's biological diversity, IPRs and the interests of researchers, be those plant breeders or the farmers/ farming communities. These relevant Acts are: i) the Protection of Plant Varieties and Farmers' Rights Act (PPVFRA), 2001; ii) the Biological Diversity Act (BDA), 2002; and iii) the Geographical Indication of Goods (Registration and Protection) Act, 2000. These legislative measures, in addition to providing enhanced intellectual property protection, emphasise the importance given to the rights of the farmers, the traditional knowledge,

and the biological resources of the country. Having been associated with the framing and facilitating the process, it was highly satisfying to see that both laws got approved by the Parliament in a record time. The PPVFRA is a unique act, being the first in the world, that provides rights to the farmers to produce, sell and use their own seeds, besides the typical rights to them equivalent to those of breeders and researchers for the valuable genetic resources conserved by them. Hence, the law aims to protect the plant varieties developed through public and private sector research as well as those developed and conserved by the farmers and farming communities. Accordingly, under the provisions of this Act, a PPVFRA Authority has been established that not only registers the new varieties developed by the breeders and farmers but also ensures fair and equitable benefit sharing through the provision of a national Gene Fund.

The primary objective of the Biological Diversity Act, 2002, is to protect India's rich biodiversity and associated traditional knowledge against their use by others without sharing the benefits arising out of such use. It provides for the establishment of a National Biological Authority (NBA), State Biodiversity Boards and Biodiversity Management Committees with extensive powers to promote conservation, sustainable use and documentation of biological resources. Foreign organisations do require NBA approval in order to access biological resources. Provisions have also been made to set up biodiversity funds and management committees at the national, state and local levels.

The Geographical Indication of Goods (Registration and Protection) Act, 2000 aims to provide a comprehensive framework to facilitate the registration, conservation and protection of goods with a unique geographical identity. The Act provides for the establishment of a Geographical Indication Registry and an Appellate Board to take necessary action against infringement, if any.

## Germplasm Flow under the New Regimes

In the pre-CBD era, all biodiversity was considered, managed and used as global public good, with easy access, and exchanged freely in the absence of ownership issues. In the present context, it would have been almost difficult for NI Vavilov to carry out his historical collection expeditions. India was importing more than 60-70 thousand accessions per year prior to CBD which has significantly gone down. India was also exporting around 20-25 thousand accessions per year, which has also declined significantly. Imagine, what would have been the food options for us had these regulations been in place prior to CBD when seeds of food crops like corn, potato, tomato, pepper, soybean etc. were shared to become our major food crops.

As a consequence of enacting legislative measures, the process of germplasm exchange invariably got declined globally. In retrospect, we have slowed down the whole process of germplasm exchange and use. Fortunately, many countries did share the germplasm with CG Centres, which is a major resource presently for multilateral exchange of crops listed under Annex I of the Treaty (ITPGRFA). Having been associated with the negotiations of the Treaty, it was decided then that a call would be taken later to include more crops but more than 20 years have passed and not a single species has been added to the Annex 1 list of 64 crops. Under the CBD, germplasm beyond the multilateral system (under the FAO umbrella of the CG system) can possibly be exchanged, under bilateral agreements and collaborative research projects. For bilateral exchange, the Nagoya Protocol has been developed, which now needs to be understood and followed by all the parties to the CBD for access to and benefit sharing derived from germplasm. So what has happened? Exchange of genetic resources, which was earlier decided by the scientists, has after the CBD, ITPGRFA and Nagoya Protocol, been taken care of by the bureaucrats and lawyers. Obviously, this is one of the major paradigm shifts that have occurred in GR management.

In India, there is still unsettled debate concerning exchange of germplasm both for the public and private seed sectors engaged in plant breeding. Even SMTA has not yet been put into practice for want of procedural clearances and lack of proper understanding. During mid-eighties, Indian Council of Agricultural Research (ICAR), as a policy, allowed free access to the parental lines of hybrids bred by the public system recognising well that seeds of these hybrids would otherwise not reach the end users i.e., the smallholder farmers. This very policy decision not only accelerated the coverage under hybrid seeds, resulting in increased crop productivity, but also strengthened existing private seed sector in India. On the contrary, there is an obvious hesitation to share the germplasm, either for the fear of loss of ownership or for biopiracy. Hence, there is an obvious need for trust-building and partnership. This would demand an

enabling policy environment and clear understanding for sharing the germplasm as well as information between public and private sectors engaged in plant breeding.

### Think Globally and Act Locally

In the present scenario, it is necessary that we think globally but take concrete measures to act locally. Action at the national/regional level is so critical today to research, document and conserve the available germplasm before it is lost forever. Despite the year 2016 being an International Year of Pulses, there was greater realisation that research on pulse crops had been quite inadequate. Charity begins at home. India is a gene rich centre. As one of the 8 mega gene centres of the world, it also has a strong national research and institutional system in place with adequate human resource. India also has a strong national agricultural research system (NARS). With respect to genetic resources, there are five bureaux dealing separately with plants, animals, fish, insects and microbes. Scientific and economic value of genetic materials are difficult to assess, as future problems and needs cannot be precisely anticipated. Moreover, feeding the ever-increasing world population would require either intensification of existing agricultural systems or by expansion into new lands. This means that optimal management of agricultural ecosystems and diversity of GR would be an essential part of any overall strategy for achieving this goal. In the past, national agricultural research systems, including that of India, had strong national breeding programs for developing improved varieties and hybrids. However, subsequently there became greater dependence on pre-breeding materials provided by the CG Centers. Unfortunately, over the years, efforts on pre-breeding also got declined at these Centers due to resource constraint. On the contrary, a paradigm shift from household food security to that of household nutritional security, demands much higher investments towards intensified scientific understanding of agriculturally important species (be those of crops, animals, insects, aquatic and microbial) as future genetic resource of considerable potential.

### Conservation through a Continuum

During the second half of the 20$^{th}$ century, *ex situ* methods of germplasm conservation, especially the seed genebanks, were considered to be the panacea in the management of genetic resources. Everybody thought that because there was danger of extinction of diversity of plant genetic resources, their seeds be collected and conserved in the genebanks–irrespective of whether they are useful or otherwise. In most cases, once collected, seeds were retained in these genebanks for long term storage with not much efforts on their evaluation for the useful traits and documentation for use by the researchers. Hence, often these genebanks were considered as Black Box. On the contrary, less emphasis was given to protect vegetatively propagated plants or those which were considered recalcitrant. As a consequence, in many cases, useful variability got lost for want of alternative scientific storage systems such as tissue culture banks or cryobanks.

In retrospect, we now need those conservation measures that are low cost and more sustainable at varying eco-system level involving communities that are known to be the gene saviours. Also there is an urgency to develop a 'conservation continuum', encompassing *in situ*, on-farm, *ex situ*, permafrost and other conservation methods with adequate funding support.

Further, it is of prime importance that the farmers, livestock keepers, aquaculture practitioners or foresters, engaged in conserving useful varieties, breeds and species, derive direct (financial) or indirect (livelihood security) benefits for remaining engaged in such conservation activities. There must be a compensation mechanism for these unique conservation practices by the farming communities. We cannot expect them to continue serving the society while living at sub-sustenance level. Hence, national leaders/policy makers do have a responsibility towards ensuring that the process of natural evolution remains well supported in the best interest of future generations.

The first and second reports on the 'State of the World's Plant Genetic Resources', brought out by the United Nations Food and Agriculture Organisation (FAO) provided authentic assessment of various conservation methods and the state of germplasm collections of plant genetic resources. It has documented more than 1,750 individual genebanks worldwide, of which about 130 hold more than 10,000 accessions each. Currently, about 7.4 million accessions are maintained globally. Analyses suggest that between 25–30% of the total holdings (or 1.9–2.2 million accessions) are quite distinct, with the remainder being duplicates held either in the same or, more frequently, a different collection. Crop wild relatives (CWR) do comprise 10% of these collections, but not much of them have been used so far. Around the globe, genetic resources are

maintained in the genebanks at the local and national level by governments, universities, botanical gardens, NGOs, companies, farmers and others in the private and public sectors. They do house a wide range of different types of collections: national collections maintained for the long-term, working collections maintained for the medium- or short-term, collections of genetic stocks and others. When we look at the national genebanks around the world, to begin with, the N.I. Vavilov Genebank in Russia (VIR) was the largest in the past. But now, the Genebank in the USA is number one followed by those of India, China, Russia, Brazil, Japan and Korea. On the contrary, in some countries of the Central Asia and Caucus like Armenia, Georgia, Kazakhstan, Turkmenistan and Kyrgyzstan, where I had the privilege to work with their NARS, not even 2-3 scientists were deployed to work on their valuable genetic resources with practically no infrastructure for the national genebanks. Such national systems do need support, both in terms of infrastructure and capacity building. It is satisfying to note that in last more than a decade, each one of them have established their functional genebanks.

Programmes on *in situ* and on-farm conservation have recently gained tremendous impetus as these protect germplasm in their natural habitat and take into account social and cultural factors such as farmer's perceptions and knowledge. On-farm conservation entails the active participation of local communities in the documentation and description of local species and varieties in a catalogue or register, establishment of nurseries for multiplication and distribution of unique plant or seed material, the promotion of nutritional values and traditional recipes, the development of enterprises and market linkages for the sales of products or services based on local unique crop diversity, and safeguarding of unique species and varieties found on their farms. Thus, *in situ* and on-farm conservation efforts remain ineffective without participation of the local community. Traditionally, local farmers are known to maintain several indigenous crops on their farms, especially fruit species or varieties. Such farmers have been designated as 'Custodian Farmers', identified for actively maintaining and promoting agrobiodiversity and related indigenous technical knowledge, at farm and community level. Linking such farmers to the research institutions and genebanks for characterization and evaluation of the elite genotypes, providing technology for rapid multiplication and distribution of plants is the need of the hour. Documentation of traditional knowledge is another activity that not only ensures its protection against theft but also ensures financial benefits to the knowledge holder when commercial sectors exploit the knowledge. Scientific validation of such traditional knowledge is also essential for improved understanding of the ecological functions of agrobiodiversity especially in the context of physical environment and the socio-economic factors. There is urgent need to promote use of more nutritious species such as millets, indigenous fruits, vegetables, roots and tubers, as compared to major emphasis that we gave in the past to only few selected staples. We now need to ensure up-scaling and out-scaling of innovations to achieve dietary diversity and improved nutrition at household levels. Information systems are still weak and capacity building is urgently required.

It is indeed satisfying that permafrost conservation for plant genetic resources has now been put in place. The Svalbard Global Seed Vault (SGSV), established in 2008 inside a mountain on a remote Island in Svalbard archipelago, located half way between mainland Norway and 1000 km from North pole, provides a great safety as duplicate storage facility for all seeded PGRFA. It is a state-of-the-art seed storage facility built to withstand natural and man-made disasters. The Seed Vault is managed by Norway government. The seed samples are stored in a reinforced concrete tunnel drilled 70 m into a mountain, stored in foil packets at -18°C, and are expected to remain viable for thousands of years. Unlike the hundreds of existing seed banks, the vault does not rely solely on artificial refrigeration systems but even if the power fails, the temperature are expected to never rise above freezing. The SGSV is built to store a massive 4.5 million varieties of crops, with each variety containing around 500 seeds. The Global Crop Diversity Trust works in conjunction with the Norway government to manage the seeds in the vault. The vault currently holds 880,837 seed samples of 5,403 species belonging to 71 institutes. These seeds were donated by almost every country in the world, so there is a massive variety of seeds represented. All germplasm from CGIAR genebanks has been safely duplicated here. If a crop is lost through natural disaster or war and a seed bank is destroyed, a government could request replacement seeds from the vault. A recent example of this was witnessed when ICARDA retrieved part of its seed collection that from the SGSV to fulfil requests for germplasm use. ICARDA's

original Gene Bank in Aleppo, Syria was forced to be shifted, after the war in the area. ICARDA had replicated over 80% of its collection in the SGSV, prior to the conflict. The seeds in ICARDA are globally sought due to unique landraces and wild relatives of cereals, legumes and forages collected from the Fertile Crescent of Western Asia. A total of 38,073 seed samples were sent to Lebanon and Morocco, ICARDA's new sites for genebank facilities, in the cropping seasons 2016 and 2017. Of these 15,000 accessions (including bread and durum wheat, lentil, faba bean, chickpea and grass pea) multiplied in 2016 have been sent back for safe duplication to SGSV on February 22, 2017. This proves to be a classical demonstration of the collective wisdom of policy makers, scientists and farmers who have contributed in the genetic resources movement in the past few centuries!

## Genetic Diversity–Use it or Lose it!

What we now know is that there is less use of genetic diversity today than yesteryears which led to attaining the Green Revolution. The Food and Agriculture Organization of the United Nations (FAO) has, therefore, initiated with the support of Bill and Melinda Gates Foundation (BMGF), a project to strengthen plant breeding capacity and research on global scale, so that use of genetic resources is enhanced globally. This project, known as the Global Partnership Initiative for Plant Breeding Capacity Building (GIPB), is a multi-partner platform with an aim to improve the institutional capacity for effective crop variety development and their distribution through seed systems. More details are available at: http://www.fao.org/in-action/plant-breeding/en/.

It is well documented that the use of PGR has globally declined. Many countries are not laying enough emphasis on pre- breeding and generation of genetic variability for crop improvement. They are largely dependent on import of pre-breeding materials mainly from the CG centres. In view of this, plant breeding must be brought back in the forefront.

Many stalwarts like Drs Norman Borlaug, GS Khush and SK Vasal had achieved great strides in varietal improvement and adaptation, mainly due to extensive use of genes from landraces and wild relatives. No doubt, working with wild relatives and species is more difficult and require good infrastructure facilities, yet they are very important in the current context of climate change.

Of course, there are several other reasons for the decline in use of germplasm. As already mentioned, access to useful germplasm is becoming more difficult due to existing new regulatory regimes. In addition, the research on traits of interest and the partnership in sharing germplasm is badly lacking. Over all, efforts on pre-breeding are declining due to lack of funding to the National Agricultural Research Systems (NARS) and CG Centers. On the other hand, the requests for germplasm by the breeders has also declined due to lack of digitization, proper evaluation for useful traits, germplasm characterisation and the existing regulatory systems.

## Advances in New Science for Agrobiodiversity Management

We are currently in an exciting scientific era, were genome decoding of organisms is becoming almost a routine activity and the possibility to precisely tailor structure and function of organisms is becoming a reality with new tools of biotechnology, especially gene editing using Crisper-Cas technology, advances in omics, space technology and bioinformatics unraveling deeper mysteries of life. New technologies pervading agriculture in terms of smart-phones, satellite imaging, phenotyping using drones, IPM, automated farm practices, decision support systems for NUE etc. are helping farmers to grow more food on their land while reducing cost on water, fertilizer, pesticides etc.

However, the availability of appropriate planting material/breeds remains the most critical factor for enhancing productivity, adaptability and resilience of agro-ecosystems. Developments in science and technology in the areas of genetic engineering, genomics, biotechnology, nanotechnology, bioinformatics, synthetic biology etc. have increased the speed, scale and efficiency in research outputs. These technologies are the game changers that will dictate how genetic resources are researched in future and used effectively. Nonetheless, existing agrobiodiversity would remain the "hardware and software codes of nature" requiring systematic deciphering for designing agricultural crops and breeds for their use through new science. Before the emergence of modern era of use of 'gene guns' by the biotechnologists or plant breeders to transfer the desirable new genes into designer crops, the farming

households assessed in their fields and courtyards the semi-wild and semi-cultivated plants for their existing strengths and weaknesses, and selected desirable traits while minimising the undesirable. Nevertheless, the products of biotechnology will also have to be field-tested besides undergoing biosafety tests before their identification and release as superior varieties for commercial cultivation. An important aspect with application of new technologies for agricultural production would be to generate awareness and dispel fears in the minds of general public about the use of new products (*e.g.* golden rice) that are outcomes of cutting-edge technologies as international public goods. With new advances for gene editing, the opportunities to accelerate crop breeding and use of germplasm have increased significantly.

## Conclusions

Paradigm changes in agrobiodiversity management in the scientific, social, legislative/regulatory and governance realms have been inevitable, and will continue to happen in the future. That's because human needs and expectations do keep on changing from time to time. To ensure synergy among agrobiodiversity management and agricultural development, the role of stakeholders is crucial, especially in the developing countries that are considered gene-rich. Also a main paradigm shift in agriculture is needed to move from sustained food security to that of household nutritional security. For this, there is an urgent need for higher research investments and more intensified scientific investigations of agriculturally important species (be those of crops, animal, aquatic and microbial). Ecosystem services must ensure synergies between conservation, sustainable agricultural production and sustainable livelihoods.

As transboundary problems continue to rise (e.g. Ug 99 and blast in wheat, Fusarium wilt race 4 in banana etc.), it becomes imperative to carry out research in partnership mode, across national boundaries. To do so, there is great need to understand, adopt and practice access and benefit sharing (ABS) mechanisms, through enabling policy environment, proper public awareness and capacity building. Also the NARS need to build their Gene Funds to sustain activities around agrobiodiversity conservation and management while broadening the genetic base to diversify the current food basket.

Further, for an effective management of genetic resources a paradigm shift from conservation to that of conservation through use is necessary. This would require a holistic approach around *ex situ*, *in situ* and on-farm conservation involving all the stakeholders (farmers, breeders, researchers etc.). Most importantly, emphasis should now be on livelihood perspective, where genetic resources form important asset for much needed livelihood security, going beyond their direct contribution to food and income to more dynamic and less visible ways in which they enable rural households to manage various forms of uncertainty and risk, maximise use of other productive assets, and facilitate both diverse and sustainable livelihood strategies. Time is now for action and not just talk in order to ensure better future for coming generations.

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# Perspectives in Biodiversity, Food and Future for India

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The last two centuries have brought the world unprecedented environmental problems that we must control if we wish our civilization to persist. The problems have resulted from an increase in the total human population over the past two centuries from one billion people to the present 7.4 billion; an even more rapid rise in consumption; and the failure of technology to keep pace with the changing numbers of people and their demands for consumption. Even more frightening is the fact that our numbers are projected to grow to nearly 9.9 billion within the next 34 years (by 2050), at an average increase of 200,000 people net per day during that period. Over the same 34 years, the current population of 1.3 billion people in India is projected to rise to 1.7 billion (www.prb.org). In view of the current demands we are placing on the environment in India and throughout the world, those predictions are alarming in the context of what we actually are doing and what we may be willing to do about them.

How did we reach our current challenging condition? At the time when our ancestors developed crop agriculture and domesticated animals, about 12,000 years ago, the global human population numbered only about one million people, with about 100,000 in Europe. As agriculture has spread around the world to encompass about a third of the planet's land surface, the numbers of people have grown rapidly, so that 500 years ago there were about 500 million people on earth, with about a third of them, some 170 million, living in India. In about 1810, the global human population reached one billion people for the first time, with about 270 million, roughly a quarter of them, in India. The population of India was growing more slowly than that of other regions.

The past two centuries have been more tumultuous than any earlier period in our history. A few decades after the Industrial Revolution reached full stride, the whole world was consolidated into nations and colonies, and rivalries between them increased greatly. Britain and France outstripped earlier colonial powers in seizing lands all over the world, with Russia and the United States annexing territories along their borders and Japan, with Germany and Italy when they were consolidated, attempting to set up their own colonies. As this process has continued over those past 200 years, some 200 million people have been killed in wars over land and other kinds of wealth. The world sadly remains filled with national and regional rivalries that are continually bursting out and leading to even more deaths. Most nations and groups of people seem to want to consume more than its rivals, and many remain willing to go to war to attain those ends. Changing national boundaries and internal moves for independence are based on the same principles, but do not move us collectively any closer to a sustainable world that can manage its planetary ecology sustainably.

A serious problem is that there are not enough resources to go around. Global Footprint Network (www.footprintnetwork.org) estimates that the people of the world combined are consuming about 164% of our planet's capacity for sustainable productivity on a continuing basis. In other words, it would require about 64% more capacity for sustainable productivity than exists on earth for us to attain collective stability at the present population level. Theoretically, we could achieve stability by attaining a level population, adopting socially acceptable levels of consumption throughout the world, and improving our technology, but we are not gaining on the problem at present. Even if we did so, we would not be gaining on our current levels of hunger, malnutrition, or poverty, even though we would no longer be permanently destroying our planet's resources that might otherwise be used for the future. Fifty years ago, we were consuming about half as much of the world's capacity for sustainable productivity as we are now. The subsequent doubling of our population and even greater rise in our consumption have sent us well past our planet's capacity for sustainable productivity, and we must face the consequences.

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Some countries consume more than their share of the world's productivity. Since our overall use of 164% of the total global capacity for sustainable productivity exceeds the total available, a given country can increase its consumption, or standard of living, only through improved technology, improved resource management, or by gaining some kind of an advantage over other countries. India's Ecological Footprint, a measure of the total amount consumed within the country, has doubled since 1961, while its population has nearly tripled from 460 million to 1.3 billion people. Thus the average amount consumed per person in India has decreased during this period. Up to 264 million people in India are estimated to have reached a middle class income level during this period, so that the average lot of the poor in India has declined over this same 60 years. In view of these circumstances, it will take an incredible amount of care for India to shift from an economy that has grown at the expense of its environment to one that flourishes by nurturing and preserving it.

During the same period (1961 to the present), while India's population has tripled and its consumption doubled, China's population has doubled while its consumption has tripled. Much of China's growth in consumption has been fueled from abroad, with China now consuming 2.5 times its internal capacity for sustainability, compared with India's 1.8 (www.footprintnetwork.org). The more that a nation exceeds its internal capacity, the more food and other commodities it has to seek around the world and pay for them one way or the other; as this process unfolds, the situation worldwide becomes increasingly unstable. With the U.S. consuming 1.9 times its internal capacity, Britain 3,5 times, Switzerland 4.2 times, and Japan 7.1 times, part of the reason for the difficulties inherent in international relationships become obvious, as does the need for reform and greatly enhanced global cooperation. Many specific environmental problems for which we share a common responsibility have become obvious however our divided and fractious world chooses to deal with them.

Global climate change is the most widely recognized of the environmental challenges that face us. A fruitful conference of the parties to the United Nations Framework Convention on Climate Change Intergovernmental Panel on Climate Change was held in Paris in December, 2015. The parties agreed to a goal of holding global temperature increase to 2°C, and to attempt to hold them to 1.5°C, and their agreement has subsequently been ratified by a sufficient number of nations and come into effect. If all nations continued with a "business as usual" scenario, we would likely force a 4°C change in average global temperatures, in which case large sections of the world would become uninhabitable. Even with a successful pursuit of the goals set in Paris, the effects on agricultural lands will be massive and our ability to keep pace with the demands of a rapidly growing population will be subject to serious doubt.

India will have a very difficult time achieving its emissions goals and meeting the targets set in Paris although Prime Minister Modi's government is determined to do so. The complexity of multiple missions and agencies involved in achieving progress makes effectively dealing with the situation difficult. Much of the India's (and the world's) economic progress has been based on relatively cheap energy from many sources, a number of them highly polluting and forcing climate change. Alternatives must be found and deployed on a massive scale that would seem to require international subsidies in many directions and of many kinds. At a global level, it may already have become impossible to hold global temperature increases within the 2°C target set in Paris. The global level of carbon dioxide in the atmosphere, 280 ppm at the start of the Industrial Revolution, reached 400 ppm in the autumn of 2016 and is still increasing, with 350 ppm probably the level at which the earth can continue to support the activities to which we are accustomed. For India, increased monsoons, higher temperatures, melting glaciers, the intensified use of water that accompanied the Green Revolution and the projected 2 meter rise in sea level by the end of this century will all adversely affect agricultural productivity, which will suffer major losses both locally and globally unless climate change is limited through common action.

Biological extinction receives less attention than climate change, but it is in fact a much more serious problem, simply because it is irreversible. Five major extinctions have taken place nearly the roughly four billion year history of life on earth, and our growth in numbers coupled with greed for every more consumption is now driving the sixth. By studying the fossil record, we can determine by extrapolation that there has been about 1 extinction per million species per year over the past 66 million years, but that now this has grown to

at least 1,000 species the historical rate (Pimm et al., 2014). The massive extinction we are causing is such that many geologists believe that our era deserves a special name, the Anthropocene, signifying our total dominance and the destruction that we are causing to our life support systems. The world in which we live now is very different from the one in which our ancestors lived a few thousand years ago, and it is not clear whether we will be able to adjust to the rapidly-changing new conditions we have brought about. As tropical ecologist Daniel Janzen of the University of Pennsylvania pointed out half a century ago, "The world is a garden, and we're all its gardeners." Whatever is saved, we will save; whatever is lost, we will destroy. This time, and the opportunities it represents, will never come again.

The loss of species seems a bad thing intellectually and perhaps morally, but it is much more than that. We base our lives entirely on the properties of organisms, which have not only created the conditions on this planet into which we evolved, but continue to provide all of our food, more than half of our medicines, and many other substances that we use directly. The ecosystems that they comprise maintain the quality of the atmosphere and the waters and provide for balance in the living systems in which we live as members. Destroying plant, animals, fungi, and microorganisms is the worst thing that we could possibly do in relation to the prospects for our civilization to last decades or centuries into the future. Nevertheless, the destruction of habitats for agriculture and urban expansion, global climate change, the spread of invasive plants and animals and diseases all over the world, and the overharvesting of particular plants and animals from nature – all of these combined relentlessly drive the process of extinction.

## Agriculture for the Future

We collectively are confronting a major problem in maintaining the sustainability of our agricultural systems and it will undoubtedly get worse unless we take a number of strong measures now. At present, we devote about a third of the Earth's surface to agriculture, most of it to grazing, and yet we are not feeding the people who are here now adequately – much less laying the foundations for the 2.5 million additional people projected to be added to our population over the next 33 years. It may seem somewhat strange that India, while consuming an estimated 1.8 times its sustainable productivity, is currently a net exporter of food: in fact, the world's seventh largest. The food is one of the commodities being traded, in effect, for goods from abroad to support a rising rate of consumption. India's trade balance is substantially negative. Even with a level population, India would need to increase its internal productivity greatly to live within the boundaries of its own sustainable productivity.

With specific respect to food and hunger, many millions of Indians starved to death from the time of the Bengal Famine (1943) to the beginning of the Green Revolution (1967). There are now three times as many people to feed as there were during those years. India's Green Revolution resulted in increasing the extent of croplands, double-cropping through intensive irrigation, applying more fertilizer, and introducing improved genetic strains of crop plants. Despite these measures, the population continued to increase more rapidly than food production during this whole period. No level of agricultural productivity can feed a continually growing population.

To feed all people adequately, we would need to maintain a level human population that might not be as large as the rapidly-growing one that we have now. Socially-justifiable consumption levels that could be accommodated through sustainable productivity would need to be adopted worldwide, a process that would necessitate the full empowerment of women and children everywhere. Technology would need to be improved as one element of the equation. Obsolete economic theories that imply that the goods we get from nature will be replenished as the demand for them grows will need to be modified to take into account the actual conditions on the planet we inhabit. On a finite planet, it is basically immoral to assume that economic prosperity can be attained by continually adding more young children to a given population – sort of a perpetual motion machine that cannot possibly lead to long-term stability when we are all dealing with limited resources. India would need to accept and implement these policies in order to find its own stability in a world that it would help to create.

Meanwhile, India faces great challenges in improving its agricultural productivity so that it can feed its people, even the poor ones, sustainably and into the future. For the whole history of agriculture in the country, improved genetic varieties of crops have been employed, and the sunflowers, potatoes, tomatoes, rice, and maize grown in India today bear faint resemblance to the earliest strains of those species that were cultivated, thanks

to genetics. By the way, all of those crops are from North or South America originally, except of course, rice. With three times as many people in India as at the time of the Green Revolution, it is not strange that some agricultural practices that proved fruitful then have now come into question. Heavy fertilization and application of pesticides and herbicides, double cropping (sometimes now triple, with no regard for the soil), and wasting water all contribute to the problem. These, along with the burning of agricultural straw that causes dense, unhealthy pollution over much of northern India once the monsoon season ends) might be considered excesses left over from the Green Revolution. Those who initiated the improvement of agriculture in India, however, never intended that every step they recommended would be followed endlessly until it caused serious harm in a country where the population meanwhile was tripling and the demand for consumption also shooting upward.

The major damage being done both to India's agricultural lands and its environment in the name of increased productivity, seemingly carrying on what were once agricultural improvements to extremes, should make one question the sustainability of India's position as a net food exporter. In effect, does pounding the last bit of productivity out of overused soils simply amount to a way of helping to make up India's trade deficit while rapidly lowering its internal capacity for sustainable productivity? The declining condition of the soils, the need to counter the effects of salt water seeping in around the coasts, and the effects of pollution everywhere would certainly seem to call for a very serious re-examination of agricultural regulations and practices worldwide.

A key element in maintaining the sustainability of our agricultural systems is the genetic diversity of the crops themselves – agrobiodiversity. When agriculture first became widespread, several hundred generations (some 10,000 years) ago, there was a great of local experimentation with different strains of the crops that were being used. Even at the time of the voyages of Columbus, five centuries ago, global commerce was still in the future, and there were only about 500 million people in the world. Very distinct centers of agriculture had been developed in the Eastern and Western Hemisphere, as well as throughout Eurasia and Africa, and all farming was practiced on a small scale. As a result of this dispersion of centers for agriculture, there was a great deal of diversity among crops and domestic animals, and many more species were involved in feeding people than is the case at present, when about 100 plant species provide more than 90 per cent of our food and three – rice, wheat, and maize – almost two-thirds of the total. Many species of plants that were once important food sources locally are no longer used anywhere or are very rarely used as crops.

As the global population grew from 500 million in 1500 to 7.4 billion today, large areas were brought under cultivation and the small-scale farmers that had maintained crop genetic diversity earlier gradually began to operate on a larger scale that by our time has become a vast scale. Relatively large fields and grazing areas are now characteristic of Europe, and much larger ones in North and South America. Even where small-holders continue to form the backbone of agriculture, as in China and India, they collectively farm vast areas. Under these circumstances, genetic diversity has suffered, even though attention is still paid to finding the best genetic strains for particular areas. For example, in the United States many hundreds of strains of soybeans and maize are grown, and there is really no other option considering the diversity of the farm belt there. Thousands of strains of rice are still cultivated locally in India and China.

To a degree, differences in climate and soils still demand that our crops remain diversity, but global agriculture today presents a very different picture from the one that occurs where small farmers are more scattered, as in southern Mexico or elsewhere in developing countries, with each selecting the particular genetic mix that they grow each year and the whole system remaining diverse. Clearly there is a continuing loss of agrobiodiversity as the intensity of interchange and the desire for ever-higher yields grows. This situation presents a real dilemma, because the rural agriculturists who have served as the guardians of a great deal of the world's agricultural diversity largely live in poverty. Although we might wish them to continue maintaining diversity for us, we cannot expect them to do so with very low incomes and limited access to the higher levels of consumption that so many of us take for granted. Subsidies of some kind will be required if we expect these rural farmers to continue living as they do, and we must also continue to use seed banks as ways to preserve agrobiodiversity properly. Just as for the loss of biodiversity generally, we have a clear moral obligation to avoid the erosion of the diversity that is left.

Why is this so? Simply put, we have altered and are continuing to alter the global conditions in which

agriculture has been developed over the past 10,000 years. It is certain that we shall need a great deal of genetic diversity to keep production going and increase it while maintaining stable conditions in the face of exploding human numbers and the ill effects of conditions such as global climate change that threaten everything we have taken for granted in today's agriculture. We might bring back many crops that have been or are being cultivated somewhere to build productivity in specific areas, or to bring great nutritional benefit to people; a number of these forgotten crops. I have earlier in this paper outlined the truly challenging situation that Indian agriculture is facing at present and must solve for the sake of its people in the future.

Contemporary genetic methods offer great possibilities for the enhancement of sustainable productivity everywhere, and it should be noted that the genes most likely to be helpful in enhancing the properties of a given crop may exist in their close relatives, or even in particular strains of that species. This clearly is an important reason to preserve what remains of agrobiodiversity and the living systems that support it.

The conservation of biodiversity generally is also important for supporting agriculture improvement, and improvement in the characteristics of other productive living systems, because modern genetics has for some four decades offered the possibility of transferring genes from one organism to another. Undoubtedly, our capabilities in that area will increase in the years to come, and it is clear that we are still very far from understand the way genetic systems operates in different parts of the dizzying variety of organisms that share this planet with us and make possible our lives here. If the people of the world really understood what we are losing, and the peril of doing so, they would rise up and devote major resources to saving as much as possible of the rich and largely undiscovered biological diversity that still exists today.

In thinking about how agriculture could be improved if we had the will, it is worth noting the bizarre and completely unfounded opposition to transgenic plants that has been fostered by private groups and alarmed people in such a way as to decrease their chances of improving their health and their lives generally.

Concerning transgenics, the level of confusion can only be called appalling. For India, a particular obstacle to feeding people adequately has been the arbitrary rejection of plants produced by particular breeding protocols, such as transgenics. When scientists learned to transfer genes between one kind of organism and another so as to change the characteristics of the recipient, they were simply mimicking a process that is extremely common in nature, a way in which organisms become better adapted to their environment. When a gene moves from one organism to another, it may be integrated into the genome of the recipient, specify a novel allele or protein that has a positive role, and then becomes a regular part of its host's genetic instructions.

Since the production of GM crops involves specific transfers of individual genes to a specific recipient organism, the resulting transgenic individuals have no traits in common. Specifically, they produce no chemical substance that is common to all GM organisms; whatever they do produce depends on the specific properties of the gene transferred. Consequently, to treat "GMOs" as a class of organisms that should be banned or scrutinized more carefully than other new crop strain is illogical. Crops or animals produced in this way may have desirable, neutral or undesirable characteristics, like those produced in any other way. They deserve neither less nor more evaluation of scrutiny than any other crop strains. Since there is nothing in common between them, there is no way that GMOs could be dangerous as a class, and clear that they bring nothing common to foods *produced* from plants or animals in whose origin this particular genetic strategy has been employed.

In the light of these findings, I have as a conservationist always found it a disgrace that the Cartagena Protocol was enacted in 2003 as part of the Convention on Biological Diversity, consuming large amounts of money and effort for no real purpose. It cannot be demonstrated that a single species of plant or animal has been saved or will be saved as a result of the operations of the Protocol, so why is it part of the CBD? The Convention has had enough trouble saving species, which have mostly slid down hill in numbers and vigor during the 24 years since it was enacted, so why should it, or agricultural productivity be encumbered by a Protocol based entirely on false premises? In the light of contemporary knowledge, writer Andrew Porterfield has aptly dubbed the Protocol a "relic of [an] earlier era promoting GMO fears." It is time to move on.

It is significant that no academy of sciences anywhere in the world, and there have been many dozens of

comprehensive studies, has ever found any potential harm from consuming food produced by GM crops. These include the academies in India, China, Brazil, Mexico, the U.K., the U.S., and everywhere else that this matter has been considered over more than 15 years. A comprehensive review conducted under the auspices of the National Research Council – National Academy of Sciences in the U.S. has reinforced the scientific basis for our understanding (National Research Council, 2016). The same year, 2016, a significant proportion of living Nobel Prize Laureates, exasperated by the non-scientific arguments that were holding back efforts of farmers and nations to produce the food we need, issued a proclamation along similar lines (http://supportprecisionagriculture.org/). The consensus opinion has never changed, but become ever stronger, as the evidence has accumulated, and the opposition that has grown up therefore must be assumed to be either political or fund-raising in character. When and how can this unfortunate situation be resolved so that people may benefit from science rather than suffer as a result of propaganda?

It is also worth pointing out that many medicines (including virtually all insulin used worldwide) and virtually all beer, cheese, and bread produced anywhere use genetically modified organisms in their production. No one seems either to fear them or call attention to the methods of their production, but if the claims about GM crops were true, they would presumably all be poisonous too. Economics triumphs once again? It is fervently hoped that India will through off the burdens imposed on it by false worries and join the rest of the world in realizing the benefits of GM crops, predominant in the United States with no harm having been detected. The apparent benefits of GM cotton, which has been grown profitably in India since 2002, ought to help make the case locally. This one improvement in a major crop is estimated to have added $18.3 billion in farm incomes in India over the past 14 years

Golden rice, in which a single gene was transferred from a bacterium to one of the original strains all of which have been developed much further by conventional methods, provides an example that is particularly painful to contemplate. Using a single innocuous fact about its origin as a basis for combatting the introduction of β-carotene-fortified rice, Greenpeace together with some individuals have denied a dependable source of vitamin A to society, thus condemning hundreds of thousands of children each year to blindness and, in many cases, death. Considering that there is not one shred of evidence pointing to dangers from such rice, these groups and individuals must bear the responsibility for their actions and consider who benefits from their promotion of such non-scientific, unfounded assertions. Having prevented the full development of Golden Rice and kept it unavailable for more than a decade, some are now claiming that it isn't "real." What strange logic that seems!

For people living in the tropics, these methods could afford a way to save their main staple crops instead of to starve. The yield of cassava, for example, is greatly reduced through Africa by a virus disease that could in principle be cured by these methods, and yet their adoption and even testing has been slowed down for years by false worries and fears promoted by a rich and prosperous Europe. At the same time, the worldwide banana crop is in danger of being destroyed completely by three rapidly-spreading fungus diseases, which, according to studies carried out at the University of California, Davis, could be controlled by the thorough investigation of their genes and the application of modern genetic methods to produce improved varieties of these critical food plants.

One of the logical snares inherent in all of the discussions of GMOs and the imaginary damages they might cause is the idea that "if they can be avoided, let's do so," to avoid the implied harm. This relationship needs to become explicit and exposed for what it is – nonsense. If no one has even proposed a credible theory by which plants of transgenic origin could, as a class, inflict harm, then we should absolutely grow them when their characteristics warrant it – not avoid them as a group. Writers and speakers repeat to the point of tedium that GMO are not a "magic bullet," but so what? There is virtually no such thing in any field of human endeavor, only factors that can be helpful in moving us in a particular direction. We really do need to move on to the next stages in the development. Until we do so, we shall simply be trying to solve major problems with our hands tied behind our backs.

The challenges of developing a robust, sustainable, and productive agriculture are huge, both in India and generally. Agriculture must change both to limit and to resist global climate change, and to limit its other pressures on the environment. All are made more severe

by inefficient agriculture and urban sprawl. I have spent much of my life fighting to conserve biological diversity and to work toward a sustainable world. India is fully dependent on its biological diversity and likely to lose even more than half of its species, the great majority of them unknown, during the next few decades. India's biodiversity is among the world's richest, with most groups except vertebrates and plants very poorly known. Meanwhile, bureaucratic snarls coupled to a degree with lack of interest in the subject are retarding both the study of India's organisms and their conservation.

We derive all of our food from plants, directly or indirectly, and, in India, most medicines also. We are just starting to understand the ways in which diverse ecosystems protect our soils and our water supply, absorb pollution, and determine the qualities of our atmosphere and its effect on us. We cannot build a sound future for India or for the world as a whole without paying much better attention to these problems, embracing both their value and the moral precepts that we have built up over the years to protect them.

There at least four important steps that would lead to agricultural improvement in India and generally:

1. Adequately fund studies to help us understand and preserve our remaining agrobiodiversity, in part by encouraging the small farmers who preserve it people who maintain it.
2. Inventory and conserve as much of existing wild biodiversity – so poorly known – as possible.
3. Use scientific principles to determine the future of agriculture, disregarding the false representations of those who benefit from polemics that greatly lower the quality of life for billions of people throughout the world. Blindness, starvation, and premature death are prices that we cannot afford to pay for their lies.
4. Invest much more heavily in agricultural research and development everywhere. Agriculture is in general very poorly understood, which is amazing in view of our utter dependence on it.

The question is not whether we can do better – we simply must. Only by overcoming our inherent selfishness, understand our differences and helping one another to lead better lives can help us to build a sustainable world. The alternative is catastrophe for everyone, sooner than we imagine it might come. As American representative to the United Nations Adlai Stevenson stated a half century ago (1965),

"We travel together, passengers on a little spaceship, dependent upon its vulnerable reserves of air and soil, all committed for our safety to its security and peace; preserved from annihilation only by the care, the work, and, I will say, the love we give our fragile craft. We cannot maintain it half fortunate, half miserable, half confident, half despairing, half slave to the ancient enemies of man, half free in a liberation of resources undreamed of until this day. No craft, no crew can travel safely with such vast contradictions. On their resolution depends the survival of us all."

Those words remain true today, and we must find ways to heed them. The 3.3 billion people who lived then have grown to today's 7.4 billion, and our demand on the world's sustainable productivity has grown past its total capacity, having increased 2.5 times over that half century. If we do not find ways to respond to the challenges we face adequately, we shall have only ourselves to blame for the consequences.

## References

Pimm SL, CN Jenkins, R Abell, TM Brooks, JL Gittleman, LN Joppa, PH Raven, CM Roberts, JO Sexton (2014) The biodiversity of species and their rates of extinction, distribution, and protection. *Science* **344:** 1246752 (2014). DOI: 10.1126/science.1246752

US National Research Council (2016) "Genetically Engineered Crops: Past Experience and Future Prospects," National Academy Press, Washington, D.C.

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# Application of Genomics to Enhance Utilization of Plant Genetic Resources

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Genomics may greatly enhance utilization of plant genetic resources (Brozynska *et al*., 2016). This is especially critical with the prospect of major climate change (Aberton *et al.*, 2016). New cereal genotypes are needed to deliver desirable nutritional and functional characteristics in the environments of the future (Henry *et al*., 2016). Analysis of wild and domesticated genetic resources may identify new sources of genetic variation for breeding. Genomic analysis of cereal (especially rice and wheat) genetic resources may contribute significantly to global food security. Whole genome sequencing and transcriptome sequencing can contribute to discovery of valuable new genes and alleles and explain the molecular basis of economic traits. Utilizing plant genetic resources requires analysis of large amounts of genomic data (Rossetto and Henry, 2014)

## Progress in Key Species

The following is a review of our recent progress in major plant species using DNA sequencing technology to discover the genes controlling key traits and use the increased understanding of their molecular basis to deliver new insights into strategies for accelerated plant improvement.

## Rice

Re-sequencing of domesticated rice reveals parts of the genome that have little or no diversity in the domesticated gene pool (Krishnan *et al*., 2012). Sequencing of the genomes of wild rice (*Oryza*) populations has revealed new ancestral populations that widen the effective gene pool of rice for breeding. These newly identified genetic resources will provide a new source of diversity for use in breeding for disease resistance and tolerance to climate change in rice. These resources and genomics tools facilitate the development of rice genotypes to satisfy the quality requirements of increasingly discerning rice consumers (Anacleto *et al*., 2015). The breeding of hybrid rice may benefit from the use of genome re-sequencing to select parents (Waters *et al*., 2015). The diversity of repetitive sequences across the *Oryza* genus has been analysed (Copetti *et al*., 2015)

### *The AA Genome Primary Gene Pool of Rice*

The primary gene pool of rice includes the wild *Oryza* species with AA genomes that are inter-fertile with domesticated rice. Analysis of the whole chloroplast genome of these species has been used to define their evolutionary relationships (Wambugu *et al*., 2015). Diverse grain quality attributes may be found in this gene pool (Wang *et al*., 2015). This gene pool also provides a source of biotic and abiotic stress tolerance genes for current and future environments.

### *New Sources of Genetic Diversity for Rice*

Recent research has identified large poorly characterized populations of *Oryza* in northern Australia (Brozynska *et al*., 2014). Phylogenetic analysis of the AA genome taxa indicates that they are sister groups to the clade including domesticated taxa suggesting that this region may be an important centre of diversity for rice. Reference genome sequences for these taxa have been produced recently as a tool to facilitate analysis of diversity in these wild populations. This whole genome analysis (Brozynska *et al*., 2016) has suggested that northern Australia may be a centre of diversity and possibly of origin of the A genome clade that includes the domesticated rice in Asia and Africa. Sequencing of DNA from bulks of individuals is being used for association of polymorphisms with traits at the whole genome level in populations segregating for key traits.

## Wheat

Sequencing of the transcriptome of developing seeds of diverse wheat germplasm has revealed genetic diversity that explains differences in carbon assimilation (Rangan *et al.*, 2016), flour yield in milling and bread quality on baking (Furtado *et al.*, 2015). Together these gene discoveries offer a significant opportunity to accelerate the rate of genetic gain in wheat breeding.

### *Carbon Assimilation*

Photosynthesis in the pericarp of wheat proceeds by a C4 pathway. Genetic variation in grain photosynthesis

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by this recently defined pathway (Rangan *et al*., 2016) may explain differences in yield due to re-fixation of carbon respired to support protein and starch biosynthesis during endosperm formation. Selection for enhanced photosynthesis in the grain may result in higher yields in environments limited by harsh conditions during late grain filling. The influence of heat stress on expression of this pathway and the apparent substantial variation in this trait within the wheat gene pool is being studied.

### *Flour Yield*

The yield of flour obtained when wheat is milled is controlled by genes that have been identified by analysis of levels of expression in wheat genotypes differing in flour yield. This discovery will avoid the need to have large amounts of grain to assess flour milling performance and provide tools for early generation selection in wheat breeding.

### *Grain Hardness*

The genetic variation in the hardness of wheat grain has been associated with the *pin* genes. Transcriptome analysis has demonstrated that the expression levels of these genes and not just their protein structures is the key to wheat hardness (Nirmal *et al*., 2016).

### *Breadmaking Quality*

A highly differentially expressed gene encoding a small sulphur rich protein in wheat endosperm may explain differences in the breadmaking qualities of wheat (Furtado *et al*., 2015). However this gene may not be important for products such as chapatti. The gene has an open reading frame encoding a small sulphur rich protein with potential for involvement in cross linking of larger proteins in the gluten. Knowledge of this gene may allow the development of wheat genotypes with acceptable end use quality at much lower grain protein contents improving the nitrogen use efficiency of the crop. The combination of selection for flour yield and bread quality will ensure wheat genotypes can be selected with acceptable grain quality. A modest number of genetic loci may require selection to ensure wheat breeding delivers acceptable end use quality allowing more selection pressure for grain yield.

### *Sources of Diversity for Wheat*

New hexaploids (synthetics) derived from the diploid progenitors may expand the range of variation found in wheat. The improved genomic tools identified by transcriptome analysis may also allow much more effective screening and utilization of variation within the existing hexaploid gene pool. Tools to support the analysis of sub-genome specific gene differences (at the genomic and transcriptomic levels) will greatly enhance progress in wheat genetic improvement.

### Peanut

Peanut (groundnut) is an important pulse crop. The genomes of relatives of the diploid progenitors have been characterized. Analysis of the tetraploid domesticated peanut remains challenging. Sequencing of gene enriched genomic DNA from bulks of genotypes with extremes of the traits is being evaluated for gene and marker discovery in peanut.

### Coffee

Coffee is a crop of great economic importance. The genome of coffee is being characterized (Tran *et al*., 2016). The diploid robusta coffee (Denoeud *et al*., 2014) and more complex tetraploid arabica genomes have been sequenced. Coffee bean quality results from an interaction between genotype and environment (Cheng *et al*., 2016). Introgression of genes from other species in the genus may be required to expand the gene pool of domesticated coffee to cope with the impact of climate change on current production areas. Re-sequencing of these diverse species is in progress. Sequencing of bulks is being used in association of traits with markers at the whole genome level in Arabica coffee. A transcriptome of the arabica coffee bean has been produced by long read sequencing.

### Mango

Mango is a tree crop with substantial diversity in both cultivated and wild gene pools. A genome sequence will provide a platform for exploration of genetic variation in this genepool. Breeding of species with a long generation time such as trees is greatly advantaged by the availability of genome resources facilitating molecular selection at early growth stages. Tree architecture and fruit quality are among the key traits to be advanced in this and other fruit trees crops.

### Macadamia

Macadamia is a good example of a recently domesticated crop. This species is genetically very distant from other species (a member of the Proteaceae) with characterized genomes. A genome sequence has the potential to

make a big contribution to the understanding of such phylogenetically isolated taxa. A draft sequence of the genome has been produced (Nock *et al*., 20I6). Sequencing of the wild relatives will rapidly help suggest strategies for use in breeding improved varieties with desirable traits such as smaller tree size. Re-sequencing of this recent domesticate and the four related wild species in the genus will allow targeted expansion of the gene pool.

## Sugarcane

Sugarcane is the leading industrial crop globally. This extremely complex genome is the subject of considerable sequencing effort (Souza *et al*., 2011; Hoang *et al*., 2015). The extreme polyploid of this species is a key constraint to application of genomic tools. Due to the challenge of assembly of this difficult genome, a first step towards a reference is being generated by sequencing sugarcane BAC clones that cover the sorghum genome. This 'monoploid genome' will support the analysis of the complete polyploid genome that is being generated with long read sequencing. This technology has also been used to generate a more complete set of transcripts for this complex species (Hoang *et al.*, 2016). Alternate transcripts from the same gene and transcripts from homologous genes make a very complex system in this 12X species. The genomes of the progenitor species have also been analysed. Hybrids with new combinations of these genomes and other related species from with the group may expand the sugarcane gene pool to support production of a more diverse range of products from sugarcane crops and enable production in more diverse environments.

## Eucalypts

Eucalypts are some of the most widely planted trees in the world with potential as a biomass or wood crop in many environments (Healy *et al*., 2016). New reference genome sequences are being generated for diverse species within the large group of Eucalypts. Hybrids between species show significant promise as tree crops. Sequencing of bulks of genotypes is being used to associate polymorphisms with traits. These relatively small genomes (< 400Mbp) are relatively easy targets for whole genome analysis and genotyping by whole genome sequencing. Comparative genomic analysis has explored variation across the Eucalypts from *Corymbia* to *Eucalyptus*.

## Domestication of New Species

### *Crop Wild Relatives*

Wild crop relatives may be source of novel genes for crop improvement but may also become targets for domestication in their own right (Shapter *et al*., 2013). New diversified crops will contribute to the resilience of the food production system and may deliver the genotypes necessary for production in new altered environments of the future. Re-sequencing is an important tool for the characterization of lines generated in the introgression of genes from crop wild relatives into the domesticated gene pool.

### *Totally New Crops*

Analysis of the food needs of human populations and available wild plants may identify new opportunities for totally new crop species. Most suitable plants found in agricultural societies and able to be consumed by conventional processing and food preparation technologies have probably already been domesticated. However, new regions and new technologies may reveal new possibilities. The domestication of distant relatives of rice as new food crops for production in cool climates is an example of this strategy (Shapter *et al*., 2013). In this case, the mutation of the shattering gene in a temperate grass may rapidly generate a potential new cereal crop for these environments.

## Climate Adaptation

Adapting agriculture to new and variable climates (Kole *et al*., 2015) will require a strong response in crops genetics (Abberton *et al*, 2016). Knowledge of the genome and variation in the genome in response to environmental selection in wild populations can be a critical guide to strategies for agricultural selection (Henry and Nevo, 2014). These analyses has emphasised the importance of adapting crops to the new array of pests and diseases found in new environments and that successful adaptation to higher temperatures may be largely associated with adaptation to new pathogens (Cronin *et al*., 2007; Fitzgerald *et al*., 2011).

## Future Prospects

### *Advances in Technology*

Advances in DNA sequencing technology will continue to accelerate the rate of application of genomics in crop improvement. Whole genome assembly had

been made simplified by recent advances in long read sequencing. Annotation of genomes and more complete characterization of transcriptomes has also been facilitated by these developments. Continued developments will be required to enable widespread whole genome analysis of plant genetic resources and association with phenotype to achieve routine use of whole genome sequence data in crop improvement. Advances in computing and bioinformatics will be necessary to fully realize this opportunity.

## International Collaboration

Coordinated efforts to capture and utilize genomic and other data on plant genetic resources are essential to ensure this technology is able to impact effectively crop performance and food security. The DIvseek (www.divseek.org) initiative is a program that aims to capture the progress in genomics and in phenomics to support global crop improvement for food security. These cooperative approaches will be essential to ensure optimal use of global plant genetic resources for agriculture and food production. Plant breeders need to be able to find within global genetic resources the alleles that they need to adapt their local varieties to the challenges of future environments.

## References

Abberton M, A Abbott, J Batley, A Bentley, M Blakeney, J Bryant, H Cai, J Cockram, A Costa de Oliveira, LJ Cseke, H Dempewolf, C De Pace, D Edwards, P Gepts, A Greenland, AE Hall, R Henry, K Hori, GT Howe, S Hughes, M Humphreys, AM Ismail, D Lightfoot, A Marshall, S Mayes, HT Nguyen, FC Ogbonnaya, R Ortiz, AH Paterson, PW Simon, J Tohme, R Tuberosa, B Valliyodan, R Varshney, SD Wullschleger and M Yano (2016) Global agricultural intensification during climate change: a role for genomics. *Plant Biotechnol. J*. **14:** 1095-1098.

Anacleto R, RP Cuevas, R Jimenez, C Llorente, E Nissila, R Henry and N Sreenivasulu (2015) Prospects of breeding high-quality rice in the post-genomic era. *Theor. Appl. Genetics* **128(8):** 1449-1466. doi:10.1007/s00122-015-2537-6

Brozynska M, ES Omar, A Furtado, D Crayn, B Simon, R Ishikawa and RJ Henry (2014) Chloroplast genome of novel rice germplasm identified in northern Australia. *Trop. Plant Biol*. **7:** 111-120.

Brozynska M, A Agnelo Furtado and RJ Henry (2016) Genomics of crop wild relatives: Expanding the genepool for crop improvement. *Plant Biotech. J.* **14:** 1070-1085.

Brozynska M, D Copetti, A Furtado, R Wing, D Crayn, G Fox, R Ishikawa and RJ Henry (2016) Sequencing of Australian wild rice genomes reveals ancestral relationships with domesticated rice. *Plant Biotech. J.* accepted 24/11/2016.

Cheng B, A Furtado, HE Smyth and RJ Henry (2016) Influence of genotype and environment on coffee quality. *Trends Food Sci. Technol.* doi: 10.1016/j.tifs.2016.09.003.

Copetti D, J Zhang, M El Baidouri, D Gao, J Wang, E Barghini, RM Cossu, A Angelova, CE Maldonado, S Roffler, H Ohyanagi, T Wicker, C Fan, A Zuccolo, M Chen, AC de Oliveira, B Han, RJ Henry, Y Hsing, N Kurata, W Wen Wang, SA Jackson, O Panaud and RA Wing (2015) *Oryza* Repeat Database: a resource for Genus-wide rice genomics and evolutionary biology. *BMC Genomics* **16:** 538.

Cronin, JK, PC Bundock, RJ Henry and E Nevo (2007) Adaptive Climatic molecular evolution in wild barley at the Isa Defense Locus. *Proc. Natl. Acad. Sci. USA* **104:** 2773-2778.

Denoeud F, L Paulet Carretero, A Dereeper, G Droc, R Guyot, M Pietrella, C Zheng, A Alberti, F Anthony, G Aprea, M J Aury, P Bento, M Bernard, S Bocs, C Campa, A Cenci, CM Combes, D Crouzillat, C Da Silva, L Daddiego, F De Bellis, S Dussert, O Garsmeur, T Gayraud, V Guignon, K Jahn, V Jamilloux, T Joët, K Labadie, T Lan, J Leclerc, M Lepelley, T Leroy, Li L-T, P Librado, L Lopez, A Muñoz, B Noel, A Pallavicini, G Perrotta, V Poncet, D Pot, Priyono, M Rigoreau, M Rouard, J Rozas, C Tranchant-Dubreuil, R VanBuren, Q Zhang, AC Andrade, X Argout, B Bertrand, A de Kochko, G Graziosi, RJ Henry, Jayarama, R Ming, C Nagai, S Rounsley, D Sankoff, G Giuliano, VA Albert, P Wincker and P Lashermes (2014) The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. *Science* **345:** 1181-1184.

Fitzgerald TL, FM Shapter, SMC Donald, DLE Waters, IH Chivers, A Drenth, E Nevo and RJ Henry (2011) Genome diversity in wild grasses under environmental stress. *Proc. Natl. Acad. Sci. USA* **108:** 21139-21144.

Furtado, A, P Bundock, P Banks, G Fox, X Yin and RJ Henry (2015) A novel highly differentially expressed gene in wheat endosperm associated with bread quality. *Sci. Rep.*5, 10446; doi: 10.1038/srep10446.

Healey A, DJ Lee, A Furtado, BA Simmons and RJ Henry (2015) Efficient eucalypt cell wall deconstruction and conversion for sustainable lignocellulosic biofuels. *Frontiers Bioeng. Biotechnol.* **3:** 190.

Henry RJ (2014) Genomics strategies for germplasm characterization and the development of climate resilient crops. *Front. Plant. Sci.* doi: 10.3389/fpls.2014.00068

Henry RJ and Nevo E (2014) Exploring natural selection to guide breeding for agriculture. *Plant Biotechnol. J.* **12:** 655-662.

Henry RJ, P Rangan and A Furtado (2016) Functional cereals for production in new and variable climates. *Curr. Opin. Plant Biol.* **30:** 11–18.

Hoang NV, A Furtado, FC Botha, BA Simmons and RJ Henry (2015) Potential for genetic improvement of sugarcane as a source of biomass for bioenergy. *Frontiers Bioeng. Biotechnol.* **3:** 182.

Hoang NV, A Furtado, PJ Mason, A Marquardt, L Kasirajan, PP Thirugnanasambandam, FC Botha and RJ Henry (2016) A survey of the complex transcriptome from the highly

polyploid sugarcane genome using PacBio full-length isoform sequencing compared with *de novo* assembly from Illumina RNA sequencing. *BMC Genomics* accepted 5/12/16.

Kole C, M Muthamilarasan, R Henry, D Edwards, R Sharma, M Abberton, J Batley, A Bentley, M Blakeney, J Bryant, H Cai, M Cakir, LJ Cseke, J Cockram, AC Oliveira, CD Pace, H Dempewolf, S Ellison, P Gepts, A Greenland, A Hall, K Hori, GT Howe, S Hughes, MW Humphreys, M Iorizzo, AM Ismail, A Marshall, S Mayes, HT Nguyen, FC Ogbonnaya, R Ortiz, AH Paterson, PW Simon, J Tohme, R Tuberosa, B Valliyodan, RK Varshney, SD Wullschleger, M Yano and M Prasad (2015) Application of genomics-assisted breeding for generation of climate resilient crops: Progress and prospects. *Front. Plant Sci.* 6: 563. doi:10.3389/fpls.2015.00563.

Krishnan SG, DLE Waters, SK Katiyar, AR Sadananda, V Satyadev and R Henry (2012) Genome-wide DNA polymorphisms in elite indica rice inbreds discovered by whole-genome sequencing. *Plant Biotechnol. J.* **10:** 623-634.

Nock CJ, Baten A, Barkla BJ, Furtado A, Henry RJ and King G (2016) Genome and transcriptome sequencing characterises the gene space of *Macadamia integrifolia* (Proteaceae) *BMC Genomics* **17:** 937.

Nirmal RC, A Furtado, C Wrigley and RJ Henry (2016) Influence of gene expression on hardness in wheat. *PloS One* 11(10): e0164746. doi:10.1371/journal.pone.0164746.

Rangan P, A Furtado, and RJ Henry (2016) New evidence for grain specific C4 photosynthesis in wheat. *Sci. Rep.* 6, 31721; doi:10.1038/srep31721.

Rossetto M and RJ Henry (2014) Escape from the laboratory: new horizons for plant genetics. *Trends Plant Sci.* **19:** 554-555.

Shapter FM, M Cross, G Ablett, S Malory, IH Chivers, GJ King and RJ Henry (2013) High-throughput sequencing and mutagenesis to accelerate the domestication of *Microlaena stipoides* as a new food crop. *PloS one* 8(12) e82641. doi:10.1371/journal.pone.0082641.

Souza GM, H Berges, S Bocs, R Casu, AD Hont, JE Ferreira, R Henry, R Ming, B Potier, MA Van Sluys, M Vincentz and AH Paterson (2011) The sugarcane genome challenges: Strategies for sequencing a highly complex genome. *Trop. Plant Biol.* **4:** 145-156.

Tran H, SL Lee, H Smyth, A Furtado and RJ Henry (2016) Advances in genomics for the improvement of quality in Coffee. *J. Sci. Food Agr.* **96:** 3310-3312.

Wambugu PW, M Brozynska, A Furtado, DL Waters and RJ Henry (2015) Relationships of wild and domesticated rice species based on whole chloroplast genome sequences. *Sci. Rep.* **5:** 13957 doi: 10.1038/srep13957.

Wang K, PW Wambugu, B Zhang, AC Wu, RJ Henry and RG Gilbert (2015) The biosynthesis, structure and gelatinization properties of starches from wild and cultivated African rice species (*Oryza barthii* and *Oryza glaberrima*). *Carbohydrate Polymers* **129:** 92-100. doi:10.1016/j.carbpol.2015.04.035.

Waters D, GS Krishnan, E Mani, S Singh, S Vaddadi, R Henry and A Baten (2015) Genome wide polymorphisms and yield heterosis in rice (*Oryza sativa* subsp. *indica*) *Trop. Plant Biol.* **8:** 117-125.

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# Implementing the Biological Diversity Act in India: Focus on ABS and Agro-biodiversity

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Conservation and sustainable use of biodiversity are age old traditions in India, as reflected in our ancient scriptures and the use of numerous indigenous plants in religious rituals, ceremonial offerings and local healthcare practices. The Biological Diversity Act, 2002 (BDA) provides an umbrella legal framework to affirm our commitments for this purpose. In addition, India is recognized as a mega-diverse country, in view of its spectacular biological diversity adapted to a wide range of environments available in its ten distinct eco-geographic zones. Equally significant is the fact that it has generously shared its biological resources in the past with other countries as reflected in the records of collections maintained in national genebanks of USA, Russia and Japan among others and also the international gene banks developed by the International Agricultural Research Centres under the CGIAR System.

## Meeting National Obligations under International ABS Agreements

Legally binding international treaties, multilateral agreements and global conventions often function as international laws impacting upon policy and legal framework in countries that have ratified them. India was among the lead nations who joined and adhered to the voluntary International Undertaking on Plant Genetic Resources (PGR) established in 1983, facilitated by the FAO Commission on PGR and based on the principle that PGRs were the common heritage of mankind. This era was followed by aggressive seeking of intellectual property rights (IPR) over the products of research on genetic resources by the users of PGR in developed countries, appropriating all the resulting benefits to themselves and depriving the providers (owners) of those bioresources in developing countries. The legally binding Convention on Biological Diversity (CBD), adopted in June 1992, seeks to balance the rights of providers of genetic resources and their users (including the breeders and other researchers). More recently, the Nagoya Protocol on access to genetic resources and benefit sharing (ABS), adopted in 2010, has further consolidated this global legal framework.

### *The 1992 Convention on Biological Diversity (CBD): The Turning Point*

The CBD is the first commitment of humankind towards conservation of biological diversity, sustainable use of its components and promoting fair and equitable sharing of benefits arising from their utilization. It marked the end of the 'common heritage' concept of genetic resources by recognizing sovereign rights of States over their natural resources within their boundaries and accepting that the authority to determine access to genetic resources rests with the national governments subject to national legislation. This Treaty is nearly universal with 196 Contracting Parties, the United States being the only major country that has not yet ratified it.

Implementing CBD gained momentum soon after its entry into force in December 1993 as several nations passed legislation to claim sovereign rights over their bioresources and to implement CBD's provisions. For example, the Philippines established a system for access to biological resources by an executive order issued in 1995 and the Andean Community, in its Decision No. 391 taken in 1996, adopted a Common Regime on Access to Genetic Resources. India enacted the Biological Diversity Act in 2002 and framed Rules in 2004 for implementing it, with the Union Ministry of Environment, Forests & Climate Change as the nodal ministry.

### *The Trade Related Intellectual Property Rights, 1995, WTO*

The TRIPS Agreement under WTO, which entered into force on 1 January 1995, is to date the most comprehensive multilateral agreement on IPRs. This treaty requires Member States to make patents available for any invention, whether product or process, in all fields of technology without discrimination, subject to the normal tests of novelty, inventiveness and industrial

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applicability. It has been provided further that the Members may exclude plants and animals (other than micro-organisms) and essential biological processes for the production of plants or animals (other than non-biological and microbiological processes). However, any country excluding plant varieties from patent protection must provide for an effective *sui generis* system of their protection. India has amended its Patents Act, 1970 to permit patenting of products (and also of micro-organisms) and also enacted the Protection of Plant Varieties and Farmers' Rights Act, 2001 to meet its national obligations. Union Ministry of Commerce & Industry is the nodal ministry for implementing this Treaty.

### *The International Treaty on Plant Genetic Resources for Food and Agriculture*

Recognizing the interdependence of countries for crop genetic resources, the FAO revised the text of its 1983 IU on PGR to bring its provisions in harmony with those of CBD and then adopted it on 3 November, 2001 as the legally binding International Treaty. This Treaty presently covers designated accessions of 64 Annex-1 food and forage crops (which are in public domain and managed by the national governments) and upholds the Farmers' Rights subject to national legislation.

Unlike the bilateral system of agreements under CBD for accessing PGRs, this Treaty provides for a Multilateral System (MLS) of ABS to facilitate exchange of PGRs which are in public domain, covering initially only 35 food crops and 29 genera of forages. Union Ministry of Agriculture & Farmers Welfare is the nodal Ministry for implementing the ITPGRFA, assisted by the DARE and NBPGR. A notification has been issued exempting the exchange of designated accessions of genetic resources of crops listed in Annex-1 of the ITPGRFA from the provisions of Sections 3 and 4 of the BD Act for research, breeding and training purposes.

### *The Nagoya Protocol to CBD on ABS, 2010*

The Nagoya Protocol to CBD, the new legally binding international treaty specific to ABS, elaborates implementation of benefit sharing provisions under the Convention's Article 15 and sets out core obligations for its contracting Parties to take appropriate measures related to access to genetic resources, benefit sharing and compliance. The provider Parties need to create legal certainty, clarity and transparency for access to genetic resources; provide fair and non-arbitrary rules and procedures for such access; establish clear procedures for prior informed consent and mutually agreed terms; and provide for issuance of an internationally acceptable certificate when access is granted. The user Parties are also required to ensure that their researchers and other users of genetic resources must comply with the national legislation of provider countries by monitoring through the ABS-Clearing House mechanism operated by the CBD Secretariat.

The National Biodiversity Authority (NBA) has been designated as the National Competent Authority for implementing this Protocol and the format for the Internationally Recognized Certificate of Compliance has also been approved. A Core Expert Group has also been constituted to designate the Check Points and notify the user and provider country measures.

### National Legislation in India for Implementing the International Treaties on ABS

Under the CBD, the Sovereign Authority to determine access to genetic resources rests with the national governments and it is subject to their national legislation. The Biological Diversity Act, 2002, was enacted in India to fulfill this requirement. It also provided suitable linkage to the provision for patenting of products and processes/technologies, based on the use of bio-resources and associated traditional knowledge (TK), under Section 10 (4) of the Patents (Amendment) Act, 2002. In addition to promoting conservation and sustainable use of all categories of bio-resources, this umbrella legislation regulates access to them while determining mode/ quantum of fair and equitable benefit sharing, and signing agreements with the users based on mutually agreed terms. For major achievements in implementing the national obligations under the CBD, please see Box 1.

This Act has adopted a common but differentiated approach [Sections 3 and 19], as adopted by the CBD principle on responsibilities of the developing and developed countries, under which the following categories of persons/body corporate/associations/ organizations are required to obtain prior approval of NBA for seeking access to India's bio-resources (and associated TK) for research and commercial use or engaging in bio-survey and bio-utilization activities:

"A person who is not a citizen of India; a citizen of India, who is non-resident; a body corporate, association or organization – not incorporated or registered in

**Box 1. Implementing national obligations under CBD in India: Major Achievements at a Glance**

1. Enacted the Biological Diversity Act, 2002 and the Rules, 2004
2. NBA established in 2003 and SBBs constituted in all the 29 States at present.
3. BMCs formed in nearly 4,000 local bodies across 17 States.
4. Guidelines for preparing People's Biodiversity Registers updated in 2013 and 2485 PBRs prepared by BMCs across 17 States. NBA has been providing financial support towards setting up of BMCs and also for preparation of PBRs.
5. Biodiversity Rules and Regulations on ABS notified by 17 States.
6. Sixteen SBBs have been supported for ABS activities under 4 externally funded projects.
7. Notified Guidelines on International Collaborative Research Projects, 2006.
8. Notified Guidelines for the identification of Biodiversity Heritage Sites and **seven** BHS sites have been notified in three States u/s 37.
9. Threatened species have been notified in 16 States and 2 Union Territories u/s 38.
10. Notified Exemption for 385 Normally Traded Commodities u/s 40, 2014.
11. Notified Guidelines on Access and Benefit Sharing Regulations, Nov 2014.
12. Notified Exemption of ITPGRFA, Annex-1 Crops, Dec 2014.
13. Fifteen institutions have been notified as the national designated repositories u/s 39 and Guidelines on their mandates and safekeeping of deposited specimens/samples issued in March, 2016.
14. ABS Awareness and Sensitization Workshops conducted in 6 States.
15. Two media workshops attempting increased awareness conducted.
16. Number of IRCCs submitted to ABS-CH: 25 out of the total of 27 so far.
17. Winners and Runners-up of India Biodiversity Awards 2016 (including the new category on Good Practices for ABS Mechanisms) honoured on the International Day for Biodiversity 2016, organized in Mumbai on 22 May.
18. Number of complete Applications received for Forms I to IV: 1218.
19. Number of applications approved: 865.
20. Number of Benefit Sharing Agreements signed: 270.
21. Amount of monetary benefit sharing received by NBA: Rs. 34.26 Crores.
22. Amount of monetary benefit sharing received by SBBs: Over Rs. 4 Crores.

Source: NBA Secretariat, Chennai.

India; or incorporated or registered in India but has any non-Indian participation in its share capital or management".

All users are also required to seek prior approval of NBA for transferring results of research on bioresources to users of the above defined category, for applying for IPR over products of research on bioresources and also for third party transfer of the already accessed bioresources, by submitting applications in specified formats and after payment of prescribed fee for each of the above mentioned purposes [See Box 2].

Access of Indian citizens to bio-resources for research is not restricted. However, Section 7 under the Act states that no person, who is a citizen of India or a body corporate, association or organization which is registered in India, shall obtain any biological resource for commercial utilization, or bio-survey and bio-utilization for commercial use except after giving prior intimation

**Box 2. Activities covered under the BD Act and the authorities for granting approval**

| Purpose for use of bio- resources and/or traditional knowledge associated thereto | Application Form to be used | Authority for granting approvals | | |
|---|---|---|---|---|
| | | For Indian Citizens/ For Persons/ entities | Entities defined u/c 3(2) | |
| 1. a) Research | | No approval | NBA | |
| b) Bio-survey & Bio-utilization | Form I | required | NBA | |
| c) Commercial Utilization | Prescribed Fee: | No approval | | |
| **Special Forms: 1A, 1B, 1C** | Rs.10,000/- | required | NBA | |
| | No Fee | | | |
| 2. Transfer of Results of Research on Bio-resources to entities defined u/s 3(2) | Form II | SBB | | |
| | Fee: | NBA | NBA | |
| | Rs. 5,000/- | NBA | | |
| 3. Seeking Intellectual Property Rights | Form III Fee:Rs.500/- | NBA | NBA | |
| 4. Transfer of the already accessed bio-resource to entities defined u/s 3(2) | Form IV Fee: Rs.10,000/- | Not relevant | NBA | |

Source: www.nbaindia.org

to the concerned State Biodiversity Board (SBB) with the expectation that a BS Agreement may have to be signed.

### *Implementing Mechanism for the Biological Diversity Act*

A 3-tier system for implementing the BD Act has been established comprising the National Biodiversity Authority (NBA) at the national level (established by the central government), State Biodiversity Boards (SBB) at the state level (constituted by the state governments) and Biodiversity Management Committees (BMC) at the local level (constituted by the local bodies). Their roles are well defined under the Act. The Act is being implemented by NBA in partnership with SBBS and BMCs.

Established by the Central Government on 1st October, 2003, the NBA comprises the Chairperson, 10 ex-officio members representing union ministries/ departments and 5 experts nominated by the Central Government. NBA, which is essentially an inter-ministerial body assisted by five technical experts, has held 38 meetings till 4 July, 2016. SBBs have also been constituted in all the 29 States and over 4,000 BMCs have also been formed across 17 States.

Funds and grants accruing to these three partners in implementing the Act are operated under the National, State and Local Biodiversity Funds. The mechanism for passing on the monetary benefits from the National and State Biodiversity Funds to BMCs and benefit claimers where identified, as provided under the Regulations on ABS guidelines, is shown in Box 3.

NBA has constituted several Expert Committees and Core Expert Groups from time to time to provide recommendations on specific issues. Eight such ECs and CEGs are functioning at present involving a pool of 174 experts drawn from different specializations across the country.

EC on Agro-biodiversity has played a lead role in implementing the national obligations under the ITPGRFA and exempting designated accessions of Annex-1crops from provisions of Sections 3 & 4 of the BD Act. Its recommendations on facilitating the mandate of IARCs and some other important issues are under consideration by the Authority for follow up actions.

### *Restrictions Imposed on Granting Access to Bioresources*

Certain restrictions have been imposed under Rule 16 on NBA's, and also SBBs', approvals for access to bio-resources, requiring to take necessary steps to restrict or prohibit access when the request relates to any endangered taxon or endemic and rare species or it may result in adverse effect on the livelihoods of the local people or adverse environmental impact which may be difficult to control and mitigate, may cause genetic erosion or adversely affect ecosystem functioning or when the use of resources is for purposes contrary to national interest and other related international agreements entered into by India.

### *Exemptions Provided under the BD Act*

The following exemptions have been provided under this Act to promote bona fide use of bioresources for research and non-commercial use:

- Indian citizens/entities accessing bio-resources for research/ bio-survey and bio-utilization for research in India.
- Provisions of Section 3 (access to bio-resource) and Section 4 (transfer of research results), read

**Box 3. Mechanism of passing on the accrued monetary benefits by NBA/ SBBs to BMCs or the benefit claimers where identified**

**A. When approvals are granted:**
1. 5.0 % of the total amount goes to the NBA, of which 2.5% is retained by NBA and 2.5% is passed on to the concerned SBB as administrative charges.
2. 95.0 % of the amount is passed on to the concerned BMCs and / or benefit claimers where identified.

**B. When approvals are granted by SBBs**
1. 5.0 % of the total amount is retained by the SBB as administrative charges.
2. The rest 95.0 % of the amount is passed on to the concerned BMCs and/ or benefit claimers where identified.

**C. Utilization of funds**
1. For supporting conservation and sustainable use biological resources and development of areas from where such biological resources or knowledge associated thereto have been accessed;
2. For promoting socio economic development of areas from where the biological resources and knowledge are accessed, in consultation with the local bodies concerned.

Source: Guidelines on ABS Regulations, 2014.

with Section 19, shall not apply to international collaborative research projects, conforming to the guidelines issued by the Central Government on 8 November, 2006.

- Provisions of Section 6 shall not apply to any person making an application for any right under the Protection of Plant Varieties and Farmers' Rights Act, 2001.
- Accessing bioresources for conventional breeding or traditional practice in use in any agriculture, horticulture, poultry, dairy farming, animal husbandry, bee keeping, etc. in India is exempted from provisions of this Act. However, "End Uses" of biological resources for "Commercial Utilization" (such as drugs, industrial enzymes, food flavours, fragrance, cosmetics, emulsifiers, oleoresins, colours, extracts and genes used for improving crops and livestock through genetic interventions are not exempted.
- 'Value added products', which may contain portions or extracts of plants and animals in unrecognizable and physically inseparable form are exempted for trade.
- Provisions of prior intimation to SBB for commercial use shall not apply to local people and communities including village healers/*vaids*, farmers and other traditional growers.
- Items such as normally traded commodities, notified by the Central Government u/s 40, would be exempt so long as these are traded as commodities.
- Exchange of designated accessions of genetic resources of crops listed in Annex-1 of the ITPGRFA has been exempted from provisions of Sections 3 and 4 of the BD Act.

### *Notification on Guidelines on Access and Benefit Sharing*

Notification on ABS Guidelines Regulations under the Biological Diversity Act was issued on 21 November, 2014. These Guidelines provide for legal certainty, clarity and transparency, simplified procedure for the Indian researchers/Govt. institutes to carry out basic research outside India, options for benefit sharing for different users, graded benefit sharing system, supply chain system from source to the manufacturer, upfront payment on high economic valued bioresources (like Red sanders and Sandalwood), apportioning of the accrued benefits to the BMCs/benefit claimers and options for sharing benefits in monetary or non-monetary mode. For the module on terms for BS, please see Box 4.

### *Facilitating Non-commercial Research on Bioresources by Indian Researchers/Government Institutions in Other Countries*

- Through the Guidelines on ABS Regulations, NBA has introduced a special Form A for the supply chain stockists, traders and manufacturers accessing bioresources from BMCs and Form B for the Indian researches/scientists/institutes to carry/send samples of bioresources outside India for conducting research including taxonomic studies. Government institutes can also send bioresources outside the country to carry out research work abroad in face of emergencies like epidemics, natural disasters, etc.
- Another special Form C has also been introduced for deposition of microbial type cultures in any

**Box 4. Module showing benefit sharing in monetary mode under the Guidelines on ABS**

1. Commercial Utilization

| Annual gross ex-factory sale of product | Benefit sharing component |
|---|---|
| Up to Rupees 1,00,00,000 | 0.1 % |
| Rupees 1,00,00,001 up to 3,00,00,000 | 0.2 % |
| Above Rupees 3,00,00,000 | 0.5 % |

2. Transfer of Results of Research on Bio-resources — 3.0 to 5.0% of the monetary consideration received

3. Intellectual Property Rights

| | |
|---|---|
| • If applicant himself commercialize the process/product/innovation | • 0.2 – 1.0% of Annual Ex-factory gross sale (minus govt. taxes) |
| • If applicant assigns / licenses the process /product / innovation to a third party for commercialization | • 3.0 – 5.0 % of the fee received in any form. And 2.0 – 5.0 % of Royalty |

4. Third Party Transfer by u/s 3(2) received from the transferee — 2.0 to 5.0% of any amount and /or royalty Persons/Entities

Source: Guidelines on ABS Regulations, 2014.

Internationally Recognized Repository for the purpose of research publications.

- Submission of these special Forms does not require payment of any fee and such requests are usually cleared within two weeks.

**Experiences Gained from Implementing the BD Act and the Way Forward**

Following a great effort by the drafting committee, chaired by the renowned scientist Dr. M.S. Swaminathan, the process of enacting the BD Act took several years of intense consultations among different government agencies, including the Parliamentary Standing Committee, and other stakeholders to evolve in its final form in 2002, vetted by the Law Commission. Section 3, adopting the CBD principle of common but differentiated responsibilities, was included for access to GRs by the Indian citizens/entities and foreigners in view of the prevailing strong apprehensions regarding what was termed '*biopiracy*' to indicate unauthorized access (mostly relating to pharmaceuticals and industrial applications) by some users without any commitment of sharing the benefits generated from the utilization of India's bioresources and associated traditional knowledge. Some differing views notwithstanding, it is indeed a tribute to the Drafting Committee (and others who contributed to this process) that the text of this Act has stood the test of time when we compare Indian experience with those of some other countries like the Philippines, Brazil, South Africa and the Andean Community. In addition, this Act also served as the umbrella legal framework for implementing the ITPGRFA and also the Nagoya Protocol on ABS in India. Specific Guidelines on ABS Regulations, notified under this Act in November 2014, have been widely welcomed as they impose low benefit sharing terms along the supply chain while offering a slab-system and sectoral approach for benefit sharing.

Some reservations had been expressed by some government departments, and also some other major user sectors about the interpretation of some of the Act's provisions but sustained dialogues with them (including ICAR, CSIR, DBT, PPV&FRA and the Indian Patent Office) helped the NBA in resolving the difficulties. NBA gained immensely from these meaningful dialogues at the highest level and succeeded in developing strong partnerships. Similar consultation process is presently in progress with several other sectors like seed industry and pharmaceuticals. Partnership with SBBs has also been remarkably strengthened in recent years, sparked by implementation of several externally funded projects by NBA, involving more than fifteen SBBs at present. Strong competition witnessed among the contestants for India Biodiversity Awards 2016 in the category of 'Good Practices for ABS' has brought out the supportive role played by several SBBs towards capacity building of BMCs in this context.

To sum up, the BD Act stipulates norms for access to bioresources and associated TK in two broad categories. While foreign access is subject to prior approval of NBA, domestic access is based on prior intimation (approval) from the concerned SBB. Recent experience reveals that bulk users of bioresources are now better motivated to enter into ABS agreements with the concerned SBBs as compared to those who access the required bioresources only once and work afterwards with their cultures grown in laboratories. This increasing acceptability of the ABS Guidelines notwithstanding, incorporating biodiversity concerns within the natural capital framework and mainstreaming biodiversity in achieving global goals still remain major challenges for the policy makers and planners in public as well as private sectors. It needs to be appreciated, however, that 'biodiversity conservation with sustainable use' and 'inclusive sustainable development' are increasingly recognized to be mutually supportive. This is strongly reflected in the Natural Capital Protocol, launched in London in July 2016 by representatives from over 160 organisations, suggesting the way that businesses may evaluate their operations. In this context, NBA has adopted a positive approach in implementing the BD Act and remains open to suggestions/feedback from all the stake holders.

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# Genetic Resources of Pearl Millet: Status and Utilization

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Pearl millet is a very important crop of arid and semi-arid regions in Asia and Africa where it is the basis of food security of millions of people inhabiting in harsh and environmentally fragile ecosystem. Genetic resources of pearl millet including landraces, improved elite material, traditional cultivars, genetic stocks and wild relatives are very rich and, therefore, their characterization, documentation, conservation and distribution is very essential to ensure utilization in breeding programmes. This review assesses the status of pearl millet genetic resources, and identifies the gaps in their collection, conservation and utilization. A total of 56,580 accessions (including possible duplicates) of pearl millet in 70 genebanks of 46 countries across world are available. Landraces represent the largest part of pearl millet germplasm, followed by breeding/research material and wild relatives. The Indian national collection includes 7,059 accessions at the National Bureau of Plant Genetic Resources (NBPGR), New Delhi. Global collections managed by ICRISAT comprise of 22,888 pearl millet accessions from 51 countries. However, only a very small fraction of these accessions has been utilized so far. Critical assessment of collection for geographical and trait-diversity gaps using various GIS tools revealed several gaps in germplasm collection from Asian and African continents. Almost all cultivated accessions have been characterized for 23 morpho-agronomic characters following prescribed pearl millet descriptors. A large variation exists for phenotypic and phenological traits among available germplasm. In general, Indian pearl millet landraces have mainly contributed for earliness, high tillering, high harvest index and local adaptation; whereas African material has been a good source of bigger panicles, large seed size, and disease resistance. Systematic evaluation and screening of germplasm has led to the identification of specific sources of better grain quality, resistance to diseases and tolerance to abiotic stresses like drought and heat. These germplasm sources continue to play a critical role in crop improvement programmes across the world. Formation of trait-specific gene pools, core and minicore collections are likely to enhance the utilization of genetic resources to a greater degree. Strategies for further enriching the germplasm and increasing its use are discussed.

**Key Words: Diversity, Genetic resources, Germplasm, Pearl millet**

## Introduction

Pearl millet [*Pennisetum glaucum* (L.) R. Br.], a diploid species (2n=14) and member of Poaceae family, is world's 6$^{th}$ most important food crop after wheat, rice, maize, barley and sorghum. It is grown over 30 million ha mostly in Sub-Saharan Africa and Southern Asia with a production of ~31-32 m tons (Yadav and Rai, 2013). Pearl millet is mainly cultivated in India and Pakistan in Asia; Niger, Nigeria, Burkina Faso, Sudan, Mali and Senegal in Africa; in South-Eastern USA and Australia.

Pearl millet is an important crop because of its ability to grow in severely water-limited environments and on less fertile soils with minimum inputs and thus forms the basis of food security of millions of people in the world's most harsh and fragile arid- and semi-arid regions. In addition, stover of pearl millet forms the major ration for bovines during dry and lean periods in crop-livestock production system in South Asia. Further, pearl millet is also valued as green forage in South-Eastern America, Australia, and Brazil. Pearl millet is nutritionally rich crop with high iron and zinc contents (Rai *et al*., 1997) and good calcium and lipids (Klopfenstein and Hoseney, 1995) in its grain.

Genetic variability is a bed-rock on which success of crop improvement programmes depends. Plant genetic resources are a heritage and have to be conserved for their use in future in order to achieve sustainable development and to meet challenges in achieving food security requirements. Therefore, collection, conservation, characterization, evaluation, documentation, , distribution and utilization of plant genetic resources is very essential to ensure that breeders have access to genetic resources which could be useful in breeding programmes. A large

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number of germplasm accessions are conserved at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India (Upadhyaya *et al*., 2012a,b) and at Niamey, Niger (Hay *et al*., 2013). Additionally, the ICAR-National Bureau of Plant Genetic Resources (NPBGR), New Delhi, India, has a large collection of exotic and indigenous material (Radhamani *et al*., 2011). These include wild relatives, improved elite material and genetic stocks that are potential sources of specific phenotypic traits, resistance to diseases and insect-pests; and tolerance to various abiotic stresses like drought and high temperature.

Genetic resources of pearl millet are more vulnerable to genetic erosion given that hybrids are the most dominant form of commercial cultivars. Therefore, conservation of immensely valuable material is imperative in form of trait-specific gene pools, core/ mini-core collections and composites that facilitate better utilization of germplasm (Appa Rao *et al*., 1998, Singh and Jika, 1988, Upadhyaya *et al*., 2011). Some of them have been strategically utilized. The purpose of this review is to assess status of collection, conservation and utilization of germplasm in pearl millet improvement and to identify the gaps in the collection and its utilization. Attempt has also been made to further explore the possibility of enhanced use of germplasm in future breeding programmes.

## Status of Pearl Millet Genetic Resources

### *Conservation*

*Global Collections:* The global germplasm collections include 7.4 million accessions of various crops conserved in more than 1,750 genebanks including 56,580 accessions of pearl millet in 70 genebanks of 46 countries (FAO, 2010). Landraces represent 88% of pearl millet germplasm conserved in genebanks worldwide. About 3.2% are wild relatives, 0.8% are improved varieties, 6% are breeding/research materials and 2% are of unknown description (Mathur, 2012). In addition to the largest collection of pearl millet germplasm at ICRISAT genebank (22,288), other collections are 3,968 accessions at the Institute of Research for Development (IRD, France) from 16 countries, 3,821 accessions at the Canadian Genetic Resources Programme, Saskatoon, Canada including 3,390 accessions of cultivated pearl millet and *P. violaceum* (221), *P. macrourum* (1), *P. purpureum* (12), *P. orientale* (1), *P. pedicellatum* (11), *P. polystachion* (8), *P. ramosum* (3), *P. unisetum* (1) and other species (14) (Mathur, 2012). All collections from central African countries, were obtained through agreement with Bioversity International and Canada to conserve as duplicate collection (with the original at ORSTOM – IDR, France). The Agricultural Research Station of the USDA Griffin, Georgia is maintaining 1,314 accessions (Mathur, 2012).

The Indian national collection includes 7,268 accessions of pearl millet conserved at the NBPGR, New Delhi. Pakistan reported to have 193 accessions of pearl millet collections. Among African countries the collections have been reported from genebanks based in Algeria, Benin, Botswana, Burkina Faso, Burundi, Cameroon, Central African Republic, Chad, Eritrea, Ethiopia, Ghana, Kenya, Lebanon, Malawi, Mali, Mauritania, Mozambique, Namibia, Niger, Nigeria, Senegal, Sierra Leone, Sudan, DR Congo, Uganda, Zambia and Zimbabwe (Mathur, 2012). Some other countries reported to conserve pearl millet collections are Australia (253), Brazil (52), China (102), Germany (54), Russian Federation (406) and Lebanon (110). Most of the collections with Bioversity International supported mission have now become part of the global collection maintained at ICRISAT, USDA-ARS and ILRI. Not much information is available for any of the other national collections. The number of unique accessions is lower than the total number of accessions recorded as many of them are duplicates (Mathur, 2012)

*Collections at ICRISAT:* The ICRISAT has made concerted efforts to assemble pearl millet germplasm by introducing the germplasm that was already collected and conserved at different national and international institutes, universities, National Agricultural Research Systems (NARS) and by launching germplasm collection missions. The major donors include: Institute Français de Recherche Scientifique pour le Développement en Coopération (ORSTOM) (2,178), Rockefeller Foundation, New Delhi, India (2,022) and (the then) International Board for Plant Genetic Resources (IBPGR-now Bioversity International), Rome, Italy (974). ICRISAT had launched 76 collecting missions exclusively for pearl millet germplasm in 28 countries and collected 10,830 pearl millet accessions. As of now, the global collections managed by ICRISAT, Patancheru, India, comprises a total of 22,888 pearl millet accessions including 19,696 landraces, 129 improved cultivars and 2,269 breeding/ research materials and 794 wild accessions from 50 countries (Table 1).

At ICRISAT genebank, about 400 g seeds each of all accessions are conserved in medium-term store maintained at 4ºC and about 30% RH (active collection) (Upadhyaya and Gowda, 2009). About 75 g each of 17,670 accessions are conserved on long-term store basis, vacuum packed in aluminum foils, which is maintained at –20ºC (base collection). Species that do not produce seed (*e.g. P. purpureum, P. macrourum, P. lanatum, P. squamulatum*) are maintained as live plants. Limited quantity of seeds of almost all accessions is available free of cost under Standard Material Transfer Agreement (SMTA) (Upadhyaya and Gowda, 2009) for research and training purposes.

*Collections at NBPGR:* Total number of pearl millet accessions at National Genebank at NBPGR is 7,268 including indigenous collection, exotic collection, released varieties and genetic stocks. Indigenous collections are in the form of landraces, farmers' varieties and wild type from 18 states and majority of them have been made from Rajasthan (603), Andhra Pradesh (265), Gujarat (215) and Uttar Pradesh (126). A large number of accessions are also conserved with no or minimum passport data (Table 2). Exotic collections (761) are also conserved in the National Genebank at NBPGR (Fig. 1). Many collections were obtained from ICRISAT and therefore, some duplication of accessions is inevitable.

*Safety Backup of Collections:* A part of pearl millet collection is also conserved at ICRISAT regional genebank, Niamey, Niger. ICRISAT has already deposited samples of over 20,654 accessions of pearl millet germplasm as safety backup at Svalbard Global Seed Vault (SGSV), Norway.

At ICRISAT and NBPGR, pearl millet accessions are maintained in medium-term store as active collections. Accessions are regenerated when the seed viability and or the seed quantity in active collection is below the critical level (<85% viability and/or <1/4 of total quantity) (Upadhyaya and Gowda, 2009). Seed viability of active collection is tested at five years interval and that of base collection at 10 years interval. Being the cross-pollinating crop, regeneration of pearl millet germplasm accessions is expensive and involves the risk of loss of accession integrity due to foreign pollen, mechanical mixtures, genetic drifts, genetic shifts and mutations. Therefore, during regeneration, the genetic integrity is maintained by cluster bagging method of pollination control for landraces, selfing for genetic stocks and sibbing for

**Table 1. Geographical distribution of pearl millet germplasm assembled at ICRISAT genebank, Patancheru, India**

| Country | Breeding material + advanced cultivars* | Landraces | Wild | Total |
|---|---|---|---|---|
| Algeria | | 5 | | 5 |
| Australia | 8 | | | 8 |
| Benin | | 46 | | 46 |
| Botswana | | 82 | | 82 |
| Brazil | 2 | | | 2 |
| Burkina Faso | 1 | 859 | 7 | 867 |
| C. African Rep. | | 142 | 10 | 152 |
| Cameroon | 2 | 909 | 85 | 996 |
| Cape Verde | 2 | | | 2 |
| Chad | 4 | 93 | 37 | 134 |
| Congo | 8 | | | 8 |
| Ethiopia | | 2 | 1 | 3 |
| France | 11 | | | 11 |
| Gambia | | 15 | | 15 |
| Germany | 3 | | | 3 |
| Ghana | 5 | 420 | | 425 |
| Great Britain | 31 | | 1 | 32 |
| India (ICRISAT) | 1,314 (53) | | 3 | 1,370 |
| India (NBPGR) | 403 (1) | 6,064 | 142 | 6,610 |
| Kenya | | 98 | 1 | 99 |
| Korea | | 1 | | 1 |
| Lebanon | 108 | | | 108 |
| Lesotho | | | 4 | 4 |
| Malawi | 2 | 296 | 12 | 310 |
| Maldives | | 1 | | 1 |
| Mali | 8 | 1,084 | 109 | 1,201 |
| Mauritania | 1 | 5 | 31 | 37 |
| Mexico | 10 | | 1 | 11 |
| Morocco | | 4 | | 4 |
| Mozambique | | 31 | 2 | 33 |
| Myanmar | | 10 | | 10 |
| Namibia | | 1,118 | 10 | 1,128 |
| Niger | 57 (75) | 1,617 | 176 | 1,925 |
| Nigeria | 35 | 2,030 | 9 | 2,074 |
| Pakistan | 10 | 158 | 2 | 170 |
| Russia and CISs | 12 | 3 | | 15 |
| Sierra Leone | | 59 | 1 | 60 |
| Somalia | | 4 | | 4 |
| South Africa | 10 | 152 | 3 | 165 |
| Sri Lanka | | | 2 | 2 |
| Sudan | | 1,014 | 27 | 1,041 |
| Tanzania | | 478 | 47 | 525 |
| Togo | | 520 | | 520 |
| Tunisia | | 6 | | 6 |
| Turkey | | 2 | | 2 |
| Uganda | 26 | 112 | 23 | 161 |
| USA | 177 | 42 | 10 | 229 |
| Yemen | | 290 | 3 | 293 |
| Zaire | | 11 | 3 | 14 |
| Zambia | | 155 | 7 | 162 |
| Zimbabwe | 2 | 1,382 | 13 | 1,397 |
| Total | 2,269 (129) | 19,696 | 794 | 22,888 |

*Figures in parentheses indicate number of advanced cultivars available in each country

male sterile lines. In cluster bagging method, panicles from 2-4 adjacent plants in a row are covered in one parchment paper bag. This allows some cross-pollination between plants of the same accession to overcome the problem of inbreeding depression caused if individual plants are selfed. Cluster bagging method is cost-effective to regenerate more accessions in a season. Pearl millet germplasm regeneration is carried out during the post-rainy season. To minimize the genetic drifts, a sample size of about 160 plants are grown in 4 rows of 4 m long each with a spacing of 75 cm between rows and 10 cm between plants.

*Geographic Representation and Gaps in Collection:* The collection at ICRISAT genebank represents the major diversity centres of pearl millet in Africa and Asia (Table 1). India is the major contributor of pearl millet germplasm with 6,610 accessions in Asia. Nigeria (2,074), Niger (1,925), Zimbabwe (1,397), Mali (1,201), Namibia (1,128), and Sudan (1,041) were the major contributing countries in Africa. The wild relatives' collection is from 29 countries.

Though the pearl millet collections at ICRISAT genebank is large and impressive, critical assessment for geographical and trait-diversity gaps revealed several gaps. Gap analysis, using GIS tools such as FloraMap, DivaGIS, ArcGIS etc. and passport and characterization data of pearl millet collection at ICRISAT genebank has provided opportunities to identify geographical gaps, trait-diversity and taxonomic gaps in the collection. Gap analysis using 6,434 geo-referenced pearl millet landraces originating in West and Central African countries revealed 62 districts in 13 provinces of Nigeria, 50 districts in 16 provinces of Burkina Faso, 9 districts in 6 provinces each of Mali and Mauritania, 8 districts in 8 provinces of Chad and 7 districts in 3 provinces of Ghana as the major geographical gaps in pearl millet

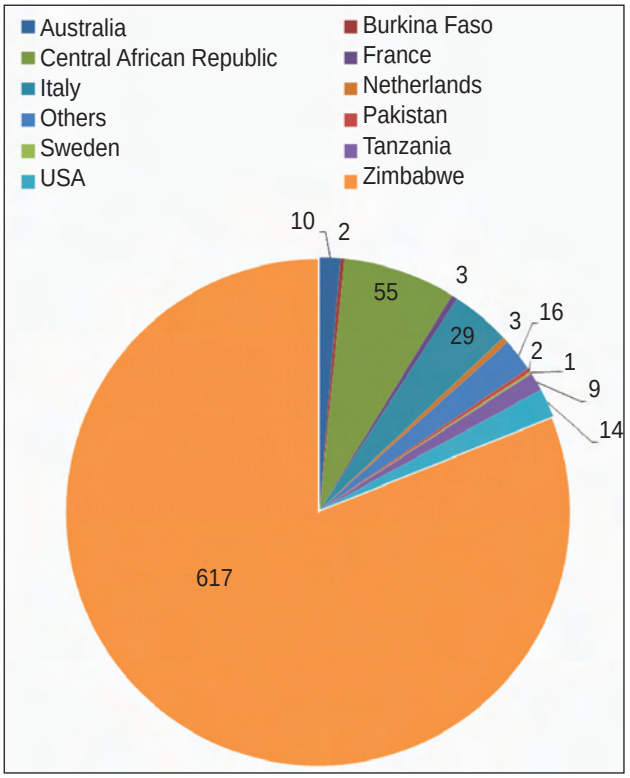


**Fig. 1. Details of pearl millet germplasm from different countries conserved in NBPGR genebank, India**

**Table 2. Details of pearl millet germplasm from different states of India conserved in the NBPGR genebank**

| State | Breeding lines | Improved cultivars | Landraces | Others | Total |
|---|---|---|---|---|---|
| Andhra Pradesh | 34 | 33 | 149 | 49 | 265 |
| Bihar | | | 1 | 3 | 4 |
| Delhi | | 5 | | | 5 |
| Goa | | | | 24 | 24 |
| Gujarat | 15 | 51 | 130 | 19 | 215 |
| Haryana | 7 | 18 | 39 | 21 | 85 |
| Himachal Pradesh | | | | 9 | 9 |
| Jammu and Kashmir | | 1 | 9 | 3 | 13 |
| Karnataka | | 1 | 38 | 4 | 43 |
| Madhya Pradesh | | 8 | 19 | 31 | 58 |
| Maharashtra | 1 | 10 | 39 | 15 | 65 |
| Mizoram | | | | 2 | 2 |
| Odisha | | 1 | 3 | 2 | 6 |
| Punjab | 7 | 7 | 73 | | 87 |
| Rajasthan | 10 | 92 | 247 | 254 | 603 |
| Tamil Nadu | 5 | 7 | 47 | 30 | 89 |
| Telangana | 8 | 5 | | | 13 |
| Uttar Pradesh | 6 | 5 | 55 | 60 | 126 |
| Other | 274 | 16 | 4,459 | 807 | 5,556 |
| Total | 367 | 260 | 5,308 | 1,333 | 7,268 |

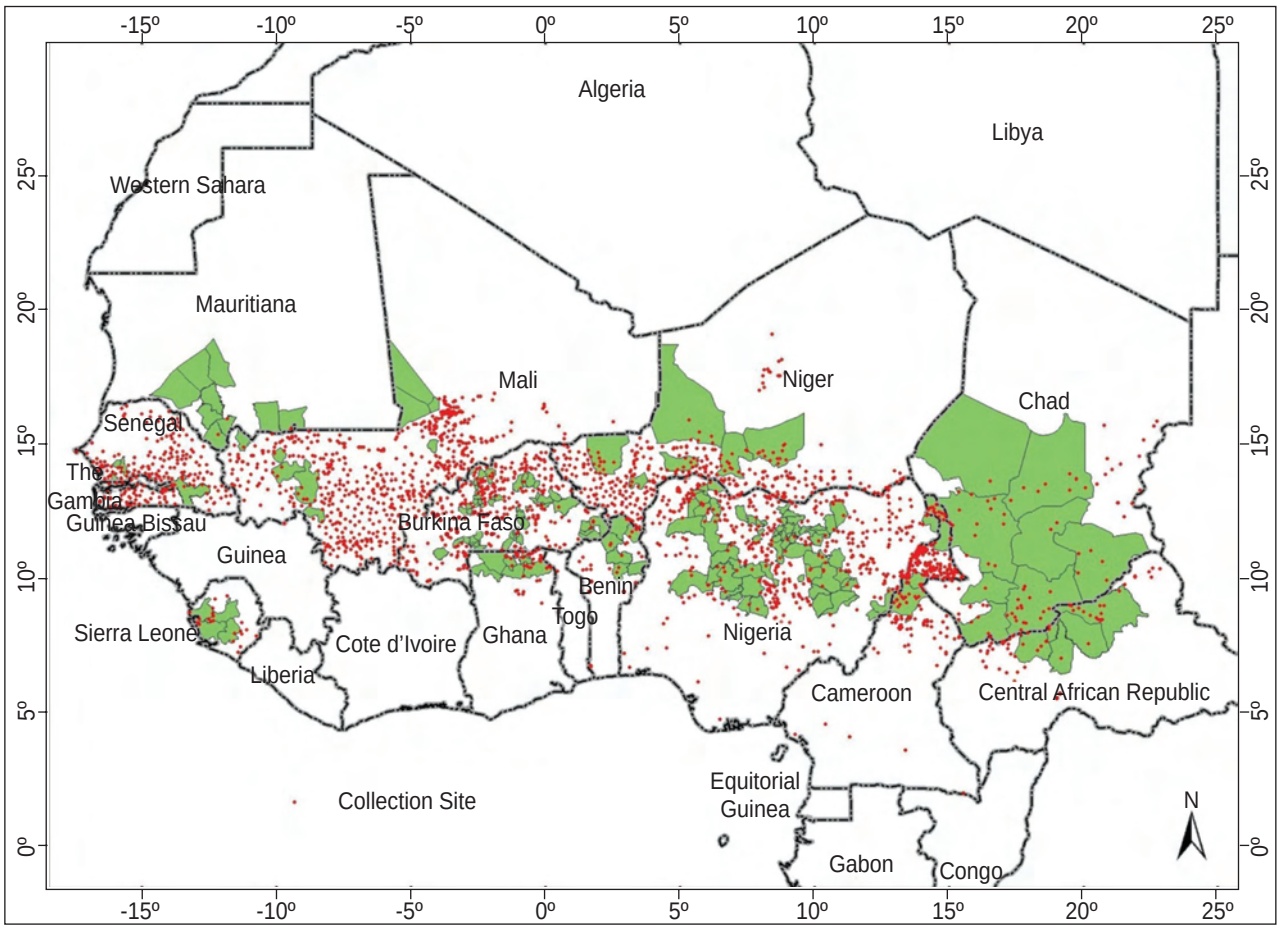


**Fig. 2. Geographical gaps (districts shaded) identified in the pearl millet germplasm from West and Central African countries and collection sites (dots) of germplasm conserved at the ICRISAT genebank, India**

collection from the region (Upadhyaya *et al*., 2009a) (Fig. 2). Gap analysis using 3,750 geo-referenced pearl millet landraces from East and Southern Africa revealed 34 districts located in 18 provinces of four East African countries and 76 districts located in 34 provinces of seven Southern African countries were identified as geographical gaps (Upadhyaya *et al*., 2012a) (Fig. 3).

Gap analysis of the collection at ICRISAT genebank represented by 5,768 landraces from India, Pakistan and Yemen in Asia revealed a total of 134 districts located in 14 provinces in India and 12 districts of Punjab province in Pakistan as the major geographical gaps in the collection (Upadhyaya *et al.*, 2010) (Fig. 4 and 5). Beed, Latur and Osmanabad in Maharashtra in India for all traits; Rajanpur, Muzaffarpur, Multan and Lodhran for panicle length and Chakwal and Sargodha for panicle thickness in Pakistan and Southern parts of Northern province and Lahiz province in Yemen were identified as gaps for trait-diversity. Gap analysis using 335 accessions of pearl millet progenitor (*Pennisetum monodii*) revealed 354 districts located in 86 provinces of eight countries in the primary center of diversity for pearl millet including most of the West and Central African countries, as geographical gaps (Upadhyaya *et al*., 2014a). When assessed for agro-ecological pattern of diversity among 5,197 pearl millet landraces collected from 20 agro-ecological regions in India, it became clear that Malwa and Bundelkhand regions are under-represented in genebank and should be explored further for additional diversity (Upadhyaya *et al*., 2007b). The mean values and the frequency distribution suggest further exploration in agro-ecological region 3 for tall plant height, region 5 for short plant height, region 6 for high panicle exsertion and large seeds, region 8 for high number of reproductive tillers, region 10 for long panicles, region 11 for thick panicles, region 12 for late flowering and high tillering and region 14 for early flowering (Upadhyaya *et al*., 2007b).

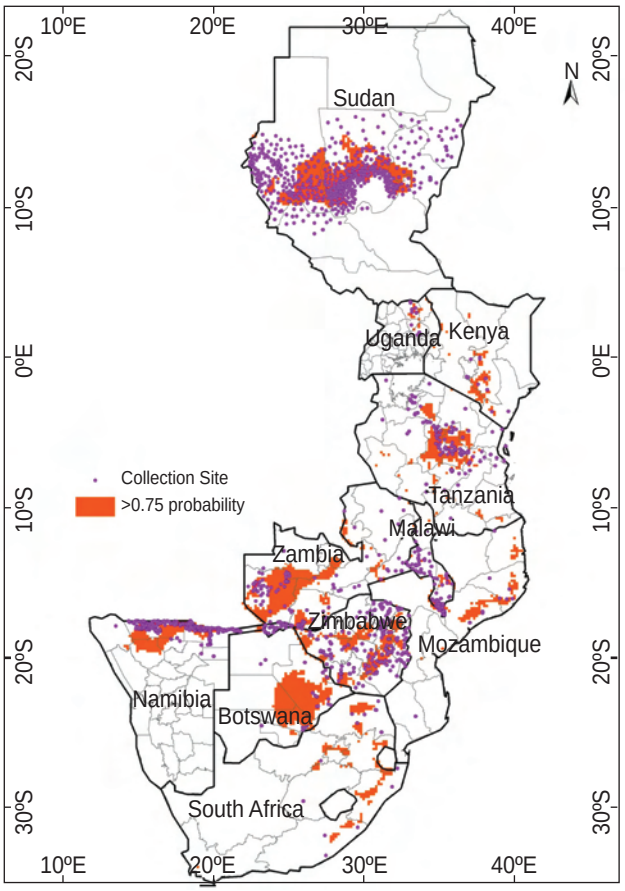


**Fig. 3. Geographical gaps (districts shaded) identified in the pearl millet germplasm from East and Southern African countries and collection sites (dots) of germplasm conserved at the ICRISAT genebank, India**

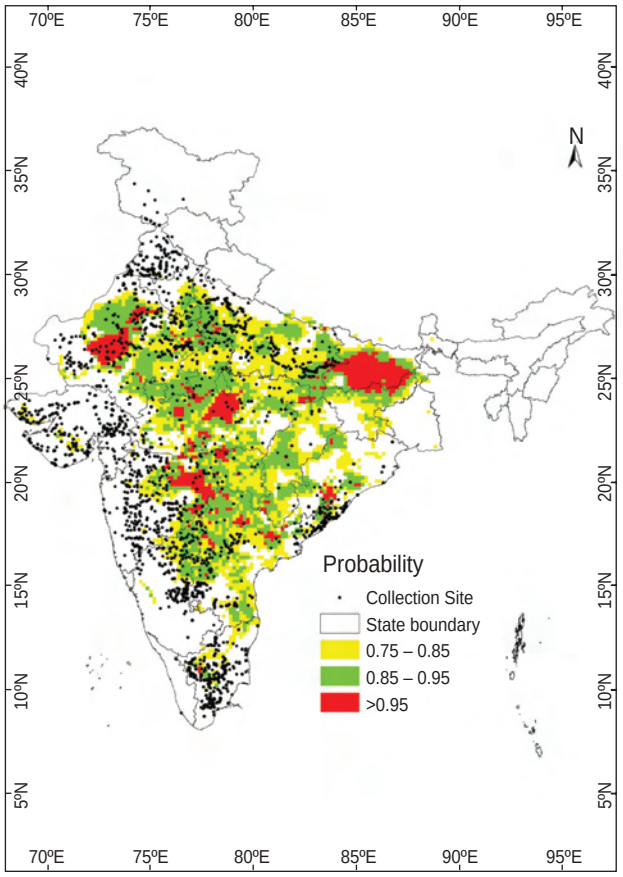


**Fig. 4. Geographical gaps (districts shaded) identified in the pearl millet germplasm from India and collection sites (dots) of germplasm conserved at the ICRISAT genebank, India**

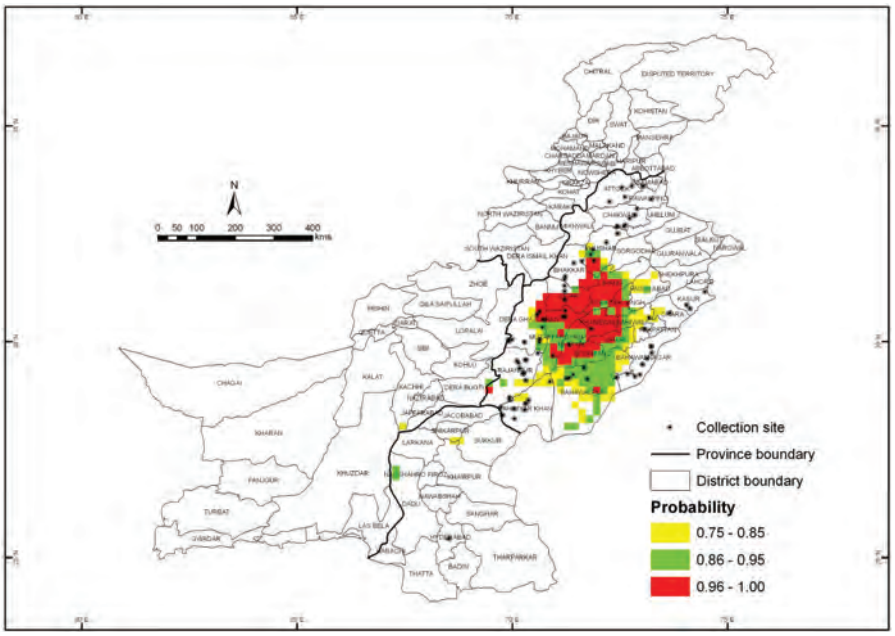


**Fig. 5. Geographical gaps (districts shaded) identified in pearl millet germplasm from Pakistan and collection sites (dots) of germplasm conserved at the ICRISAT genebank, India**

### *Characterization and Evaluation*

Characterization and evaluation are pre-requisite for the efficient utilization of conserved germplasm. The world collection of pearl millet germplasm maintained at ICRISAT was characterized in batches of 500-1000 every year at ICRISAT farm, Patancheru, in alfisols during rainy and post-rainy seasons from 1974 through 2015. Rainy season crop was raised during June to October and post-rainy season crop during November to March. Germplasm accessions were grown in an augmented block design using systematic checks, repeated for every block of 20 test accessions. Each accession was sown in two 4-m long rows. Spacing was 75 cm between rows. The seed was sown using tractor mounted four-cone planter. The crop was thinned 15-20 days after sowing to give approximately 10 cm spacing between plants within a row. Lifesaving irrigations were provided in the rainy season, but irrigation was provided at regular intervals during the post-rainy season. Fertilizers were applied at the rate of 100 kg/ha N and 40 kg/ha $P_2O_5$ in both the seasons (Upadhyaya and Gowda, 2009).

By the end of 2015, almost all cultivated accessions were characterized for 23 morpho-agronomic characters following the descriptors for pearl millet (IBPGR and ICRISAT, 1993). Days to 50% flowering, plant height, panicle length and thickness were recorded during both rainy and post-rainy seasons, whereas number of nodal, productive and total tillers per plant, panicle exsertion, synchrony of panicle maturity, panicle shape, spikelet density, bristle length, grain yield potential, fodder yield potential and overall plant aspect was recorded only during the rainy season. Synchrony of panicle maturity, spikelet density, bristle length, grain yield potential, fodder yield potential and overall plant aspect was visually scored on a 1 to 9 scale, where 1 is most undesirable and 9 most desirable. Observations on grain characters, such as 1000-seed weight, seed shape, seed color and endosperm texture were recorded during the post-rainy season after harvesting.

Further evaluation or screening of germplasm was done by specialists such as pathologists, entomologists, physiologists, biochemists *etc*. Data obtained were added to the characterization database. Accessions/ genotypes identified with useful traits were registered as genetic stocks by assigning new accession number for conservation and utilization. To realize the true potential of the accessions and to facilitate the selection of genotypes by researchers, sets of selected pearl millet germplasm were evaluated for important agronomic characters at different locations in India and several other countries in Africa. Germplasm catalogs were prepared using the multilocation evaluation data (Mathur *et al.*, 1993). To accomplish complete characterization and evaluation of accessions, a multi-disciplinary approach was followed at NBPGR and ICRISAT and the data generated in various disciplines were added to the pearl millet germplasm databases that are being maintained in the genebank.

*Diversity in Collections:* Large phenotypic diversity was observed in the pearl millet collection at ICRISAT genebank for several characters. There are accessions in the collection, which can flower as early as in 33 days and as late as in 159 days in rainy season (Table 3). Similarly, plant height ranged from 30 cm to 490 cm with a mean of 249 cm. Total tillers varied from 1 to 35. Panicle size and shape are the other important traits for which diversity was very high (Fig. 6). The 1000-seed weight varied from 1.5-21.3 g. Distribution of qualitative traits indicates occurrence of nine panicle shapes, five seed shapes and 10 seed colors in the entire collection. Considerable variability for several other traits like sweet stalks, leaf traits, high seed protein content, midrib colour, dwarfism, sources of cytoplasmic-nuclear male sterility and yellow endosperm were also observed in the collection. The Shannon-Weaver (Shannon and Weaver, 1949) diversity index (H′) was calculated to compare the diversity among germplasm accessions for various traits. Phenotypic diversity (H′) ranged from 0.427 (total tillers) to 0.632 (plant height in post-rainy season) for quantitative traits. Among qualitative traits, diversity was maximum for endosperm texture (H′=0.772) and minimum for bristle length (H′=0.443). Diversity

**Table 3. Range of variation in pearl millet collection at ICRISAT genebank, India**

| Character | Range | Mean |
|---|---|---|
| Time to 50% flowering-R (days) | 33-159 | 72.7 |
| Time to 50% flowering-PR (days) | 32 - 138 | 71.7 |
| Plant height (cm)-R | 30 - 490 | 248.5 |
| Plant height (cm)-PR | 25 - 425 | 161 |
| Total tillers (No.) | 1 - 35 | 2.7 |
| Productive tillers (No.) | 1 - 19 | 2.1 |
| Panicle exsertion (cm) | -45 to 29 | 3.5 |
| Panicle length (cm)-R | 5 - 135 | 28.9 |
| Panicle length (cm)-PR | 4 - 125 | 25.8 |
| Panicle width (mm)-R | 8 - 58 | 24 |
| Panicle width (mm)-PR | 8 - 61 | 22.8 |
| 1000-Seed weight (g) | 1.5 - 21.3 | 8.5 |

R- rainy season; PR- post-rainy season

**Fig. 6. Diversity for panicle size, shape and color in the world collection of pearl millet as observed during characterization**

for qualitative traits was higher (H′=0.610) than that for quantitative traits (H′=0.573). Averaged over all traits, the diversity index was 0.588.

*Patterns of Diversity in the Collection:* Patterns of diversity for agro-ecological regions was assessed in the collection from India. Agro-ecological region is an area of the earth's surface characterized by distinct ecological responses to macroclimate as expressed by soils, vegetation, fauna and aquatic systems. Therefore, the agro-ecological region is the land unit carved out of climatic zones. The agro-ecological regions are more homogeneous both in terms of cropping patterns and climate and thus provide a better basis for studying crop responses to climatic variations. Each climatic zone is divided in to 3-9 smaller agro-ecological regions depending on the rainfall, temperature, soils, vegetation, length of growing period etc. Division of the Indian climatic zones has resulted in three agro-ecological regions (1,2 and 3) in the arid zone, five regions (4,5,6,7 and 8) in the semi-arid zone, nine regions (9,10,11,12,13,14,15,16 and 17) in the sub-humid zone and three regions (18, 19 and 20) in the coastal zone (Upadhyaya *et al*., 2007b). When assessed for agro-ecological pattern of diversity among 5,197 peal millet landraces collected from 20 agro-ecological regions in India, region 3 for tall plant height, region 5 for short plant height, region 6 for high panicle exsertion and large seeds, region 8 for high number of reproductive tillers, region 10 for long panicles, region 11 for thick panicles, region 12 for late flowering and high tillering and region 14 for early flowering as promising regions (Upadhyaya *et al*., 2007b).

Assessing the latitudinal patterns of diversity in the world collection of pearl millet landraces maintained in ICRISAT genebank revealed Northern hemisphere as predominant source with 80% of total landraces (Upadhyaya *et al*., 2014b). The latitude ranges of $10^{o}$-$15^{o}$N and $15^{o}$-$20^{o}$S were found as important source regions for pearl millet. Landraces from the 5°–10°N latitude region flowered late and grew tall in the rainy and post-rainy seasons and produced more tillers, while those from 10°–15°N latitude region produced fewer tillers and had long and thick panicles with larger seeds. Landraces from 10°–15°S and 20°–25°S latitudes were good sources for long-bristled and bird-resistant types. Further, late-maturing, tall and high tillering landraces from lower-latitude regions (<$20^{o}$ N and S) were better sources for fodder production. Early maturing landraces producing long and thick panicles with large seeds from mid-latitude regions (10°–15°) in both hemispheres were useful for developing high-yielding cultivars. Furthermore, a study on climate data of the germplasm collection sites revealed that most accessions from latitudes ranging from $10^{o}$ to 20°on both side of the equator were highly sensitive to longer photoperiod (>12.5 h) and/or lower temperature (<12°C) (Upadhyaya *et al*., 2012b). Accessions that originated at higher latitudes (>25-35°) on both the hemispheres exhibited low sensitivity to both photoperiod and low temperature. The photoperiod and temperature insensitive accessions were represented from mid-latitudes (15-20°) in both the hemispheres.

The studies on elevation pattern of diversity using 229 landraces collected in Yemen revealed high diversity in landraces from low elevations for flowering and plant height (Reddy *et al*., 2004).

*Access to Collections:* To ensure unrestricted access to the world community, ICRISAT has placed its germplasm collections under the auspices of the Food and Agricultural Organization (FAO) of the United Nations in 1994. As per agreement with the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), ICRISAT supplies germplasm free of cost to global research community using the Standard Material Transfer Agreement (SMTA). So far, ICRISAT has distributed over 1.4 million samples accessions of mandate crops to researchers in 148 countries including

those supplied to researchers in ICRISAT. ICRISAT genebank has restored pearl millet germplasm to India (7,488), Cameroon (922) and Sudan (594), when their national collections were lost due to natural disasters or lack of proper storage facilities. Thus, national programmes have regained access to the precious heritage that would have been lost, had it not been conserved in ICRISAT genebank. NBPGR is also maintaining a trait-based database of all accessions and small quantity of seed is supplied on request.

*Documentation of Collections:* Documentation of genetic resources is essential for proper conservation, management and utilization of genetic resources. At ICRISAT genebank four categories of information on each accession is being maintained using GRIN-Global software (Upadhyaya and Gowda, 2009): (i) Passport data: information related to accession identity and collection, (ii) conservation data: information on storage, monitoring and regeneration, (iii) characterization and evaluation data: information on morpho-agronomic characteristics and reaction to pests/diseases, and (iv) distribution data: information related to seed supply. Passport and characterization data can be accessed through: (i) www.germplasm.icrisat.org, (ii) www.icrisat.org and www.nbpgr.ernet.in

## Utilization

*Sources of Specific Traits:* Germplasm collections at ICRISAT and NBPGR genebanks continue to play a major role in crop improvement programmes. Over the years, systematic evaluation of germplasm accessions available in genebanks has led to the identification of several sources of phenotypic, quality and adaptation traits, and biotic and abiotic stress resistance (Table 4). In general, Indian pearl millet landraces have mainly contributed for earliness, high tillering, high harvest index, and local adaptation (Yadav and Bidinger, 2007); whereas African material has been a good source of high head volume, large seed size, and disease resistance (Anand Kumar and Appa Rao, 1987). Several genetic stocks were used as sources of biotic and abiotic stress resistance and morphological mutants were used in academic studies.

*Trait-specific Gene Pools:* Harlan and de Wet (1971) suggested classifying each species including its related species by gene pools, rather than by formal taxonomy. Gene pools are created to provide researcher with the widest variability in germplasm accessions so as to sustain continual improvement over a longer period of time. Different methods have been employed for developing gene pools (Burton, 1978; Singh and Jika, 1988; Appa Rao *et al*., 1998). But choice of creation of gene pools is largely determined by traits most sought after/targeted by breeders in their breeding programmes. Most frequent requests of germplasm for specific traits from breeders world over led to creation of four gene pools of pearl millet at ICRISAT (Appa Rao *et al*., 1998). These include early gene pool (EGP) constituted from 1,143 accessions, high tillering gene pool (HTGP) from 1,093 accession, large spike gene pool (LSGP) from 804 accessions and large grain gene pool (LGGP) from 887 accessions selected from 21,000 accessions. Trait-specific populations, based on abiotic-stress-adapted landraces from India, have also been developed (Yadav and Bidinger, 2007).

While constituting a gene pool or trait-specific population, all accessions with a trait of interest are selected ignoring other traits. Experience in pearl millet indicated that gene pools have slightly narrowed phenotypic variation and obscured recessive traits (Burton, 1978; Appa Rao *et al*., 1998; Upadhyaya *et al*., 2007a). Nonetheless, such trait-specific gene pools and populations are attractive options to most breeders as it is much easier to look for the traits in the gene

**Table 4. Promising sources identified in the world collection of pearl millet at ICRISAT genebank, India**

| Stress/Nutritional traits | No. of accessions screened | No. of promising sources identified |
|---|---|---|
| **Abiotic stress tolerance** | | |
| Salinity | 48 | 32 |
| Drought | 115 | 8 |
| Heat | 238 | 6 |
| **Biotic stress resistance** | | |
| Ergot | 2,752 | 283 |
| Downy mildew | 4,727 | 65 |
| Rust | 2,229 | 332 |
| Smut | 1,747 | 397 |
| Downy mildew | 534 | 222 |
| **Nutritional traits** | | |
| High seed protein content (>15%) | 1,735 | 272 |
| High seed iron content (>80 ppm) | 387 | 41 |
| High seed iron and zinc content (>60 ppm) | 387 | 33 |
| High seed zinc content (>60 ppm) | 387 | 42 |
| Yellow endosperm | 137 | 2 |

pools and populations in which random-mating would have produced recombinants along with specific trait of interest. Trait-specific gene pools and populations can be easily distributed and used as a source population for improvement through single-plant selection, recurrent selection and mass selection.

*Disease Resistance:* Downy mildew caused by *Sclerospora graminicola* (Sacc.) Schroet. is the most important disease of pearl millet in Indian sub-continent and Africa. Several disease epidemics have been reported in India (Dave, 1987) and destruction of the crop in Africa has also been reported (Williams, 1984). Field evaluation of more than 3,000 germplasm accessions and stability tests across locations in India and Africa has identified several sources (ICML 12, ICML 13, ICML 14, ICML 15 and ICML 16) of high levels of downy mildew resistance (Singh *et al.*, 1990). The resistant types exhibited reduced penetration, restricted mycelial growth and complete lack of haustorial formation (Chalam *et al*., 1992). Ex-Bornu from Nigeria, 3/4 Ex-Bornu and 3/4 Hainei Kirei from Niger have contributed to downy mildew resistance (Andrews *et al*., 1985). In another study, 3,163 accessions were screened and 1,220 were found to be resistant (Singh *et al*., 1987; Mengesha *et al*., 1990). Germplasm accessions from Mali, Niger, Nigeria and Senegal were the major sources of downy mildew resistance. Upadhyaya *et al*., (2007b) have reported screening of 3,164 accessions for downy mildew reaction and identified 54 promising lines. Thakur *et al*. (2001) have reported that 863 B is resistant to three pathotypes (Patancheru, Durgapura and Jalna) and had 2-8% disease incidence against Mysore pathotype. Resistance against different downy mildew pathotypes was identified from 863 B (IP 22303), P 1449-2 (IP 21168), ICMB 90111 (IP 22319), ICMP 451 (IP 22442) and IP 18293 (Upadhyaya *et al*., 2007b). Of the 238 accessions of mini core collection, 62 exhibited resistance to two or more pathotypes of downy mildew (Sharma *et al*., 2015).

Germplasm accessions have also been rich source of resistance for other important pearl millet diseases like smut, ergot and rust (Table 4). Germplasm accessions obtained from India, Uganda, Nigeria, Lebanon and Senegal yielded six promising smut resistant lines (ICML 5, ICML 6, ICML 7, ICML 8, ICML 9, and ICML 10 (Thakur and King, 1988). Further, screening of 1,747 germplasm accessions has identified 44 smut resistant lines (<10% severity) originating from Cameroon, India, Lebanon, Uganda, Mali, Senegal, Niger, Nigeria and Togo (Thakur *et al*., 1992). Variability existed among the 106 landraces evaluated for smut in Burkina Faso; the smut infection and percent seed set varied from 0.8 – 8.4% and 7.0 – 43.9%, respectively (Wilson *et al*., 1991).

A screening effort involving 2,752 germplasm accessions obtained from 19 countries and some unknown sources did not yield any accession with acceptable level of resistance to ergot (Thakur *et al*., 1993). But, 27 accessions with low ergot susceptibility (0-10%) and >75% selfed seed set from India, Nigeria, Togo and Uganda were identified. Higher levels of ergot resistance were developed from the less susceptible lines by inter-mating and pedigree breeding. Thakur and King (1988) have registered four ergot resistant germplasm lines (ICML 1, ICML 2, ICML 3, ICML 4). Under international trials, ergot infection ranged from 1-3% among the four resistant lines. Additionally, these lines also exhibited resistance to downy mildew and smut.

Several accessions from different African countries and India were found to show 0-10% rust severity (Singh *et al*., 1997). Further, several sources of resistance to rust were identified which originated from India, Senegal, Nigeria, USA, Mali, Cameroon, Chad, and Burkina Faso. The 17 rust resistant entries identified were from Nigeria (700481-21-8, 700481-22-8, 70041-23-2), Senegal (P 1564, P 1577, P 1581, P 1591), Cameroon (P 24, P 140), Niger (D 212 P1, P 2890), Mali (IP 548, P 615), Chad (7042-1-4-4), Sudan (IP 8695-4), USA (IP 537-8) and India (IP 2084-1). Singh *et al*. (1987 & 1990) have reported some resistant germplasm accessions (ICML 11, ICML 17, ICML 18, ICML 19, ICML 20, and ICML 21) that have been registered. Three accessions (IP 7846, IP 11036 and IP 21187) have recently been reported to possess resistance to four pathotypes of blast disease (Sharma *et al*., 2013).

*Abiotic Stress Tolerance:* Drought is the most important abiotic stress impacting the pearl millet production. Therefore, identifying sources of drought tolerance is very crucial for developing improved cultivars. Germplasm accessions and other genetic stocks are a very valuable source for drought tolerance and escape (Table 4). Earliness is important especially for arid regions. Murty *et al*. (1967) characterized 1,532 accessions and reported variation for days to flowering among Indian (52-77 days) and exotic (53-85 days) collections. In another study, the days to flowering showed much wider variability (33-140

days) among the world collection of 16,968 pearl millet accessions (Harinarayana *et al*., 1988). IP 4021 (Bhilodi) collected from Gujarat was earliest with 33 days to 50% flowering in rainy season and 34 days in post-rainy season. Further, screening efforts identified two promising drought tolerant lines among the 509 accessions screened (Harinarayana *et al*., 1988). Landraces identified from Rajasthan, India exhibited wide variability for different characters. SR 15, SR 17, and SR 54 were three landraces that were identified for earliness. Three other unique landraces that showed earliness were 'Chadi' from Rajasthan, 'Bhilodi' from Gujarat and 'Pittaganti' from Eastern Ghats of India (Kumar and Appa Rao, 1987). Further, germplasm accessions IP 4066, IP 9496 and IP 9426 were identified as promising early lines. In a detailed study conducted across a wide range of environmental conditions, 105 landraces were evaluated and a wide range in the drought response was observed and landraces having high degree of drought tolerance have been identified for use in developing drought tolerant cultivars (Yadav *et al*., 2003).

Salinity is another important production constraint especially in some parts of India. Genetic variability has been reported for salinity tolerance in pearl millet (Ashraf and McNeilly, 1992; Chopra and Chopra, 1997). Among the 24 accessions evaluated for salinity tolerance, KAT/PM-2 Kitui, Kitui local and 93613 produced greater dry matter (Ashraf and McNeilly, 1992). These three accessions along with 93612 had longer shoots compared to other accessions. In another study, 45 germplasm accessions (23 landraces, 18 dual-purpose lines and 4 accessions of *P. purpureum*) that included 40 accessions from Western and Central Africa, 3 from Eastern and Southern Africa and 2 from India were evaluated (Kulkarni *et al*,. 2006). Among these IP 22269 and IP 6098 were found to be promising dual purpose lines producing about 1420 kg/ha grain yield (comparable to Raj 171 – 1492 kg/ha) and about 40-60% higher dry fodder yield compared to the check variety Raj 171 (3513 kg/ha) under field trials. Further, IP 3616, IP 6105, IP 6112 and IP 6104 were found to be promising lines for dry-fodder yield. IP 22269 is 'High Tillering Gene Pool (HTGP)' collection from ICRISAT (Appa Rao *et al*., 1988), IP 3616 a dual-purpose collection from Tamil Nadu and IP 6104 and IP 6112 are from Niger (Kulkarni *et al*., 2006). Vegetative stage salinity tolerance was evaluated using 100 entries that included 35 hybrid parents, 61 population progenies, 2 OPVs and 2 germplasm accessions (Krishnamurthy *et al*., 2007). Among these HTP 94/54, ICMP 451, CZI 9621 and IP 3757 were identified to be most tolerant entries. Additionally, 863 B and ICMB 94555 were found to be moderately tolerant. Upadhyaya *et al*. (2007b) have reported 32 promising accessions identified after screening 48 accessions for salinity tolerance. A pearl millet variety 'HASHAKI 1' has been identified for release in Uzbekistan as high forage variety for salt affected areas (Yadav *et al*., 2012).

In view of climate change and rising temperatures, tolerance of crops to high temperature during their reproductive stage has recently assumed high significance. The high temperatures have relevance at both seedling and reproductive stages of crop. Several growth processes like the rate of germination, rate of coleoptile elongation, or the rate of photosynthesis require rather high optimum temperatures, *e.g*., 35°C in pearl millet, which is indicative of good adaptation of pearl millet to the hot growing conditions. Peacock *et al.* (1993) identified a few genotypes from Rajasthan for better survival under high soil surface temperatures during initial stage of development.

Large genetic variation for tolerance to heat at reproductive stage among pearl millet breeding lines and populations has also been observed, and heat-tolerant lines have been identified (Gupta *et al*., 2015). Based on multi-locational screening, five maintainer lines ICMB 92777, ICMB 05666, ICMB 00333, ICMB 02333 and ICMB were found to have more than 60% seed set when the air temperature during flowering exceeded 42˚C. Populations like ICMV 82132, MC 94, ICTP 8202 and MC- Bulk have also been identified as sources of heat tolerance for further selection. Three germplasm accessions (IP 19799, IP 19877, IP 19743) were also identified as heat tolerant (seed set of >50%), and can also be further utilized for diversifying the genetic base of heat tolerant materials in pearl millet (Yadav *et al*., 2012)

*Nutritional Traits:* Pearl millet is a highly nutritious crop and contributes to about 19-63% and 16–56% of total iron (Fe) and zinc (Zn) intake from all the food sources (Parthasarathy Rao *et al*., 2006). Evaluation of 297 Iniadi germplasm accessions originating from Western Africa (Togo, eastern Ghana, southern Burkina Faso and western Benin) has indicated wide

variability for Fe and Zn density levels (Rai *et al.*, 2008). Fe levels in 101 accessions were equal to or higher than the commercial OPV ICTP 8203 (81 mg/kg). Among these, 92 accessions also had Zn density greater than or equal to 61 mg/kg (ICTP 8203 – 59 mg/kg). IP 17602 (121 mg/kg), IP 17673 (109 mg/kg) and IP 9404 (108 mg/kg) were the three accession with highest levels of Fe density compared to ICTP 8203 (81 mg/kg). Similarly, Zn density levels were found to be highest in IP 17602 (87 mg/kg), IP 17561 (86 mg/kg) and IP 17836 (82 mg/kg) compared to ICTP 8203 (59 mg/kg). In another trial involving 90 entries (40 hybrid parents, 30 populations and progenies and 20 germplasm accessions), 863 B was identified to contain the high Fe levels (72.7 mg/kg) (Velu *et al*., 2007) and good amount of Zn (55.8 mg/kg) (Rai *et al*., 2008). The grain Fe density among 18 OPVs and 121 commercial hybrids has been reported to vary from 42 mg/kg to 67 mg/kg, and Zn from 37 mg/kg to 52 mg/kg (Rai *et al.*, 2016).

Additionally, 260 promising accessions for high seed protein content (>15%) have been identified among the 1,270 accessions (Upadhyaya *et al.*, 2007b). Further, wide variation for grain protein content was identified among the pearl millet genotypes from Sahelian West Africa (Buerkert *et al.*, 2001). Additionally, among the 22 landraces, 22 improved varieties, 6 inbred X variety hybrids (IVHs) and 4 top-cross hybrids (TCHs), landraces outperformed the varieties, IVHs and TCHs. Further, wide variability for crude protein content (9.71-15.43%) was also observed among the 61 local pearl millet accessions from Tamil Nadu, India (Govindraj *et al.*, 2011).

Efforts are being made at global level to enhance the pearl millet nutrition including micronutrients to overcome malnutrition. The protein content in pearl millet mini core accessions ranged from 6 to 13%, averaged 10.7%. IP# 3642, 4291, 4363, 4488, 4747, 9198, 12431, 13624, 13636, 16489, 17465, and 19877 had 9-18% greater protein content than the control, IP 3616 (11%), with IP 3642 and IP 19877 having the highest protein content 13%. The genetic variation for grain Fe and Zn in mini core collection ranged from 34 to 95 ppm, averaged 69 ppm, for Fe, while from 29 to 81 ppm, and averaged 56 ppm, for Zn content. IP# 4363, 4747, 9198, 12431, 13624, 13636, and 19877 had 9-11% greater Fe (86-88 ppm) than best control (IP 17862). Likewise, accessions with 11-25% greater Zn than IP 17862 were IP# 4177, 4291, 4363, 4488, 4747, 9198, 12431, 13624, 13636, and 17465. Six of these accessions (IP# 4363, 4747, 9198, 12431, 13624, and 13636) had both high grain Fe and Zn. The control IP 17862 had 79 ppm Fe and 63 ppm Zn. The wild relatives are useful sources for various nutritional traits. In a preliminary study at ICRISAT, 101 accessions of *P. violaceum* had combination of protein, iron and zinc higher than the best controls. The research is in progress to identify stable sources to develop nutrient dense broad based open pollinated and hybrid cultivars. Seed quality traits are highly influenced by environment and genotype by environment interaction, therefore, necessitating the need for further evaluation to identify nutrient dense germplasm.

*Direct Use in Cultivar Development:* The use of germplasm in pearl millet improvement programmes in national and international research institutes has resulted in the release of commercial cultivars in different countries. Mass selection in locally adapted germplasm has been used extensively in cultivar development. Varieties like Co 1, Co 2, Co 3, Co 4, Co5, Jakharana, RSJ, RSK, Pusa Moti and S530 were developed in 1960s and 1970s (Yadav and Rai, 2013). While Co 1, Pusa Moti and S 530 were developed from African material (Harinarayana and Rai, 1989) the others were developed from Indian landraces. Later WC-C 75 and ICMS 7703 were developed from intercrossing of African and Indian material. Similarly, RCB 2 was developed from selections among the Indian landraces from Rajasthan. Development of ICTP 8203, a high yielding, downy mildew resistant and large-seeded variety was developed through direct selection within large-seeded Iniadi landrace from northern Togo (Rai *et al*., 1990). This same variety was released as Okashana 1 in Namibia and as Nyankhombo (ICMV 88908) in Malawi (Upadhyaya *et al*., 2007a). Even prior to the release of Okashana 1 in Namibia, the Iniadi-type material was available as Serere 17 (Tanzania) and Serere 6A (Botswana) in southern and eastern Africa (Andrews and Kumar, 1996). Improved version of ICTP 8203 containing higher Fe content in its grains has recently been released as Dhanshakti (Rai *et al*., 2014).

Okashana 2, a variety was developed from a cross involving Zimbabwe local landrace IP 16504 with ICCMV 87901 and ICMV 88908 and released in Namibia in 1998 (Obilana *et al*., 1997). Further, two other OPVs (ICMV 221 and RCB-IC 911) were developed from bold

seeded composite (BSEC) (Andrews and Kumar, 1996). The 'Iniadi' landrace has also been utilized in developing CZP-IC 923, which was a collaborative effort involving ICAR-CAZRI, Jodhpur and ICRISAT, India. CZP 9802, another OPV was developed from early maturing and high yielding progenies of a population from Rajasthan, India (Yadav, 2004). The varieties JBV 2 and JBV 3 were developed from Early Composite 91 and SRC II, respectively. Two other varieties *viz*., HC 10 and ICMV 155 were developed from early maturing and drought tolerant 'New Elite Composite (NELC)'.

Local landraces *per se* have been put to relatively greater direct use in western Africa for developing open pollinated varieties (OPVs). IKMP 1, a variety was developed and released in Burkina Faso by recombining selections made from landraces. Further, two varieties IKMP 3 and IKMP 5 were developed as selections from landraces CVP 417 and CVP 170, respectively (both from Burkina Faso; Upadhyaya *et al*., 2007a). Similarly, an OPV ICMV-IS 88102 was developed as selection from a landrace IP 6426 and released in Burkina Faso and Mali. Another variety, Kangara was developed from two landraces and white grain composite and released in Namibia during 1998. Kangara was also released in Zimbabwe as PMV 3 (Obilana *et al*., 1997). Several cultivars (IKMV 8108, IKMV 8109, ICMV IS 91106, and ICMV IS 91108) were developed from the Iniadi material for the west and central Africa (Andrews and Kumar, 1996). Additionally, another OPV, GB 8735 was developed from cross involving Iniadi and Souna (early maturing landrace from Mali) landraces (Andrews and Kumar, 1996). This OPV was tested and released for cultivation in Mauritania, Chad and Benin.

A significant impact of germplasm use has been on hybrid development. The male-sterile line Tift 23A was introduced in India from USA in 1962. HB 3 was a popular hybrid that was developed using Tift 23 A (seed parent) and J 104 (pollen parent). J 104 was derived from Indian germplasm material. BJ 104, and CJ 104 were two other hybrids that were developed using 5141A, bred from Indian germplasm. Three hybrids (BK 560, GHB 27 and GHB 32) were all developed using 5141A as seed parent. The pollen parents for these three hybrids were K560-230, J 2002 and J 1188, respectively and these were all developed from Indian germplasm. The pollen parent of ICMH 451 (ICMP 451) and ICMH 423 (ICMP 423) were derived from late and early composites, respectively. The pollen parent (H 77/833-2) of highly popular and early maturing hybrid HHB 67 was selected from a Rajasthan landrace. Additionally, several hybrids based on 'GHB' series were developed using pollen parents that were derived from Indian germplasm. Further, two MS lines ($L66A_2$; $L67A_3$) were developed from African germplasm at Punjab Agricultural University, Ludhiana, India. Two more male-sterile lines *i.e*. CZMS 44A and CZMS 47A were developed at CAZRI, Jodhpur using local germplasm material collected from Barmer, Rajasthan, India (Manga and Yadav, 1997).

'Iniadi' or 'Togo' population has been utilized in developing hybrid parents (male-sterile lines and restorers) that have been used in hybrid development. Several of the early-maturing hybrids developed in India are based on male-sterile lines derived from Iniadi material collected from Ghana (Dahlberg *et al*., 1997). A high yielding downy mildew resistant hybrid (ICMH 312) was developed from a cross involving ICMR 312, a restorer population developed from BSEC and 81 A (Andrews and Kumar, 1996). 863 A and ICMA 88004 are two male-sterile lines that have been developed from the Togo population. Further, A/B pair of 863 was developed from Iniadi landrace material. Studies conducted by SADC/ICRISAT SMIP jointly during the late 1980's and early 1990's observed heterotic vigor in crosses involving local landrace variety (LLV) accessions and improved released varieties (Monyo *et al*., 1996). The intervarietal hybrid developed from crossing SDMV 89003 (improved variety) and SDPM 626 (a LLV) produced 33.7% (3930 kg/ha) higher yield than the control variety, PMV 2 (2942 kg/ha). While the crosses involving LLVs from Tanzania demonstrated yield superiority of up to 89.8% over Serere 17.

*Forming Representative Core Collections for Enhancing Utilization:* With the establishment of genebanks at ICRISAT and NBPGR, the range of available pearl millet germplasm has increased tremendously. However, there are various bottlenecks to the increased use of genetic resources. The main reasons for low use of germplasm includes larger size of collections, lack of reliable data on traits of interest to the user, restricted access to the accessions, inadequate linkages between genebank and the users and limited capacity of breeding programmes to absorb new material.

To enhance germplasm utilization, core collections consisting 2,094 accessions (10% of entire collection) (Upadhyaya *et al*., 2009b), mini core collection consisting

238 accessions (10% of core or 1% of entire collection) (Upadhyaya *et al*., 2011) and reference sets of genetically most diverse accessions (Upadhyaya *et al*., 2006) were developed. Developing a core collection that represents the diversity of entire collection is an efficient approach to enhancing the use of germplasm in crop improvement (Upadhyaya *et al*., 2009b). Core collections are dynamic and need to be revised when additional germplasm and information become available. The pearl millet core collection, consisting of 1,600 accessions selected from 16,000 accessions characterized at the ICRISAT genebank up until 1998, was augmented by adding 501 accessions representing 4,717 accessions assembled and characterized later. The revised core collection consists of 2,094 accessions (five duplicate and two male-sterile accessions were deleted from the original core collection). A comparison of mean data using the Newman–Keuls test, variance using Levene's test, and distribution using $\chi 2$ test indicated that the variation in the entire collection of 20,766 cultivated accessions was preserved in the revised core collection. The Shannon-Weaver diversity index for different traits was similar in the revised core and entire collection. The revised core collection was observed to be more valuable than the original core as it has sources of resistance for important diseases including downy mildew (Upadhyaya *et al*., 2009b).

Even a core collection consisting of 2,094 accessions is large and can become too unmanageable to evaluate and characterize the accessions for economic traits. Hence, a mini-core collection of pearl millet, comprising 238 accessions was constituted following Upadhyaya and Ortiz (2001) using evaluation data of core collection accessions for 18 morpho-agronomic traits (Upadhyaya *et al*., 2011). Results indicated that almost the entire genetic variations and a majority of co-adapted gene complexes present in the core-subsets were preserved in the mini-core subsets. Due to its greatly reduced size, the mini core will serve as gateway to the entire collection of pearl millet for proper exploitation of pearl millet genetic resources for crop improvement. Molecular characterization of mini core collection and composite collection further revealed genetic usefulness of the germplasm accessions in allele mining.

Development of mini core collection (1% of total collection) representing the core and entire collection for diversity has resulted in the extensive evaluation of mini core sets and identification of several promising sources for agronomic and nutritional traits and biotic and abiotic stresses.

*Using Wild Relatives:* As there was large amount of genetic variability available in pearl millet landraces for useful traits, use of wild relatives in crop improvement was negligible. There have been a few targeted attempts and the results have been encouraging. For example, the use of *P. glaucum* subsp. *monodii* led to the identification of new source of cytoplasmic-nuclear male sterility, referred to as $A_4$ (Hanna, 1989). Hanna (1992) has summarized the use of this wild relative for new sources of resistance to leaf diseases that of *P. purpureum* for sources of forage traits, and stiff stalk and restorer genes of the $A_1$ CMS system, and that of *P. squamulatum* Fresen for apomictic gene (Rai *et al*. 1997). Crop wild relatives contain higher levels of resistance for both biotic and abiotic stresses and are promising for some agronomic and nutritional traits. Therefore, these will continue to play a vital role in crop improvement programmes, more so under conditions of climate change (Hanna, 1992). *P. pedicellatum and P. polystachion* are resistant to downy mildew, rust and leafspot and produce more tillers.

## Future Prospects

Landraces and traditional cultivars have evolved over centuries by natural and human selection under drought, high temperature or saline conditions. They are better adapted to the local conditions and would contribute in enhancing the resilience at the farm level. Such landraces and germplasm accessions could be of immense importance especially as sources of native genes conditioning resistance to various biotic and abiotic stresses and thus would be of great help to the farming community. These could also serve as excellent genomic resource for isolation of candidate genes responsible for tolerance to climatic and edaphic stresses for accelerating further genetic improvement of pearl millet as well as for their possible deployment in the genetic improvement of other crops.

There is renewed interest in pearl millet and other coarse grain cereals as health and functional food. The assessment of pearl millet germplasm as health food has indicated a good variation in several micronutrients. Pearl millet can be a useful source for carotenoids having anti-oxidant properties and pro-vitamin A activity. Available germplasm should be searched for native variation in these traits.

Additional explorations are needed in the regions where collection gaps have been indicated. *Ex situ*

conservation of genetic resources from such regions and distribution of germplasm to the stakeholders on regular basis would remain very crucial especially in the present scenario of climate change. Like other crops, the proportion of available germplasm used in breeding programme of pearl millet has been very limited. The development of core and minicore in recent past is expected to improve this situation. Developing *e*-resources with detailed information like passport data, characterization and evaluation data with respect to individual accessions would certainly help in enhancing the utilization of genetic resources in order to broaden the genetic base of commercial cultivars which is very essential to reduce the chances of disease epidemics and to mitigate the effects of climate change.

## References


Andrews DJ and K Anand Kumar (1996) Use of the West African pearl millet landrace *Iniadi* in cultivar development. *Plant Genet. Resour. Newslett.* **105:** 15-22.

Andrews DJ, SB King, JR Witcombe, SD Singh, KN Rai, RP Thakur, BS Talukdar, SB Chavan and P Singh (1985) Breeding for disease resistance and yield in pearl millet. *Field Crops Res.* **11:** 241-258.

Appa Rao S, MH Mengesha and KN Reddy (1998) Development and characterization of trait-specific genepools in pearl millet. *Plant Genet. Resour. Newslett.* **113:** 27-30.

Ashraf M and TM Mcneilly (1992) The potential for exploiting variation in salinity tolerance in pearl millet *Pennisetum americanum* Leeke *Plant Breed.* **108:** 234-240.

Buerkert A, M Moser, AK Kumar, P Fürst and K Becker (2001) Variation in grain quality of pearl millet from Sahelian West Africa. *Field Crops Res.* **69**: 1-11.

Burton GW (1978) Advances in breeding a better quality forage plant. In "Advances in Hay, Silage and Pasture Quality". Proceedings of Forage and Grassland Conference, Raleigh, North Carolina. American Forage and Grassland Council, Lexington, KY, USA.

Chalam VC, SD Singh and KC Rao (1992) Mechanisms of resistance. In: Cereals Program Annual Report 1991. ICRISAT, Patancheru, AP, India, p 33.

Chopra NK and N Chopra (1997). Performance of pearl millet genotypes at different salinity levels in western Rajasthan. *Ann. Arid Zone* **27:**183–189.

Dahlberg JA, CT Hash, S Kresovich, B Maunder and M Gilbert (1997). Sorghum and pearl millet genetic resources utilization. Intl. Sorghum and Millets Breeding Conference, Sept 22 - 27, 1996, Lubbock, TX.

Dave HR (1987) Pearl millet hybrids. In Proceedings of the International Pearl Millet Workshop, 7-11 April 1986, ICRISAT Center, India, Patancheru, A.P. 502324, India, pp 121-126.

FAO (Food and Agriculture Organization of the United Nations) (2010) http://www.fao.org

Govindraj M, B Selvi, S Rajarathinam and P Sumathi (2011) Genetic variability and heritability of grain yield components and grain mineral concentration in India's pearl millet (*Pennisetum glaucum* (L) R. Br.) accessions. *African J. Food Agric. Nutr. Development* **11:** 4758-4771.

Gupta SK, KN Rai, P Singh, VL Ameta, SK Gupta, AK Jayalekha, RS Mahala, S Pareek, ML Swami and YS Verma (2015) Seed set variability under high temperatures during flowering period in pearl millet (*Pennisetum glaucum* L. (R.) Br.). *Field Crops Res*. **171**: 41–53.

Hanna WW (1989) Characteristics and stability of a new cytoplasmic-nuclear male-sterile source in pearl millet. *Crop Sci.* **29:** 1457-1459.

Hanna WW (1992) Utilization of germplasm from wild species. In: *Decertified Grasslands: Their Biology and Management*. Academic Press, London, UK, pp 251-257.

Harinarayana G and KN Rai (1989) Use of pearl millet germplasm and its impact on crop improvement in India. In: Collaboration on genetic resources: summary proceedings of a joint ICRISAT/NBPGR (ICAR) workshop on germplasm exploration and evaluation in India. Nov 14-15, 1988, ICRISAT, Patancheru, India, 89-92 p.

Harinarayana G, S Appa Rao and MH Mengesha (1988) Prospects of utilizing genetic diversity in pearl millet. In: Paroda *et al.* (eds.) *Genetic Resources, Indian Perspective*. NBPGR, New Delhi, India, pp 170-182.

Harlan JR and JMJ de Wet (1971) Towards a rational classification of cultivated plants. *Taxon* **20:** 509–517.

Hay FR, RS Hamilton, BJ Furman, HD Upadhyaya, KN Reddy and SK Singh (2013) Cereals. In: MN Normah, HF Chin, BM Reed (eds.) *Conservation of tropical plant species*. Springer, New York, USA, pp. 293-316.

IBPGR and ICRISAT (1993) Descriptors for pearl millet (*Pennisetum glaucum* (L.) R. Br.). IBPGR, Rome, Italy and ICRISAT, Patancheru, India.

Klopfenstein CF and RC Hoseney (1995) Nutritional properties of sorghum and the millets. In: DAV Dendy (ed.) *Sorghum and millets: chemistry and technology*. American Association of Cereal Chemistry (AACC), St. Paul, MN, USA, pp. 125-168.

Krishnamurthy L, R Serraj, KN Rai, CT Hash and AJ Dakheel (2007) Identification of pearl millet [*Pennisetum glaucum* (L.) R. Br.] lines tolerant to soil salinity. *Euphytica* **158:** 179–188.

Kulkarni VN, KN Rai, AJ Dakheel, M Ibrahim, M Hebbara and V Vadez (2006) Pearl millet germplasm adapted to saline conditions. *SAT eJournal* **2:** 1-4.

Kumar AK and S Appa Rao (1987) *Diversity and utilization of pearl millet germplasm*. In: JR Witcombe and SR Beckerman (eds.) Proceedings of the International Pearl Millet Workshop, 7-11 April 1986. ICRISAT Centre, India, pp 69-82.

Manga VK and OP Yadav (1997) Development of a new male sterile line CZMS 44A of pearl millet. *Crop Improv.* **24:** 125-126.

Mathur PN (2012) Global strategy for the *ex situ* conservation of pearl millet and its wild relatives. Global Crop Diversity Trust, Rome, Italy.

Mathur PN, S Appa Rao, RC Agrawal, MH Mengesha and RS Rana (1993) Evaluation of pearl millet germplasm Part-1. NBPGR-ICRISAT collaborative programme, National Bureau of Plant Genetic Resources, New Delhi 110 012, India.

Mengesha MH, S Appa Rao and CR Reddy (1990) Characteristics and potential uses of some genetic stocks of pearl millet in the world collection. *Indian J. Plant Genet. Res.* **3:** 1-7.

Monyo ES, SA Ipinge, S Mndolwa, N Mangombe and E Chintu (1996) The potential of local landrace varieties in pearl millet improvement. In K Leuschner, CS Manthe CS (eds.) Drought-tolerant crops for southern Africa: proceedings of the SADC/ICRISAT regional Sorghum and pearl millet Workshop, 25-29 July 1994, Gaborone, Botswana. ICRISAT, Andhra Pradesh, India, 153-162 p.

Murty BR, MK Upadhyaya and PL Manchanda (1967) Classification and cataloguing of a world collection of genetic stocks of *Pennisetum*. *Indian J. Genet.* **27:** 313-394.

Obilana AB, ES Monyo and SC Gupta (1997) Impact of germplasm improvement in sorghum and pearl millet: Developing country experiences. In: *Proceedings of the International Conference on Genetic Improvement of Sorghum and Pearl Millet*. 23-27 September 1996, Lubbock, Texas, USA.

Parthasarathy Rao P, PS Birthal, BVS Reddy, KN Rai and S Ramesh (2006) Diagnostics of sorghum and pearl millet grains-based nutrition in India. *Int. Sorghum Millets Newslett.* **46:** 93–96.

Peacock JM, P Soman, R Jayachandran, AU Rani, CJ Howarth and A Thomas (1993) Effect of high surface soil temperature on survival in pearl millet. *Exp. Agric.* **29**: 215-225.

Radhamani J, A Pandey, K Srinivasan and V Tyagi (2011) Conserving millet genetic resources in India. *Proc. Indian Natl. Sci. Acad.* **77:** 295-304.

Rai KN, AK Kumar, DJ Andrews, AS Rao, AGB Raj and JR Witcombe (1990) Registration of 'ICTP 8203' pearl millet. *Crop Sci*. **30:** 959.

Rai KN, CT Hash, AK Singh and G Velu (2008) Adaptation and quality traits of a germplasm-derived commercial seed parent of pearl millet. *Plant Genet. Res. Newslett.* **154:** 20–24.

Rai KN, HT Patil, OP Yadav, M Govindaraj, IS Khairwal, B Cherian, BS Rajpurohit, AS Rao, H Shivade and MP Kulkarni (2014) Notification of crop varieties and registration of germplasm: Pearl millet variety 'Dhanashakti'. *Indian J. Genet. Plant Breed.* **74:** 405-406.

Rai KN, OP Yadav, M Govindaraj, WH Pfeiffer, HP Yadav, BS Rajpurohit, HT Patil, A Kanatti, A Rathore, AS Rao and H Shivade (2016) Grain iron and zinc densities in released and commercial cultivars of pearl millet *(Pennisetum glaucum). Indian J. Agric. Sci.* **86:** 11-16.

Rai KN, S Appa Rao and KN Reddy (1997) Pearl millet. In D Fuccillo, L Sears, P Stapleton (eds.) Biodiversity in Trust, Conservation and use of Plant genetic Resources in CGIAR Centers, Cambridge University Press, Cambridge CB2 IRP, United Kingdom, pp 243-258.

Reddy KN, NK Rao and MI Ahmed (2004) Geographical patters of diversity in pearl millet germplasm from Yemen. *Genet. Resour. Crop Evol.* **51:** 513-517.

Shannon CE and W Weaver (1949) The mathematical theory of communication. Univ. Illinois Press, Urbana.

Sharma R, HD Upadhyaya, S Sharma, VL Gate and C Raj (2015) Identification of new sources of resistance to multiple pathotypes of *Sclerospora graminicola* in the pearl millet mini core germplasm collection. *Crop Sci.* **55:** 1–10.

Sharma R, HD Upadhyaya, SV Manjunatha, KN Rai, SK Gupta and RP Thakur (2013) Pathogenic variation in the pearl millet blast pathogen *Magnaporthe grisea* and identification of resistance to diverse pathotypes. *Plant Dis.* **97:** 189-195.

Singh BB and N Jika (1988) Five pearl millet genepools in Niger. *Plant Genet Resour. Newslett.* **73-74:** 29-30.

Singh SD, DJ Andrews and KN Rai (1987) Registration of ICML 11 rust resistant pearl millet germplasm. *Crop Sci.* **27:** 367-368.

Singh SD, JP Wilson, SS Navi, BS Talukdar, DE Hess and KN Reddy (1997) Screening techniques and sources of resistance to downy mildew and rust in pearl millet. Research Bulletin No. 48. ICRISAT, Patancheru, AP, India, p 30.

Singh SD, SB King and PM Reddy (1990) Registration of five pearl millet germplasm sources with stable resistance to downy mildew. *Crop Sci.* **30:** 1164.

Thakur RP and SB King (1988) Registration of four ergot resistant germplasms of pearl millet. Crop Sci. **28:** 382.

Thakur RP, KN Rai, SB King and VP Rao (1993) Identification and utilization of ergot resistance in pearl millet. In Research Bulletin No. 17. ICRISAT, Patancheru, AP, India, p 40.

Thakur RP, KN Rai, VP Rao and AS Rao (2001) Genetic resistance of pearl millet male-sterile lines to diverse Indian pathotypes of *Sclerospora graminicola*. *Plant Dis.* **85:** 621-626.

Thakur RP, SB King, KN Rai and VP Rao (1992) Identification and utilization of smut resistance in pearl millet. In Research Bulletin No. 17. ICRISAT, Patancheru, AP, India, p 39.

Upadhyaya HD and CLL Gowda (2009) Managing and enhancing the use of germplasm – strategies and methodologies. Technical Manual No. 10., ICRISAT, Patancheru, AP, India, p 236.

Upadhyaya HD, CLL Gowda, KN Reddy and S Singh (2009b) Augmenting the pearl millet [*Pennisetum glaucum* (L.) R. Br.)] core collection for enhancing germplasm utilization in crop improvement. *Crop Sci.* **49:** 573-580.

Upadhyaya HD, CT Hash, S Senthilvel, RK Varshney, DA Hoisington, KN Rai, KN Reddy, RP Thakur and S Chandra (2006) Development of composite collection and genotyping of pearl millet [*Pennisetum glaucum* (L.) R. Br.]. Poster presented in the Generation Challenge Program Annual Research Meeting, 12-16 September, Sao Paulo, Brazil.

Upadhyaya HD, D Yadav, KN Reddy, CLL Gowda and S Singh (2011) Development of pearl millet mini core collection for enhanced utilization of germplasm. *Crop Sci.* **51:** 217-223.

Upadhyaya HD, KN Reddy and CLL Gowda (2007a) Pearl millet germplasm at ICRISAT gene bank – status and impact. *SAT eJournal* **3:** 1-5.

Upadhyaya HD, KN Reddy, CLL Gowda, MI Ahmed and S Singh (2007b) Agroecological patterns of diversity in pearl millet [*Pennisetum glaucum* (L.) R. Br.] germplasm from India. Indian *J. Plant Genet. Resour.* **20:** 178-185.

Upadhyaya HD, KN Reddy, MI Ahmed and CLL Gowda (2010) Identification of gaps in pearl millet germplasm from Asia conserved at the ICRISAT genebank. *Plant Genet. Resour. Characterization Utilization* **8:** 267-276.

Upadhyaya HD, KN Reddy, MI Ahmed and CLL Gowda (2012a) Identification of gaps in pearl millet germplasm from East and Southern Africa conserved at the ICRISAT genebank. *Plant Genet. Resour. Characterization Utilization* **10:** 202-213.

Upadhyaya HD, KN Reddy, MI Ahmed, CLL Gowda and B Haussmann (2009b) Identification of geographical gaps in the pearl millet germplasm conserved at ICRISAT genebank from West and Central Africa. *Plant Genet. Resour. Characterization Utilization* **8:** 45-51.

Upadhyaya HD, KN Reddy, S Singh, CLL Gowda, MI Ahmed and S Ramachandran (2014b) Latitudinal patterns of diversity in the world collection of pearl millet landraces at the ICRISAT genebank. *Plant Genet. Resour. Characterization Utilization* **12:** 91-102.

Upadhyaya HD, KN Reddy, S Singh, CLL Gowda, MI Ahmed and V Kumar (2014a) Diversity and gaps in *Pennisetum glaucum* subsp. *monodii* (Maire) Br. germplasm conserved at the ICRISAT genebank. *Plant Genet. Resour. Characterization Utilization* **12:** 226-235.

Upadhyaya, HD and R Ortiz (2001) A mini core collection for capturing diversity and promoting utilization of chickpea genetic resources in crop improvement. *Theor. Appl. Genet.* **102:** 1292-1298.

Upadhyaya, HD, KN Reddy, MI Ahmed, N Dronavalli and CLL Gowda (2012b) Latitudinal variation and distribution of photoperiod and temperature sensitivity for flowering in the world collection of pearl millet germplasm at ICRISAT genebank. *Plant Genet. Resour. Characterization Utilization* **10:** 59–69.

Velu G, KN Rai, V Muralidharan, VN Kulkarni, T Longvah and TS Raveendran (2007) Prospects of breeding biofortified pearl millet with high grain iron and zinc content. *Plant Breed.* **126:** 182-185.

Williams RJ (1984) Downy mildews of tropical cereals. *Adv. Plant Pathol.* **2:** 1-103.

Wilson JP, GW Burton, JD Zongo and IO Dicko (1991) Disease resistance and morphogenic traits of pearl millet landraces from south Burkina Faso. *Crop Sci*. **31:** 641-645.

Yadav OP (2004) CZP 9802–a new drought-tolerant cultivar of pearl millet. *Indian Farming* **54:** 15-17.

Yadav OP and FR Bidinger (2007) Utilization, diversification and improvement of landraces for enhancing pearl millet productivity in arid environments. *Ann. Arid Zone* **46:** 49-57.

Yadav OP and KN Rai (2013) Genetic improvement of pearl millet in India. *Agric. Res.* **2:** 275-292.

Yadav OP, E Weltzien-Rattunde and FR Bidinger (2003) Genetic variation for drought response among landraces of pearl millet (*Pennisetum glaucum*). *Indian J. Genet.* **63:** 37-40.

Yadav OP, KN Rai and SK Gupta (2012) Pearl Millet: Genetic Improvement for Tolerance to Abiotic Stresses. In: Improving Crop Resistance to Abiotic Stress. N. Tuteja, S. S. Gill and R. Tuteja (eds.). Wiley VCH Verlag GmbH & Co. KGaA, pp. 261-288.

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# On-farm Status and Collection of Rice (*Oryza sativa* L.) Genetic Resources of Sikkim Himalayas

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Exploration trips were conducted to rice growing belts of Sikkim for collection and assessing on-farm status of rice landraces. Total of 52 traditional rice landraces collected along with record of passport data, features of cultivar and other aspects related to its cultivation and use. Inferences have been drawn based on observations on-field and interviews with local people regarding factors influencing rice diversity and reasons for their depletion. Probable strategies for conservation and maintenance of these landraces for their sustainable use have been discussed.

**Key Words: Rice landraces, Genetic erosion, On-farm status, Northeastern India**

## Introduction

Half of the planet's population consumes rice (*Oryza sativa* L.) as staple food. It has played a key role in human nutrition and culture for the past 10,000 years. The human population is expected to reach 9.6 billion by 2050, suggesting the need to increase rice production which could feed the burgeoning human population. Rice is one of the most important food crops of India being grown in an area of 43.95 million ha with production and productivity of 106.54 million tonnes and 2239 kg/ha respectively, during 2013-14 (Anonymous, 2014a). Traditional rice cultivars are known for their valuable alleles which inevitably are the source material for development of new lines and tailoring the genotypes to withstand the impact of stresses as a result of climate change. Heterogeneous microclimate is a feature of hilly ecosystems where genetic variability and on-farm conservation of traditional varieties is a source of genes for rice improvement (Ikeda *et al.*, 1994; Rai 2007). Various workers have studied on-farm status of the rice diversity of Himalayan regions (Agnihotri and Palni, 2007; Mehta, 2010; Rana, 2009 and Sultan and Rao, 2013). The entire Northeastern region of India is known worldwide for its rice diversity (Singh *et al.,* 2006; Ngachan *et al.*, 2011; Choudhury *et al*., 2014). Sikkim is a small beautiful hill state of Northeastern India and is a biodiversity hotspot in Eastern Himalayan region. Rice is the most important staple food of the local people as inferred from the epiphet "Denzong" means the valley of rice. It is cultivated in 11.16 (000' ha) with production of 20.26 (000' tonnes) and productivity of 1815.74 kg/ha (Anonymous, 2014b). Scanty literature is available on rice germplasm of Sikkim (Kapoor *et al*., 2014; Roy *et al*., 2015). Rapid change in land use practices and land cover of various agro-ecosystems has resulted in loss of genetic resources. Due to limited conservation and information on the available rice germplasm in the state, it is prerogative to explore knowledge of the existing landraces and the factors affecting genetic diversity. This study was done with the objective to (a) explore the on-farm status of rice diversity (b) factors causing genetic erosion and (c) suggest conservation strategies for sustainable use.

## Materials and Methods

### *Description of Study Area*

Sikkim has a total geographical area of 7,096 sq Km which lies between latitudes 27º5'N to 20º9'N and longitudes 87º59'E to 88º56'E. Due to mountain barriers of Northeast India and the influence of Bay of Bengal, it is also one of the wettest regions in the Himalayan belt. The state receives an annual rainfall of 2000 mm to 4000 mm. July is the wettest month and rainfall is heavy and well distributed during the months of May to September. The hottest months are July and August and coldest are December and January. Sikkim's agro-ecological systems are divided in to lower hills consisting of tropical (300-500 m) and sub-tropical regions (500-

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1500 m), midhills (1500-2000 m), high hills (2000-5000 m) and very high hills (above 5000 m). The state is multiethnic. Eighty percent of the population lives in rural areas where agriculture plays a dominant role in the state economy with the total cultivable land by around 68,000 hectares (12% of the total geographical area). Moreover, the choice of crop is mostly consumption oriented and system of cultivation has established in low input, low risk, low yield technology because the primitive forms of agriculture is still most dominant.

## Data and Sample Collection

Exploration trips were conducted during the year 2012 and 2013 to all the rice cultivated areas of Sikkim viz., East, West, North and South Sikkim (Figure 1). Samples were collected directly from the household along with passport data such as collector name, vernacular name of variety, latitude, longitude, elevation, common name, unique feature, frequency of occurrence, sampling method, habitat and other pertinent information collected for each sample. Seed sample of each accession were collected only once to avoid duplication. Validation of the cultivar identity was done by observing the seed colour and other morphological characters which have been authenticated by interviewing local farmers, extension functionaries and other local sources. Complete information on the rice landraces were collected by interviews with the farmers. We used structured unstructured and participatory approach for generating information related to its cultivation, past history and unique feature of the cultivar. Help of extension functionaries, village level workers and Panchayat heads were also taken for better interaction with the farmers and understanding of local knowledge. Due to the scattered inhabitation of the population in the remote locations and non-availability of data related to the approximate area under different rice cultivars, the inferences drawn are based on observations and interview with the local people from where the germplasm collected. Our data set contains information on the types of rice varieties the farmer grows, reasons for selection of the variety, unique features and limitations of the variety, common morphological traits in variety, maintenance of variety, seed management systems and probable reasons for depletion of genetic resources. The rice samples were collected from an elevation ranges from 475 m to 1758 masl.


**Fig. 1. Areas surveyed during rice germplasm collection in Sikkim**

## Results

### *Description of Rice Growing Belts of Sikkim*

Rice is predominantly cultivated in terraces with narrow and serpentine fields (*Dhan Bari*) both in high altitude (*lekh* area) and low altitude areas (*owl* area). Rice is cultivated during *kharif* season (June-July) by traditional method. Rice cultivation is mainly done under rainfed lowland conditions where irrigation source is usually located at the topmost field from where water flows to another adjacent field with gravity flow. Seedlings are generally transplanted at 30 days after sowing but often delayed up to 45 days due to lack of good rainfall and scarcity of water in water streams (*Jhoras*) for impounding rice fields. For better seedling establishment, chopping top portion of seedlings is a common practice in late transplanting. Five to six seedlings are transplanted per hill. Rice monocropping is a common practice. The paddy fields are occupied with the crop up to November month owing to late maturity of cultivars. In upland rice cultivation direct seeding is done (only in small patches of North Sikkim) on slopy areas under slash and burn system. Transplanting at higher altitudes is done during second week of May to escape cold spells which arrive

**Table 1. Rice genetic resources under cultivation in Sikkim Himalayas**

| S.No. | Cultivars and major cultivated areas | Frequency | Distribution | Farmers' criteria of nomenclature |
|---|---|---|---|---|
| North Sikkim | | | | |
| 1 | Red Zomu | Rare | Localized | Morphological |
| 2 | Nepal Dhan | Rare | Localized | Place of origin |
| 3 | Zomu | Rare | Localized | Morphological |
| 4 | Takmaru | Rare | Localized | Morphological |
| 5 | Takmaru I | Rare | Localized | Morphological |
| 6 | Zokub | Rare | Localized | Morphological |
| 7 | Chini Dhan | Occasional | Localized | Place of origin |
| 8 | Taichung | Occasional | Localized | Morphological |
| 9 | Dharmali | Occasional | Localized | Morphological |
| 10 | Kalo Dhan | Occasional | Localized | Morphological |
| West Sikkim | | | | |
| 11 | Pahelo Dalle | Rare | Localized | Morphological |
| 12 | Tauli | Rare | Localized | Morphological |
| 13 | Brihmphool | Rare | Localized | Morphological |
| 14 | Dudhey Juari | Rare | Localized | Morphological |
| 15 | Pusa Sugandha –II | Rare | Widespread | Govt. seed (Sarkari Dhan) |
| 16 | Sijali | Rare | Localized | Morphological |
| 17 | Bhangeri | Rare | Localized | Morphological |
| 18 | Ram Saree | Occasional | Localized | Morphological |
| 19 | Dhutraj | Occasional | Widespread | Morphological |
| 20 | Ram Bhog | Occasional | Localized | Morphological |
| 21 | Japani | Occasional | Localized | Morphological |
| 22 | Kalsati | Occasional | Widespread | Morphological |
| 23 | Lal Bacchi | Occasional | Widespread | Morphological |
| 24 | Musuli | Occasional | Widespread | Morphological |
| 25 | Katti | Frequent | Widespread | Morphological |
| 26 | Marsee | Frequent | Widespread | Morphological |
| 27 | Kataka | Frequent | Widespread | Morphological |
| 28 | Champey | Frequent | Widespread | Morphological |
| 29 | Doodh Kalam | Frequent | Widespread | Morphological |
| 30 | Kaley Bungay | Frequent | Localized | Morphological |
| 31 | Khimti | Frequent | Widespread | Morphological |
| 32 | Timburay | Frequent | Widespread | Morphological |
| South Sikkim | | | | |
| 33 | Chari Nangrey | Occasional | Widespread | Morphological |
| 34 | Yeidehi | Occasional | Widespread | Morphological |
| East Sikkim | | | | |
| 35 | Phool Patta | Rare | Localized | Morphological |
| 36 | Kalo Nunia | Occasional | Localized | Morphological |
| 37 | Zornali | Occasional | Widespread | Morphological |
| 38 | Chirakey | Occasional | Widespread | Morphological |
| 39 | Dhanase | Occasional | Localized | Morphological |
| All over Sikkim | | | | |
| 40 | KRH-2 | Occasional | Widespread | Govt. seed (Sarkari Dhan) |
| 41 | PD-10 | Frequent | Widespread | Govt. seed (Sarkari Dhan) |
| 42 | VL-82 | Frequent | Widespread | Govt. seed (Sarkari Dhan) |
| 43 | VL-85 | Frequent | Widespread | Govt. seed (Sarkari Dhan) |
| 44 | Tabrey | Frequent | Widespread | Morphological |
| 45 | Jhapaka | Frequent | Widespread | Morphological |
| 46 | Attey | Abundant | Widespread | Morphological |
| 47 | Thulo Attey | Abundant | Widespread | Morphological |
| 48 | Sano Attey | Adundant | Widespread | Morphological |
| 49 | Krishna Bhog | Abundant | Widespread | Morphological |
| South and West Sikkim | | | | |
| 50 | Chari Masini | Occasional | Widespread | Morphological |
| 51 | Anandhi | Frequent | Widespread | Morphological |
| 52 | Ram Zeera | Occasional | Widespread | Morphological |
| 53 | Sano Khamti | Frequent | Widespread | Morphological |
| East and South Sikkim | | | | |
| 54 | Bael Butty | Rare | Localized | Morphological |
| 55 | Tulasi | Abundant | Widespread | Morphological |
| West and East Sikkim | | | | |
| 56 | Phouryal | Frequent | Widespread | Morphological |
| East, South and West | | | | |
| 57 | Khamti | Frequent | Widespread | Morphological |

early in these areas. Majority of the rice fields are located below 1000 m asl (37.30%), 13.90% at 1000-1200 masl, 27.90% at 1200-1500 masl and 20.90% at a height more than 1500m asl. Direct seeded rice cultivation known as *Ghaiya Dhan* was a common practice in many rainfed areas of Sikkim, but this practice have been relinquished by farmers some 20-25 years back.

### *Genetic Variability*

A total of 57 rice accessions were assembled which comprised of 52 local and 5 improved high yielding varieties (HYVs) (Table 1). Rice varieties presently under cultivation in Sikkim comprise of local landraces, obsolete varieties and improved high yielding varieties including hybrid. HYVs constitute around 12% of the total rice varieties grown. Varieties released for hilly areas like *VL-62* and *VL-85* were found under cultivation at higher altitude. Obsolete varieties like *Taichung* is still grown in small patches of North Sikkim.

Majority of the landraces were late maturing (150-175 days). Large variation observed in plant height which varied from 69.9 cm to 140 cm.

*Kalsati* bears long grains. About half of the total landraces were of short grain type. *Anandhi*, *Taichung* and *Timburey* are of broad grain type. Seeds of *Ramzeera* were smallest resembling to cumin. *Rambhog, Marsee, Kaley Bungey, Chirakey, Ramsaree, Musuli, Krishnabhog, Phool patta* and *Lal Bacchi* bear long panicles while *Tabrey, Taichung* and *Zornalli* bear short panicles. Maximum 1000 grain weight recorded in *Anandhi* (33.0 g).

*Tulasi* and *Champey Dhan* are aromatic and tasty rice mostly used as powdered rice, stuffed rice and Sathua. *Phouryal*, *Japani, Kalsati* and *Attey* for preparing *sale roti* (a local dish), *Dhanase* for chewda; *Tabrey*, *Brihmphool* and *Tulasi* for popped rice; *Krishnabhog, Kalonunia and Brihmphool* are known for their aroma and quality. Most popular rice cultivars are *Krishnabhog, Attey, Kalo nunia, Jhapaka, Tulasi, Champey* or *Champasari and Khamti.*

*Attey* is the most widely grown cultivar having two variants *Sano Attey* and *Thulo Attey* having small and bold type grains respectively. These are cultivated up to 1500 m asl. *Namfafzu, Dhanase, Takmaru, Dharmali, Juari Dhan, Red Zomu, Sirkey* are grown in high altitudes. *Sano* Attey is known for lodging resistance.

**Table 2. Factors responsible for replacement and erosion of rice landraces in Sikkim Himalayas**

| Factors responsible | Percentage |
|---|---|
| Lack of manpower | 40% |
| Area diversion to cash crops (Changes in cropping system) | 25% |
| Lack of irrigation sources | 10% |
| Low income | 10% |
| High yielding varieties (HYVs) | 10% |
| Low yield | 5% |

Awns were shorter in *Chirakey*, *Krishnabhog, Taichung* and *Takmaru* whereas highly conspicuous in *Brihmphool* and *Champey*.

The farmers' nomenclature of rice varieties is based on morphological characters and on location where these have been cultivated and found. Cultivars with small sized grains are annoted with *Sano* and *Masino* Dhan while long type with *Thulo* or *Lamo* Dhan. Cultivars like *Kaley Bungey, Kalo nunia* denotes black coloured lemma of the grain. *Tabrey* denotes the awns which are inseparable from rice grains. Largest variation in landraces recorded in West Sikkim.

Varietal mixture is one of the feature of local seed systems in Sikkim. Various varietal seed mixtures of *Brihmphool + Attey, Tulasi + Attey, Ananadhi + Attey* were found during seed collection.

### Factors Affecting On-farm Rice Diversity and Varietal Choice

Agriculture in Sikkim is of subsistence type where rice is grown mostly for household consumption and some special rice varieties are grown for market purpose**.** Factors responsible for replacement and depletion of rice landraces in Sikkim are shown in Table 2**.** Agro ecology is the major factor affecting varietal preference. The important variable under it is the altitude and the irrigation availability. Irrigation sources were more in the low altitude areas where farmers cultivate two to three rice varieties. The high yielding varieties are mostly cultivated by progressive and socially well farmer who have access to modern technologies through Government interventions (state Agriculture departments and ICAR). The land availability with the farmer decides the number of landraces to be grown. Farmer cultivates rice varieties according to their needs as some rice varieties are grown primarily for processing and preparation of special products. Kalo nunia, a short grain aromatic type grown primarily for market purpose. Characters most preferred

by the farmers in rice cultivar include tallness, high biomass yield, disease tolerance, grains with medium amylose content. Cultivar mixture has been observed to be a common feature in farmer's field. In one way it maintains the diversity in field and buffering against biotic and abiotic stresses. The seed supply system is basically local where the farmer retains the farm saved seed. The straw is also sold at a premium price in local market mostly used as fodder. A variety has both desirable and undesirable characters associated with it, thereby no single variety meets all the farmer needs (Bellan and Brush, 1994).

### *Erosion of Genetic Diversity*

Based on interviews with the farmers and local heads probable reasons have been recorded for depletion of rice landraces, the inferences drawn are:

Rice cultivation in hills is a labour intensive operation. Shortage of agricultural laborers and manpower identified as the most important reason. Agricultural labourers have diverted to better employment opportunities due to which large stretches of rice fields remain uncultivated.

Lack of adequate irrigation sources for rice fields due to drying of temporary water streams *(Jhoras*) have decreased the area under the crop.

Due to small landholdings, farmers have diverted rice fields to cultivation of remunerative cash crops mainly vegetable production which are more profitable than paddy cultivation. Rice fields have been replaced by beans, cole crops, seasonal vegetables and other local vegetables which fetches premium price in market. Consistent poor yield of local cultivars adds to this crop shift.

Aromatic rice, which fetches premium price in the market has been slowly gaining acreage in the region. Farmers who were earlier cultivating 2-3 rice cultivars have now prefer aromatic rice due to its better market value and high demand.

In some areas introduction of HYVs have significantly decreased the area under local landraces. For example a drastic reduction in cultivable area of one of the high altitude rice cultivar *Phudungey* have been noticed and it could not be collected during our exploration. Similar trend recorded for *Brihmphool*, *Phouryal*, *Dharmali* and *Sirkey*. *Phouryal Dhan* was grown in lower Soreng belts of West Sikkim some years back but have been replaced by HYVs. Mehta *et al.* (2014) have reported replacement of approximately three dozens of traditional varieties from different agro-eco-niches by HYVs in Garhwal and Uttarakhand.

Sikkim has been declared as organic state where crops like ginger, large cardamom and buckwheat have gained prime importance due to their promotion under organic brand. Rice remained neglected in this regard. Factors like drought and erratic rainfall, poor yield of local varieties, availability of HYVs and change in crop sequences have also been reported by Mehta *et al.*, (2014) for erosion of traditional varieties. Rana *et al*. (2009) and Mehta *et al*. (2014) have studied the factors responsible for genetic erosion of the western Himalayan and Garhwal region of Uttarakhand respectively.

## Discussion

Cultivation of genetically diverse landraces and mixture of different cultivars are most suitable cropping system in highly heterogeneous climatic and edaphic conditions of Himalayan region to averse risk of crop failure and maintain crop diversity on-farm. The reason seems most plausible for preponderance of traditional farming, is the remote and far flung inhabitation where input supply and technology flow is slow and strongly influenced by cultural and economic factors. Being a small state, having small cultivable area, variation in rice cultivars is noteworthy. These landraces are a result of conservation efforts and selection by the farmers and natural forces. Diversity in cultivated landraces depends mainly on farmer's choice being influenced by cultural and social factors. This demands for periodical exploration trips usually in period of 5 years for updating rice diversity status. There is ample scope for improvement of these landraces by employing pureline selection and hybridization with elite rice varieties. Improvement in post harvesting processing of quality rice along with better market linkages ensure remunerative prices to the farmers. The communities actively involved in diversity conservation should be compensated through allocation of funds to promote germplasm maintenance which can further be sustained through better seed storage facilities on-farm. In this era of Intellectual Property Rights (IPR) regime, new laws such as Protection of Plant Varieties and Farmers Rights Act (PPV&FRA act 2001), have been enforced in India to safeguard farmer's rights over their variety. Awareness regarding benefits of protecting rice varieties and benefit sharing accruing out of it

will motivate farmers towards conservation. Adoption of high yielding rice varieties are must for increasing rice productivity in the region but adoption should be in line with the conservation of the replaced landraces. Maintenance and conservation efforts at community or village level would be more appropriate rather than at individual level, especially in hilly ecosystems. In this aspect, maintenance and updating of biodiversity registers have been initiated by Sikkim State Biodiversity Board (Department of Forests, Sikkim).

Categorization of landraces as widespread common, widespread rare, localized-common and localized rare based on pattern of occurrence in the region indicates their population structure (Khatiwada *et al.*, 2000). Rare localized cultivars viz., Red Zomu, Zokub, Nepal Dhan, Zomu, Takmaru, Pahelo dale, Tauli, Brihmphool, Dudhey Juari, Bael Buty, Sijali and Bhangeri needs immediate protection due to their small population size. Conservation *in-situ* ensures that the ongoing processes of evolution and adaptation of crops to their environments are maintained within farming systems and conservation at ecosystem level, species and genetic level. *Ex-situ* conservation efforts are equally important in these marginal areas due to their small population size, chances of erosion are more thereby maintaining seeds of accessions under controlled conditions and regenerating periodically will conserve it for long time. ICAR Research Complex for NEH Region, Sikkim Centre has initiated steps in this regard and have been maintaining and evaluating these landraces for different traits. For a biodiversity hotspot like Sikkim, it is important to have institution linkage for effective conservation plans by involving local, national or international bodies for effectively plan and execute conservation strategies. This will be successful only through greater participation of local leaders and farmers.

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## References

Agnihotri RK and LMS Palni (2007) On-farm conservation of landraces of rice (*Oryza sativa* L.) through cultivation in the Kumaun region of Indian central Himalaya. *J. Mt. Sci*. **4**: 354-360.

Anonymous (2014a) Agricultural Statistics at a glance, 2014, Directorate of Economics and Statistics, Ministry of Agriculture, Govt. of India (http://www.dacnet.nic.in/eands).

Anonymous (2014b) ENVIS Centre Sikkim. http://www.sikenvis.nic.in/Database/RiceSikkim_4078.aspx.

Bellon MR and S Brush (1994) Keepers of maize in Chiapas, Mexico. *Economic Botany* **48**:196-209.

Brush SB (1995) *In-situ* conservation of landraces in centres of crop diversity. *Crop Sci.* **35:** 346-354.

Choudhury B, ML Khan and S Dayanandan (2013) Genetic structure and diversity of indigenous rice (*Oryza sativa*) varieties in the Eastern Himalayan region of Northeast India. *Springer Plus* **2**: 228. http://www.springerplus.com/content/2/1/228.

Choudhury DR, N Singh, AK Singh, S Kumar, K Srinivasan, RK Tyagi, A Ahmad, NK Singh and R Singh (2014) Analysis of genetic diversity and population structure of rice germplasm from North-Eastern region of India and development of a core germplasm set. *http://journals.plos.org/plosone/article* id=10.1371/journal.pone.0113094.

Das B, S Sengupta, SK Parida, B Roy, M Ghosh, M Prasad and TP Ghose (2013) Genetic diversity and population structure of rice landraces from Eastern and North Eastern states of India. *BMC Genet.* **14**: 71.

Hore DK (2005) Rice diversity collection, conservation and management in northeastern India. *Genet. Resour. Crop Evol*. **52**: 1129-1140.

Ikeda R, DA Vaughan and N Kobayashi (1994) Landraces and wild relatives of rice (*Oryza sativa* L.) as a source of useful genes. *JIRCAS Int. Symp. Ser (Japan)* **2**:104-111.

Kapoor C, RK Avasthe, P Chettri, R Gopi, H Kalita and SV Ngachan (2014) Indigenous Sikkim rice cultivars. *ICAR News: A Science and Technology Newsletter* **20(3):** July-September, 2014 pp 7.

Khatiwada SP, BK Baniya, DK Rijal, CL Paudel, RB Rana, P Chaudhary, PR Tiwari, MP Upadhhyay, YR Pandey and A Mudwari (2000) Population genetic structure. Nepal. In: D Jarvis, B Sthapit and L Sears (ed.). Conserving Agricultural Biodiversity *In situ*: A Scientific basis for Sustainable Agriculture. International Plant Genetic Resources Institute, Rome, Italy, pp. 134-138.

Mehta PS, KS Negi, AK Trivedi and SN Ojha (2010) On-farm management of rice varieties in Kumaon Himalayas of Uttrakhand. *Indian J. Plant Genet. Resour*. **23**: 126-131.

Mehta PS, SN Ojha, KS Negi, , SK Verma, A Rayal and RK Tyagi (2014) On-farm status of rice (*Oryza sativa* L.) genetic resources in Garhwal Himalaya of Uttarakhand, India. *Genet. Resour. Crop Evol*. (Published online: 02 Apil 2014).

Myers N (1994) Protected areas-protected from a greater what? *Biodiversity and Conservation,* **3**: 411-418.

Ngachan SV, AK Mohanty and A Pattanayak (2011) Status paper on rice in North East India. http://www.rkmp.co.in. Rice Knowledge Management Portal (RKMP) Directorate of Rice Research, Rajendranagar, Hyderabad 500030.

Paroda RS and SS Malik (1990) Rice genetic resources, its conservation and use in India. *Oryza* **27:** 361-369.

PPVFRA (Protection of Plant Varieties and farmers' Rights Act, 2001. http://plantauthority.gov.in/)

Rai M (2007) Rice culture in agriculture. An Indian perspective. In: PK Agrawal, JK Landha, RK Singh, C Devkumar and B Hardy (ed.) Science technology and trade for peace and prosperity. Proceedings 26th International Rice Research Conference, New Delhi, pp 89-99.

Rana JC, KS Negi, SA Wani, S Saxena, K Pradheep, A Kak, SK Pareekh and PA Sofi (2009) Genetic resources of rice in Western Himalayan region of India: current status. *Genet. Resour. Crop Evol*. **56**: 963-973.

Roy S, A Banerjee, B Mawkhleing, AK Misra, A Pattanayak, GD Harish, SK Singh, SV Ngachan and KC Bansal (2015) Genetic diversity and population structure in aromatic and quality rice (*Oryza sativa* L) landraces from North-Eastern India. http://journals.plos.org/plosone/article id=10.1371/journal.pone.0129607.

Singh PK, MN Mishra, DK Hore and MR Verma (2006) Genetic divergence in lowland rice of North eastern region of India. *Communications in Biometry and Crop science* **1**: 35-40.

Sultan SM and LVS Rao (2013) Germplasm collection from last remnants of rice landrace genetic diversity in high altitude areas of Kashmir Himalayas. *Int. J. Conserv. Sci.* **4**: 467-476.

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# Assessment of Distinctiveness, Uniformity and Stability of Finger Millet (*Eleusine coracana*) Varieties

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Characterization of 12 finger millet varieties was carried out over two seasons using morphological descriptors given by the Bioversity International, 1985. Data was recorded on 28 morphological characters (13 visual and 15 measurable). Among thirteen visually assessed characters five were monomorphic, six were dimorphic and two were polymorphic in nature. No intra-varietal variation was observed for any of the visual characteristics and expression of characters in different varieties remained same for the two consecutive years confirming the uniformity and stability of varieties. COYD (combined over years distinctiveness) analysis with respect to 15 measurable traits indicated that all the varieties were absolutely distinct from each other. COYD analysis was supported with MJRA (Modified Joint Regression Analysis) in which the slope of the MJRA curve and regression probability was calculated, which indicated that characteristics under study were not completely independent but interacting with each other as well as with the environment. COYU (combined over years uniformity) analysis revealed that all the varieties were more or less uniform for measurable characteristics.

**Key Words: Combined over years distinctiveness, Combined over years uniformity, DUS, Finger millet**

## Introduction

*Eleusine coracana* commonly known as finger millet or *ragi* is an alloteraploid cereal **(**2n= 4X=36, genome composition = AABB), that includes two distinct subspecies: subsp. *coracana* (finger millet) and subsp. *africana* (wild finger millet). It is an important staple food in semi-arid regions of East Africa and Southern India. India has enormous diversity of millets in both cultivated and wild species. Obviously there is a need of consolidated system in the country to protect such vast variability present in the species and proper sharing of benefits derived out of them. In order to achieve this goal, India ratified the agreement on Trade Related aspects of Intellectual Property Rights agreement (TRIPs) in 1994. Under the Article 27.3(b) of the TRIPs agreement, member countries are required to grant protection to plant varieties either by a patent or by an effective system of *sui generis* protection, or a combination of these two. In this context, Government of India has chosen a *sui generis* system and passed an Act in 2001, named as Protection of Plant Varieties and Farmers' Rights Act (PPV&FR). The PPV&FR Act, 2001 encourage public/ private investment in research and development of new plant varieties by giving protection to different categories of plant varieties against unauthorized multiplication of seeds or propagating materials for a specific period (Anonymous 2001). The plant varieties must fulfill the distinctiveness, uniformity and stability (DUS) criteria for protection under the Act. Hence there is a need to characterize finger millet varieties especially farmers' varieties on the basis of DUS criteria and to register them with PPV&FR Authority on behalf of the farmers otherwise valuable germplasm which is being conserved by the farmers could be lost or misused without giving any beneficial advantage to the farmer. However, DUS descriptors for finger millet were not developed at the time of conducting the experiment. Hence, this is the first report taken up with the objective to develop DUS descriptors for characterisation and identification of finger millet varieties.

## Materials and Methods

The experimental material consisted of 12 genotypes of finger millet varieties comprising 10 released varieties and two farmer's varieties. The trials were conducted during *kharif* season of 2012 and 2013 in randomized block design with three replications. Each variety was accommodated in a plot of two rows of 3 m length spaced at 25 cm row to row and 15 cm plant to plant

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distance. The observations were recorded at different growth stages as per the descriptors for finger millet (The International Board for Plant Genetic Resources, 1985) from 30 plants or parts of 30 plants, which were divided among 3 replications (10 plants per replication). Finger millet varieties were distinguished by recording observations on 28 morphological characteristics which included 13 visually assessed characteristics and 15 measurable characteristics.

For determining distinctiveness in case of visually assessed characters, differences between two varieties were considered clear if the expression of one or more characteristics fell into two different states. Analysis of measurable characteristics was carried out with the help of DUSNT software (Watson *et al.*, 1998) comprising of COY-D (combined over years distinctiveness) for analysis of distinctiveness (Anonymous 2008a) and COY-U (combined over years uniformity) for analysis of uniformity (Anonymous 2008b). $F_1$ and $F_2$ ratios were calculated for COY-D analysis of 15 measurable characteristics which were variety MS by variety × year MS and variety × year MS by variety × replication MS, respectively. Modified Joint Regression Analysis (MJRA) was also used as a part of COY-D analysis. This MJRA model took account of systematic annual increases or decreases in character expression across all varieties by fitting extra terms, one for each year, in the analysis of variance. Each term represented the linear regression of the observations for the year against the variety means over all years, as described by Digby (1979).

The COY-U analysis involves ranking references and candidate varieties by the mean value of the characteristics. Standard deviation (SD) of each variety is taken and the mean SD of the most similar varieties is subtracted. A candidate variety will be considered to be sufficiently uniform, if using a COYU analysis the standard deviation for each characteristic is not greater than the mean standard deviation for the same characteristic in comparable varieties at 1% probability level. COYU test compared within-plot standard deviations between varieties, hence, if there is no variation within-plot, this test cannot be performed.

Phenotypic coefficient of variation (PCV), genotype coefficient of variation (GCV), heritability and genetic advance were calculated from the pooled data of the measurable characters over two years and compared for the analysis of stability.

## Result and Discussion

Out of thirteen visually assessed characteristics five were monomorphic, six were found to be dimorphic and two were polymorphic (Table 2). These visually assessed characteristics did not show any variation in their states of expression over two years of study. Further, no off type plants were observed hence, these characters were considered to be uniform. Expression of each characteristic was found to be stable in both the two years for the respective varieties, thus confirming their consistency and stability. The stability of visually assessed characteristics can be attributed to a low genotype × environment interaction in their expression. This is due to the fact that most of the visually assessed characters are controlled by single or two genes with simple dominant or recessive relationship.

Data recorded on 15 measurable characteristics were subjected to COY-D statistical method at 0.1 percent level of significance. Each variety at a time was considered to be a candidate variety and compared to rest of the varieties as reference varieties to obtain a pair-wise distinctiveness matrix using COYD analysis (Table 3). Analysis revealed that all the varieties showed distinctiveness with respect to each other.

**Table 1. Details of finger millet varieties studied with their pedigree and source**

| S.No. | Genotype | Parentage | Year of release | Released from |
|---|---|---|---|---|
| 1 | VL 149 | VL 204 × IE - 882 | 1991 | Vivekananda Parvatiya Krishi Anusandhan Shala, Almora |
| 2 | GE 149 | Germplasm | – | Champawat, Lauhaghat |
| 3 | HR 911 | UAS-1 × IE 927 | 1986 | U.A.S. Bangalore |
| 4 | VR 708 | VMEC-36 | 1998 | Agril Res. Station, Vizianagaram (AP) |
| 5 | Indaf 8 | Hullu bele × IE 929 | 1988 | U.A.S. Bangalore |
| 6 | PES 110 | Selection from IC germplasm | 1985 | G.B.P.U.A.T. Pantnagar |
| 7 | PRM-1 | Pureline selection from Ekeshwar local | 2006 | G.B.P.U.A.T. Pantnagar |
| 8 | PRM-2 | Selection from Tehri local | 2010 | G.B.P.U.A.T. Pantnagar |
| 9 | PES 400 | Selection from IC germplasm | 1986 | G.B. .U.A.T. Pantnagar |
| 10 | PR202 | Sarada × EC 158 | 1976 | U.A.S. Bangalore |
| 11 | Parvati | Farmer's Variety | – | Kanalchhin, Gundoli Gaon, Pithoragarh |
| 12 | Gausari | Farmer's Variety | – | Dabri Tholdar block, Tehri Garhwal |

**Table 2. Morphological characterization of visually assessed characteristics in finger millet genotypes**

| Varieties | Characteristics | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Anthocyanin colouration of first leaf sheath | Node pigmentation | Growth habit | Leaf sheath pubescence | Node pubescence | Spike exertion | Discontinuity of spikelets on finger | Varieties | Anther Colour | Athocyanin pigmentation of glume | Spike shape | Finger branching | Pericarp persistence after threshing | Seed coat colour |
| VL 149 | Absent | Purple | Erect | Absent | Absent | Complete | Absent | VL 149 | Purple | Present | Open | Absent | Partial | Brown |
| GE 149 | Absent | Green | Erect | Absent | Absent | Complete | Absent | GE 149 | Yellow | Absent | Semi Compact | Absent | Persistent | Brown |
| HR 911 | Absent | Green | Erect | Absent | Absent | Complete | Absent | HR 911 | Yellow | Absent | Semi Compact | Absent | Partial | Brown |
| VR 708 | Absent | Green | Erect | Present | Absent | Complete | Absent | VR 708 | Yellow | Absent | Semi Compact | Present | Partial | Brown |
| Indaf 8 | Absent | Green | Erect | Absent | Absent | Complete | Absent | Indaf 8 | Yellow | Absent | Semi Compact | Present | Partial | Brown |
| PES 110 | Absent | Green | Erect | Present | Absent | Complete | Absent | PES 110 | Yellow | Absent | Semi Compact | Absent | Persistent | Brown |
| PRM-1 | Absent | Green | Erect | Present | Absent | Complete | Absent | PRM-1 | Yellow | Absent | Compact | Present | Partial | Brown |
| PRM-2 | Absent | Brown | Erect | Absent | Absent | Complete | Absent | PRM-2 | Yellow | Present | Compact | Present | Partial | Dark Brown |
| PES 400 | Absent | Purple | Erect | Present | Absent | Complete | Absent | PES 400 | Purple | Present | Compact | Absent | Partial | Brown |
| PR202 | Absent | Green | Erect | Present | Absent | Complete | Absent | PR202 | Yellow | Absent | Semi Compact | Absent | Persistent | Brown |
| Parvati | Absent | Green | Erect | Present | Absent | Complete | Absent | Parvati | Yellow | Absent | Compact | Absent | Partial | Brown |
| Gausari | Absent | Green | Erect | Absent | Absent | Complete | Absent | Gausari | Yellow | Absent | Semi Compact | Present | Partial | Brown |
| | Monomorphic | Polymorphic | Monomorphic | Dimorphic | Monomorphic | Monomorphic | Monomorphic | | Dimorphic | Dimorphic | Polymorphic | Dimorphic | Dimorphic | Dimorphic |

COY-D analysis of 15 measurable characters using MJRA model was also carried out (Table 4). The MJRA analysis revealed that the $F_1$ ratio which takes into account the variety mean square and variety × year mean square was significant for all the measurable characters under the study except for peduncle length, finger number and maturity period at 1% probability. It indicated that there was less role of environment in expression of all the characters except peduncle length, finger number and maturity period. The significant $F_2$ ratio was observed only for the characters, namely leaf length, head emergence and days to flowering at 1% probability, indicating that the pattern of distinctiveness was inconsistent over the two years of experiment for these characters or in other words environment played a greater role in determining the pattern of distinctiveness among the varieties for these characters thereby, limiting their scope to establish varietal distinctiveness among the present set of varieties. However, the present experimental material with respect to these characters should be tested for one more year or at different locations before arriving at conclusions.

The slope of the MJRA curve and regression probability was calculated for both the years by the DUSNT software which indicated that characteristics under study were not completely independent rather they are interacting with each other as well as with the environment, which emphasize the need for testing the present experimental material in another year and other location.

Measurable characteristics were subjected to COYU analysis for assessment of uniformity using DUSNT software (Table 5) but standard deviation was found to be zero for finger width, days to head emergence, days to flowering, maturity period and 1000 seed weight among all the varieties. Hence, there was no variation within the plot for these characters as a result COYU test could not be performed.

A perusal of Table 5 indicated that out of 12 finger millet varieties, 3 varieties VL 149, HR 911 and PES 110 showed uniformity for all the nine characters followed by GE 149 and VR 708 for eight characters. In addition to this, non-uniformity was observed for majority of the characters but within the acceptable limits of UPOV criteria (Anonymous 2008b). Such non uniformity has been reported earlier in *sorghum* varieties for some characters in local varieties by COYU analysis in maize (Singh *et al.*, 2013), in French bean (Mall and Chawla,

**Table 3. Pair-wise distinctness matrix of finger millet varieties obtained from COYD analysis**

| S.No. | Candidate varieties | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | VL 149 | - | D | D | D | D | D | D | D | D | D | D | D |
| 2 | GE 149 | D | - | D | D | D | D | D | D | D | D | D | D |
| 3 | HR 911 | D | D | - | D | D | D | D | D | D | D | D | D |
| 4 | VR 708 | D | D | D | - | D | D | D | D | D | D | D | D |
| 5 | Indaf 8 | D | D | D | D | - | D | D | D | D | D | D | D |
| 6 | PES 110 | D | D | D | D | D | - | D | D | D | D | D | D |
| 7 | PRM-1 | D | D | D | D | D | D | - | D | D | D | D | D |
| 8 | PRM-2 | D | D | D | D | D | D | D | - | D | D | D | D |
| 9 | PES 400 | D | D | D | D | D | D | D | D | - | D | D | D |
| 10 | PR202 | D | D | D | D | D | D | D | D | D | - | D | D |
| 11 | Parvati | D | D | D | D | D | D | D | D | D | D | - | |
| 12 | Gausari | D | D | D | D | D | D | D | D | D | D | D | - |
| Overall distinctness | | D | D | D | D | D | D | D | D | D | D | D | D |

**Table 4. Combined over years distinctiveness analysis of 15 measurable characteristics in finger millet varieties using Modified Joint Regression Analysis (MJRA)**

| | Flag leaf: Length (cm) | Flag leaf: Width (cm) | Leaf: Length (cm) | Leaf: Width (cm) | Leaf sheath length (cm) | Plant height (cm) | Peduncle length (cm) | Spike length (cm) | Finger number | Finger length (cm) | Finger width (cm) | Time of spike emergence (Days) | Time of flowering (Days) | Maturity period (Days) | 1000 seed weight (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Year MS | 2.203 | 0.003 | 185.589 | 0.008 | 132.031 | 35.900 | 2.229 | 0.312 | 0.151 | 4.488 | 0.003 | 3.249 | 3.379 | 34.032 | 0.009 |
| Variety MS | 91.645 | 0.146 | 66.156 | 0.074 | 9.828 | 104.701 | 6.619 | 20.029 | 0.909 | 15.122 | 0.035 | 417.564 | 415.958 | 548.564 | 0.145 |
| Var. year MS | 4.786 | 0.003 | 10.679 | 0.003 | 1.909 | 17.183 | 1.727 | 0.669 | 0.252 | 0.505 | 0.001 | 21.367 | 19.946 | 125.127 | 0.017 |
| F1 Ratio | 19.147 | 49.907 | 6.195 | 25.425 | 5.149 | 6.093 | 3.832 | 29.955 | 3.611 | 29.930 | 36.711 | 19.543 | 20.855 | 4.384 | 8.490 |
| Var.Rep MS | 1.960 | 0.001 | 1.950 | 0.004 | 1.582 | 6.488 | 1.596 | 1.187 | 0.086 | 0.397 | 0.001 | 6.125 | 6.262 | 129.871 | 0.020 |
| F2 Ratio | 2.442 | 2.188 | 5.476 | 0.699 | 1.207 | 2.648 | 1.082 | 0.564 | 2.913 | 1.271 | 0.802 | 3.489 | 3.185 | 0.963 | 0.861 |
| Between SE | 0.893 | 0.022 | 1.334 | 0.022 | 0.564 | 1.692 | 0.537 | 0.334 | 0.205 | 0.290 | 0.013 | 1.887 | 1.823 | 4.567 | 0.053 |
| Within SE | 0.572 | 0.015 | 0.570 | 0.026 | 0.513 | 1.040 | 0.516 | 0.445 | 0.120 | 0.257 | 0.014 | 1.010 | 1.022 | 4.652 | 0.058 |
| MJRA Slope | 0.990 | 1.045 | 1.212 | 1.103 | 1.155 | 0.819 | 1.209 | 0.956 | 0.891 | 0.894 | 1.046 | 1.011 | 1.012 | 0.396 | 1.044 |
| MJRA Slope | 1.010 | 0.954 | 0.778 | 0.897 | 0.837 | 1.173 | 0.774 | 1.044 | 1.105 | 1.106 | 0.953 | 0.989 | 0.988 | 1.513 | 0.955 |
| Regr F Val | 0.020 | 1.130 | 3.503 | 3.568 | 1.215 | 1.988 | 1.679 | 0.587 | 0.313 | 4.871 | 0.837 | 0.024 | 0.028 | 13.094 | 0.152 |
| Regr Prob | 89.155 | 31.273 | 9.075 | 8.824 | 29.622 | 18.894 | 22.415 | 46.116 | 58.792 | 5.182 | 38.183 | 87.880 | 87.058 | 0.470 | 70.496 |

$$F_1 \text{ ratio} = \frac{\text{Variety MS}}{\text{Variety} \times \text{Year MS}} \quad F_2 \text{ ratio} = \frac{\text{Variety} \times \text{Year MS}}{\text{Variety} \times \text{replication MS}}$$

2012), and in basmati and aromatic rice varieties (Patra *et al.*, 2010 and Joshi *et al*., 2011).

High heritability and high genetic advance were observed for flag leaf: blade width (94.57%, 26.50%), spike length (76.59%, 33.30%), finger length (92.01%, 43.62%), time of spike emergence (97.06%, 24.89%) and time of flowering (97%, 23.72%). This implies that, these traits were not much influenced by environmental factors which in turn indicated that these traits are mostly controlled by additive and /or additive × additive gene interactions. High heritability coupled with moderate genetic advance was observed for characters like flag leaf: blade length (83.64%, 19.61%), leaf: blade length (92.18%, 14.50%), leaf: blade width (68.28%, 12.14%), leaf sheath length (61.91%, 15.06%), finger width (75.51%, 11.02%) and maturity period (90.03%, 12.57%). Moderate heritability (36.24%) coupled with low genetic advance (4.8%) was observed for peduncle length. Hence both additive and non-additive gene effects are equally important in the inheritance of these traits. Panse and Kharagonkar (1957) suggested that, if the heritability of a particular character is high in a specific environment coupled with low genetic advance, then it could be mainly due to non-additive gene action. In the present study high

**Table 5. Combined over years uniformity analysis of nine measurable characteristics in finger millet varieties**

| Candidate Variety | Flag leaf: Blade Length (cm) | Flag leaf: Blade Width (cm) | Leaf Blade Length (cm) | Leaf Blade Width (cm) | Leaf sheath length (cm) | Plant height (cm) | Peduncle length (cm) | Spike length | Finger number |
|---|---|---|---|---|---|---|---|---|---|
| VL 149 | 90 | 109 | 102 | 91 | 87 | 82 | 86 | 90 | 105 |
| GE 149 | 100 | 114 | 101 | 109 | 110 | 94 | 114:1 | 80 | 105 |
| HR 911 | 101 | 100 | 92 | 97 | 84 | 100 | 101 | 87 | 112 |
| VR 708 | 103 | 94 | 107 | 160+1 | 84 | 97 | 109 | 88 | 102 |
| Indaf 8 | 93 | 103 | 93 | 106 | 135+1 | 106 1 | 114:1 | 108 | 114 |
| PES 110 | 98 | 115 | 87 | 92 | 86 | 93 | 99 | 115 | 91 |
| PRM-1 | 114:1 | 87 | 116 1 | 86 | 98 | 102 | 102 | 116 2 | 93 |
| PRM-2 | 96 | 90 | 96 1 | 69 | 92 | 96 | 89 | 81 | 117 1 |
| PES 400 | 95 | 83 | 88 | 104 | 103 | 114 1 | 95 | 114 1 | 62 |
| PR202 | 95 | 95 | 119:1 | 93 | 107 1 | 106 | 93 | 103 | 103 |
| Parvati | 115:2 | 107 | 98 | 89 | 113 1 | 91 | 96 | 82 | 85 |
| Gausari | 99 | 104 | 101 | 104 | 102 | 118 1 | 101 | 136:2 | 111 1 |

Symbols :
+ -SD exceeds over-years criterion after 2 years with probability 0.01
: - SD not yet acceptable after 2 years with probability 0.05
1,2,3 - the number of occasions the within-years SD exceeds the UPOV criterion

**Table 6. Genetic parameters for measurable characters in finger millet**

| Characters | Variance | | | Coefficient of variation | | | Heritability (h2) % | Genetic advance (%) |
|---|---|---|---|---|---|---|---|---|
| | Genotypic variance | Phenotypic variance | Environmental variance | GCV (%) | PCV (%) | ECV (%) | | |
| Flag leaf: Blade length (cm) | 13.940 | 16.691 | 2.727 | 10.40 | 11.38 | 4.60 | 83.64 | 19.61 |
| Flag leaf : Blade width (cm) | 0.025 | 0.026 | 0.001 | 13.33 | 13.71 | 3.19 | 94.57 | 26.50 |
| Leaf: Blade length (cm) | 10.697 | 11.622 | 0.906 | 7.32 | 7.63 | 2.13 | 92.18 | 14.50 |
| Leaf: Blade width (cm) | 0.010 | 0.014 | 0.004 | 7.00 | 8.48 | 4.78 | 68.28 | 12.14 |
| Leaf sheath length (cm) | 1.350 | 2.180 | 0.830 | 9.31 | 11.83 | 7.30 | 61.91 | 15.06 |
| Plant height (cm) | 16.201 | 19.977 | 3.836 | 3.35 | 3.72 | 1.63 | 80.75 | 6.2 |
| Peduncle length (cm) | 0.699 | 1.925 | 1.231 | 3.85 | 6.39 | 5.11 | 36.24 | 4.8 |
| Spike length (cm) | 3.040 | 3.970 | 0.929 | 18.49 | 21.13 | 10.22 | 76.59 | 33.30 |
| Finger number | 0.143 | 0.200 | 0.057 | 5.09 | 6.02 | 3.21 | 71.59 | 8.9 |
| Finger length (cm) | 2.483 | 2.699 | 0.215 | 22.10 | 23.04 | 6.51 | 92.01 | 43.62 |
| Finger width (cm) | 0.006 | 0.007 | 0.002 | 6.31 | 7.27 | 3.59 | 75.51 | 11.02 |
| Time of spike emergence (days) | 76.988 | 79.263 | 2.342 | 12.27 | 12.45 | 2.14 | 97.06 | 24.89 |
| Time of flowering (days) | 154.613 | 74.772 | 77.093 | 16.81 | 11.69 | 11.87 | 97 | 23.72 |
| Maturity period (days) | 44.607 | 49.595 | 4.941 | 6.43 | 6.78 | 2.14 | 90.03 | 12.57 |
| 1000 Seed weight (g) | 0.023 | 0.037 | 0.014 | 5.34 | 6.72 | 4.09 | 63.03 | 8.92 |

heritability coupled with low genetic advance was observed for plant height (80.75%, 6.2%), peduncle length (36.24%, 4.8%) finger number (71.59%, 8.9%) and 1000 seed weight (63.03%, 8.92%) as shown in Table 6. It may be concluded from the present investigation that the morphological descriptors used in this study are sufficient to discriminate the present set of varieties.

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## References

Anonymous (2001) Manual of Patent Examining Procedures. 8th Edn. pp. 21-50.

Anonymous (2008 a) International union for the protection of New varieties of plants-Associated document-examining distinctness. In: *UPOV TGP/9/1*. 1-36.

Anonymous (2008 b) International union for the protection of New varieties of plants-Associated document- examining uniformity. In: *UPOV TGP/10/1*. 1-14.

Digby PGN (1979) Modified joint regression analysis for incomplete variety environment data. *J. Agric. Sci.* **93:** 81-86.

Joshi DC, PK Shrotria, R Singh, MK Srivastava, HS Chawla (2011) Assessment of RAPD and ISSR marker systems for

establishing distinctiveness of forage Sorghum (*Sorghum bicolor* (L.) Moench) varieties as additional descriptors for plant variety protection. *Indian J. Genet.* **71:** 1-11.

Joshi DC, PK Shrotria, R Singh, and HS Chawla (2009) Assessment of Distintiveness, Uniformity and Stability of Sorghum (*Sorghum bicolor* (L.) Moench) varieties based on morphological descriptors. *Indian J. Genet.* **69:** 1-11.

Mall N and HS Chawla (2012) DUS characterization of French bean (*Phaseolus vulgaris* L.) varieties based on morphological descriptors. *Crop Imp.* **39:** 18-25.

Panse VG and H Kharagonkar (1957) Genetics of quantitative characters in relation to plant breeding. *Indian J. Genet.* **17:** 318-327.

Patra N, RC Agrawal and HS Chawla (2010) Assessment of distinctiveness, uniformity and stability of basmati rice (*Oryza sativa* L.) varieties based on morphological descriptors. *Indian J. Genet.* **70:** 48-57.

Singh R, N Mall and HS Chawla (2013) Establishing distinctiveness in local maize (*Zea mays* L.) varieties using RAPD marker as additional descriptor for protection under PPV & FR Act. Indian *J. Plant Genetic Res.* **26:** 50-56

Watson S, J Ward and STC Weathurup (1998) Distinctness, uniformity and stability trait (DUST) analysis system. UPOV TWC 16/9.

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# Comparisons of Major Biochemical Constituents and Mineral Composition in Six Cultivars of Aromatic Rice in Manipur

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Six aromatic rice varieties collected from the valley districts of Manipur were analyzed for their morpo-physiochemical and mineral composition of the grains. All aromatic rice varieties had protein contents in the range of 4.25 to 7.54%, soluble sugar from 7.5 to 10.27 mg/g and total phenolics in the range of 0.52 to 3.90 mg/g with the highest phenol content recorded in Ching Chakhao (3.9 mg/g). Starch was uniformly distributed to all the aromatic varieties ranging from 34.23 to 37.79%. Higher content of K (680.37), Ca (70.17), Mg (34.43), Mn (1.73) and Zn (4.37) was recorded in Chakhao while higher content in Cu and Fe was equally shared by Ching Chakhao and Chakhao Anganba. Among the varieties, Lamsang Chakhao recorded minimum amounts of K (408) while, Chakhao Amubi recorded least amounts in Ca (11.30), Mg (32.63) and Cu (0.57), Phumlou Chakhao in Mn (0.87) and Zn (0.57 mg/100 g). Trace amounts of Co were detected in all the aromatic varieties with the highest being observed in Lamsang Chakhao (0.43 mg/100 g).

**Key Words: Aromatic rice, Biochemical constituents, Mineral composition, Physiochemical**

## Introduction

There are several types of rice around the world, which are categorized on the basis of color like white rice, brown rice, red rice, black rice etc. Rice can also be classified as aromatic and fine (non-aromatic) rice on the basis of aroma.

Generally, the price of the aromatic rice is three to four times higher than that of the non-aromatic or ordinary rice varieties in the state. Although, rice is a rich source of carbohydrate, it contains moderate amounts of protein, fat and B vitamins (Fresco, 2005). Rice carbohydrate is mainly starch which is composed of amylose and amylopectin. As rice being the staple food for more than three billion people in Asia (Bhattacharjee *et al*., 2002), understanding of the biochemical and mineral composition of the different varieties of rice becomes imperative for improve breeding programmes. Moreover, it is generally assumed that aromatic rice is a good source of different phytochemicals (Asaduzzaman *et al*., 2013). These components are most likely involved in the reduction of degenerative human diseases due to their antioxidative and free radical scavenging properties (Basu *et al*., 2012). In recent years, there has been a global trend toward the use of phytochemicals from natural resources such as vegetables, fruits, oilseeds and herbs, as antioxidants and functional ingredients. Therefore, natural antioxidants from plant extracts especially from rice would be of considerable importance due to their safety and easy availability. Based on the above information, a research experiment was conducted to compare the physiological, biochemical and mineral composition of six genotypes of aromatic rice available in the valley districts of Manipur.

## Materials and Methods

The cultivars collected from the four valley districts were grown in the experimental field of the College of Agriculture. One hill of each genotype was transferred along with the field soil and raised in the plastic pots. First flowering, 50% flowering and 100% flowering were recorded. Plant height, number of tillers, number of panicles and panicle length were studied. Freshly harvested paddy samples in duplicate were manually dehulled and dried at 50ºC. While dehulling, it was attempted not to disturb the bran as far as possible. The grains were powdered and stored under reduced pressure until analysis. Crude protein was determined by estimating the total nitrogen (Kjeldahl method) in a Kel-Plus Supra-LX nitrogen auto analyzer following the procedure of Humphries (1956). Total soluble sugar was determined as per the method of Morris (1948).

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Starch and total phenols were estimated following the procedures of Hedge and Hofreiter (1962) and Bray and Thorp (1954). For evaluation of minerals, wet digestion method of Capar *et al*. (1978) was followed. K was estimated in a systronics-105 flame photometer. Ca, Mg, Fe, Zn, Mn, Cu and Co were analyzed in a Perkin Elmer Atomic Absorption Spectrophotometer, Analyst AA-200. Calibration curves of each element were prepared from standards of E. Merck Germany.

### Statistical Analyses

All data were analyzed by the Analysis of Variance (ANOVA) procedure using SPSS software version 10 (for windows). Dendrograms were generated using average linkage between groups. Interrelationships among traits values were estimated using the Pearson correlation coefficient.

### Results and Discussion

The physiological and yield parameters of the different cultivars are indicated in Table 1. First flowering and first 50% flowering was recorded in Lamsang Chakhao, however, early date of maturation was recorded in Chakhao Anganba (146 days) which was followed by Lamsang Chakhao (148 days). All the other varieties took 152 days to maturation. Chakhao was the shortest plant (112.7 cm), while Chakhao Amubi was the tallest with 127.2 cm high. Maximum length of panicle was recorded in Chakhao Amubi (26.5 cm) and Ching Chakhao (23.4cm) however, higher number of panicles were recorded in Phumlou Chakhao (8) and Chakhao (8). The biochemical composition of the genotypes is given in Table 2. Protein content ranged from 4.52 to 7.54% with a mean value of 6.49±0.49. These values were in agreement with the reports of Saikia *et al.* (2012) and Sompong *et al.* (2011). Starch content in rice is one of the most important criteria of rice quality in terms of cooking and gelling properties, especially the amylose fraction (Abu-Kwarteng *et al.*, 2003). Starch content in the local aromatic varieties ranged from 68.46 to 77.96% with a mean of 73.56±1.34. These values were in agreement with the report of Asaduzzaman *et al.* (2013) who reported starch content of six aromatic rice varieties in Bangladesh to be in the range of 63.193 to 72.60/100 g. Chakhao Amubi recorded higher content of soluble sugar (10.27 mg/g), followed by Phumlou Chakhao (8.85 mg/g) and Chakhao (8.77 mg/g). Total phenolic content ranged from 0.52 to 3.9 mg/g with maximum content being recorded in Ching Chakhao (3.90 mg/g). Except Ching chakhao, all the other varieties had very less total phenol content ranging from 0.52 to 1.15 mg/g with the least being recorded in Lamsang Chakhao. Variations in total phenol content among the aromatic

**Table 1. Important morphological observations in six cultivars of aromatic rice collected from the valley districts of Manipur**

| S. No. | Cultivar's Name | Date of Sowing | Date of Transplanting to the pod | 1ST Flowering | 50 % Flowering | Date of Harvesting | Total Duration in Maturity (days) | Plant height (cm) | Panicle Length (cm) | Panicle No. | No. of tillers |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Lamsang Chakhao | 03/07/10 | 04/08/10 | 24/09/10 | 03/10/10 | 19/11/10 | 148.0 | 122.2 | 21.3 | 7 | 8 |
| 2 | Ching Chakhao | 03/07/10 | 04/08/10 | 27/09/10 | 07/10/10 | 23/11/10 | 152.0 | 119.8 | 23.4 | 7 | 8 |
| 3 | Phumlou Chakhao | 03/07/10 | 04/08/10 | 26/09/10 | 04/10/10 | 23/11/10 | 152.0 | 120.5 | 22.3 | 8 | 10 |
| 4 | Chakhao Anganba | 03/07/10 | 04/08/10 | 03/10/10 | 10/10/10 | 17/11/10 | 146.0 | 122.2 | 21.2 | 6 | 7 |
| 5 | Chakhao | 03/07/10 | 04/08/10 | 27/09/10 | 12/10/10 | 23/11/10 | 152.0 | 112.7 | 22.6 | 8 | 9 |
| 6 | Chakhao Amubi | 03/07/10 | 04/08/10 | 28/09/10 | 13/10/10 | 23/11/10 | 152.0 | 127.2 | 26.5 | 7 | 7 |
| Mean± S.Em | | - | - | - | - | - | 150.33±1.09 | 120.77±1.93 | 22.88±0.80 | 7.17±0.31 | 8.17±0.48 |
| C.V. | | - | - | - | - | - | 1.77 | 3.91 | 8.55 | 10.5 | 14.31 |

**Table 2. Major biochemical constituents in six aromatic rice cultivars collected from valley districts of Manipur (Mean±SD)**

| S.No. | Cultivar name | % Protein (N%×6.25) | % Starch (in terms of glucose × 0.95) | Soluble sugars in terms of glucose (mg/g) | Phenolics in terms of catechol (mg/g) |
|---|---|---|---|---|---|
| 1 | Lamsang Chakhao | $4.25\pm1.29^{a}$ | $74.10\pm4.23^{a}$ | $7.50\pm0.50^{a}$ | $0.52\pm0.20^{a}$ |
| 2 | Ching Chakhao | $6.87\pm1.44^{b}$ | $68.46\pm3.88^{b}$ | $8.03\pm0.55^{a, b}$ | $3.90\pm0.20^{b}$ |
| 3 | Phumlou Chakhao | $7.54\pm2.18^{b}$ | $77.96\pm5.87^{c}$ | $8.85\pm0.80^{b}$ | $0.90\pm0.15^{c}$ |
| 4 | Chakhao Anganba | $6.12\pm1.60^{b}$ | $73.68\pm3.56^{a}$ | $7.60\pm0.56^{a}$ | $0.57\pm0.11^{a}$ |
| 5 | Chakhao | $7.07\pm2.34^{b}$ | $71.56\pm2.0^{a}$ | $8.77\pm0.78^{b}$ | $0.87\pm0.08^{d}$ |
| 6 | Chakhao Amubi | $7.08\pm1.96^{b}$ | $75.58\pm4.27^{a, c}$ | $10.27\pm0.97^{c}$ | $1.15\pm0.15^{e}$ |
| | Mean±S. Em | 6.49±0.49 | 73.56±1.34 | 8.50± 0.42 | 1.32±0.52 |
| | S.Ed± | 0.77 | - | 0.45 | 0.06 |
| | CD at 5% | 1.73 | 2.86 | 1.01 | 0.12 |
| | CD at 1% | 2.46 | 4.06 | 1.44 | 0.17 |

Note: Different letters in the column indicate significance at 5% level

**Table 3. Correlation matrix of four biochemical constituents among the six aromatic rice cultivars**

| | Protein | Starch | Phenolics | Sugars |
|---|---|---|---|---|
| Protein | – | 0.076 | 0.276 | .643 |
| Starch | | – | -0.717 | 0.359 |
| Phenolics | | | – | -.057 |
| Sugars | | | | – |

rice varieties were also reported by Asaduzzaman *et al*. (2013). These values were in agreement with the reports of Saikia *et al.* (2012). The lesser amount of biochemical constituents in different aromatic rice varieties might be due to none application of nitrogenous and other fertilizers as they had been subjected to the field soil only (Buresova *et al*., 2010).

The correlation coefficients among the biochemical constituents is shown in Table 3, however, none of the values were statistically correlated. Such observations were also reported in other studies (Eggum, 1979). The dendrogram (Fig. 2) indicated different groupings of the genotypes due to biochemical variations. Out of the 3 clusters, cluster-I consists of maximum number of genotypes (Lamsang Chakhao, Chakhao Anganba and Chakhao) while, cluster-II consists of 2 genotypes (Phumlou Chakhao and Chakhao Amubi) and cluster-III consist of only one genotype (Ching Chakhao). The separation of Ching Chakhao into a different cluster is justified due to the fact that it is the only genotype originated from the hills (Ching = Hills; Chakhao = Tasty rice) others are all valley originated.

Genotypes varied considerably in macro mineral composition (Table 4). K, Mg and Ca were the major elements found in all the genotypes. Higher content of K (680.37 mg/100 g), Mg (70.17 mg/100 g) and Ca (34.43 mg/100 g) were recorded in Chakhao, which was followed by Ching Chakhao (645.33 mg/100 g K, 64.97 mg/100 g Mg and 26.90 mg/100 g Ca) and Chakhao Anganba (643.33 K and 27.37 mg/100 g Ca).

Among the minor elements, Mn, Zn, Fe and Cu were found to be fairly uniformly distributed in all the genotypes (Table 4). Higher content of Mn (1.73 mg/100 g) and Zn (4.37 mg/100 g) was recorded in Chakhao, which was followed by Ching Chakhao (1.30 mg/100 g) and Chakhao Amubi in Mn (1.30 mg/100) and Chakhao Anganba in Mn (1.33 mg/100 g) and Zn (4.13 mg/100 g). Higher contents of approximately equal values of Cu and Fe were recorded in Ching Chakhao (4.63 and 33.87 mg/100 g) and Chakhao Anganba (4.63 and 33.17 mg/100 g), which was followed by Phumlou Chakhao in Cu (3.83 mg/100 g) and Chakhao (24.83 mg/100 g), Chakhao Amubi (23.97 mg/100 g) and Lamsang Chakhao (23.33 mg/g) in Fe. Trace amounts of Co were detected in all the aromatic varieties ranging from 0.10 to 0.43 mg/100 g with a mean of 0.21±0.05 with the highest being observed in Lamsang Chakhao (0.43 mg/100 g).

The variability observed in the mineral composition was neither restricted to the ecological zones from which they were collected nor peculiar to the colour of the varieties. The values of all the cultivars studied seemed to be elevated which may be due to the fact that the grains used for analyses were dehuled manually thereby most of the rice bran responsible for higher minerals was not disturbed (Pederson and Eggum, 1983). These findings were in agreement with the reports of Oko *et al.* (2012) and Anjum *et al.* (2007). Table 5 indicated correlation coefficients of 8 elements. Among the macro elements, Ca is found to be positively correlated with Mg, while K and Mg to Cu and Zn. The correlation with respect to Ca and Mg is very high reaching up to 84% ($p<0.01$). Similarly, the correlation coefficients between Mn and Zn is also very high (90%) indicating to be highly positively correlated ($p<0.01$). Correlations between K-Cu and Mg-Zn were also observed though of moderate degree.

**Table 4. Mineral content in six aromatic rice cultivars of Manipur (Mean±SD)**

| S. No. | Cultivar name | K (mg/100g) | Ca (mg/100g) | Mg (mg/100g) | Mn (mg/100g) | Zn (mg/100g) | Cu (mg/100g) | Fe (mg/100g) | Co (mg/ 100g) |
|---|---|---|---|---|---|---|---|---|---|
| 1 | Lamsang Chakhao | 408±12.17$^{a}$ | 24.07±1.02$^{a}$ | 58.47±2.10$^{a}$ | 1.03±0.06$^{a}$ | 2.37±0.15$^{a}$ | 4.30±0.50$^{a, b}$ | 23.33±2.27$^{a}$ | 0.43$^{a}$ |
| 2 | Ching Chakhao | 645.33±10.78$^{b}$ | 26.90±0.75$^{b}$ | 64.97±3.31$^{b}$ | 1.30±0.00$^{b}$ | 3.07±0.06$^{b}$ | 4.63±0.29$^{a}$ | 33.87±0.75$^{b}$ | 0.30$^{a, b}$ |
| 3 | Phumlou Chakhao | 578.67±10.07$^{c}$ | 22.0±0.70$^{a}$ | 44.00±2.65$^{c}$ | 0.87±0.06$^{c}$ | 0.57±0.06$^{c}$ | 3.83±0.38$^{b}$ | 32.93±0.38$^{b}$ | 0.10$^{b}$ |
| 4 | Chakhao anganba | 643.33±7.64$^{b}$ | 27.37±0.29$^{b}$ | 57.00±2.51$^{a}$ | 1.33±0.12$^{b}$ | 4.13±0.06$^{d}$ | 4.63±0.12$^{a}$ | 33.17±0.12$^{b}$ | 0.13$^{b}$ |
| 5 | Chakhao | 680.37±12.80$^{d}$ | 34.43±0.91$^{c}$ | 70.17±3.65$^{d}$ | 1.73±0.00$^{d}$ | 4.37±0.11$^{e}$ | 3.80±0.00$^{b, c}$ | 24.83±0.35$^{a}$ | 0.20$^{b}$ |
| 6 | Chakhao amubi | 582±12.17$^{c}$ | 21.30±0.46$^{a}$ | 32.63±0.23$^{e}$ | 1.30±0.00$^{b}$ | 2.80±0.00$^{f}$ | 3.07±0.06$^{d}$ | 23.97±0.76$^{a}$ | 0.10$^{b}$ |
| | Mean± S.Em | 589.62± 39.74 | 26.01± 3.13 | 54.54± 5.67 | 1.26±0.12 | 2.89±0.56 | 4.04±0.25 | 28.68±2.09 | 0.21±0.05 |
| | S. Ed± | 4.80 | 0.94 | 1.98 | 0.05 | 0.07 | 0.22 | 0.86 | 0.09 |
| | CD at 5% | 10.69 | 2.09 | 4.42 | 0.12 | 0.17 | 0.49 | 1.92 | 0.20 |
| | CD at 1% | 15.21 | 2.97 | 6.28 | 0.17 | 0.24 | 0.69 | 2.74 | 0.29 |

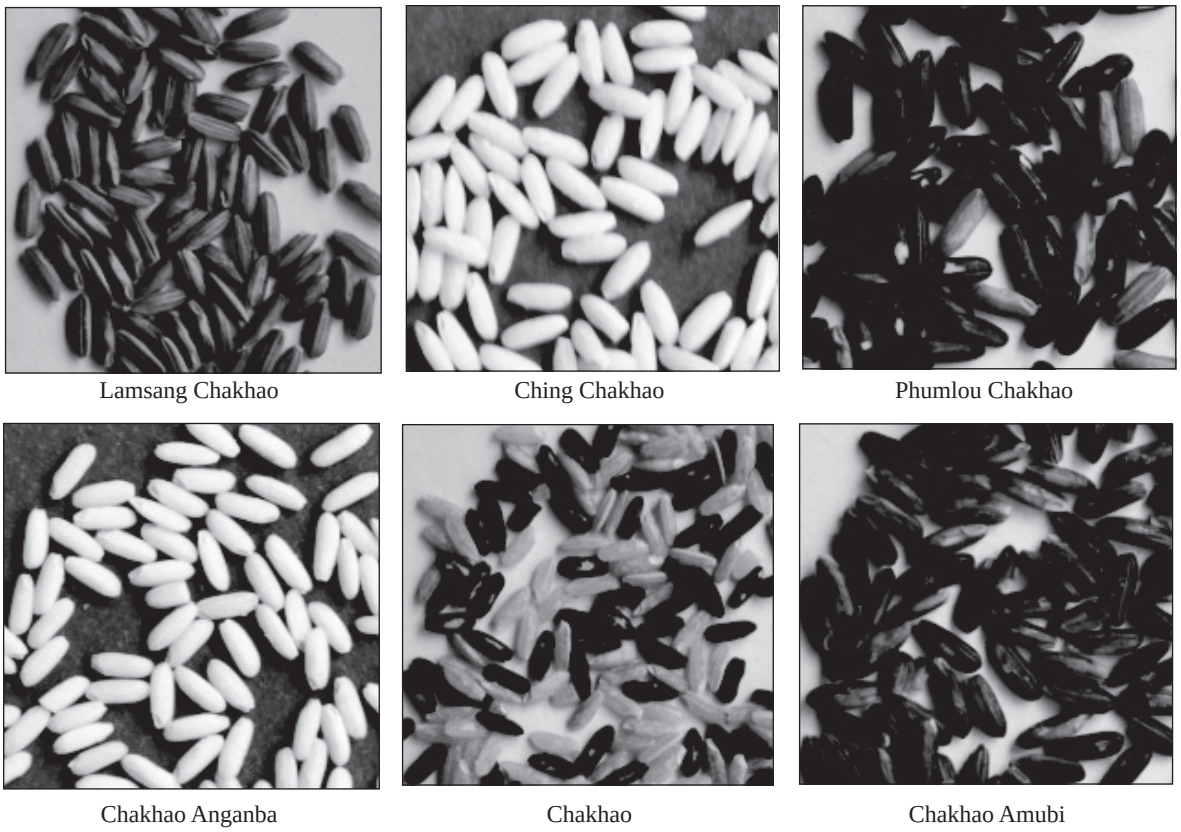


**Fig. 1. Photographs of the dehulled grains of six aromatic cultivars of rice collected from four valley districts of Manipur**

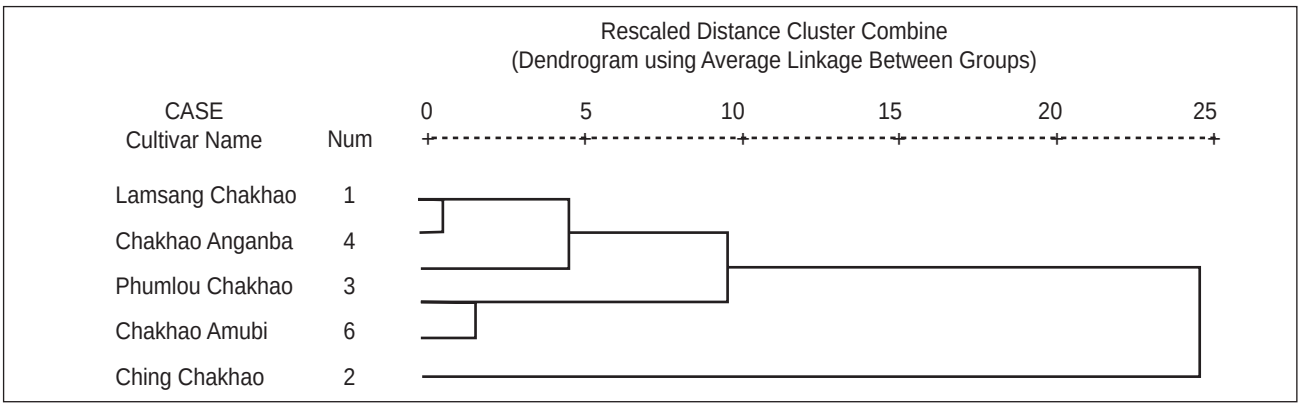


**Fig. 2. Dendrogram showing relationship among varieties in respect of 4 biochemical constituents**

The dendrogram at Fig. 3 indicated clusters of the genotypes due to variations in mineral composition. Out of the 2 clusters, cluster I consists of 4 genotypes, while cluster II consists of 2. Cluster I is the grouping of genotypes with superior mineral composition out of which genotype, Chakhao recorded highest values in K, Ca, Mg, Mn and Zn, while Ching Chakhao and Chakhao Anganba recorded highest values in Cu and Fe. Significant correlation among the mineral elements suggested that their inter-relationship must be considered, while selecting in a breeding program meant for the improvement of mineral content in rice (Oko *et al.*, 2012).

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**Table 5. Pearson correlation of eight elements among six aromatic rice cultivars**

| | Potassium | Calcium | Magnesium | Manganese | Zinc | Copper | Iron | Cobalt |
|---|---|---|---|---|---|---|---|---|
| Potassium | – | 0.649 | 0.601 | -0.152 | -0.072 | 0.809* | 0.436 | 0.660 |
| Calcium | | – | 0.836** | 0.489 | 0.493 | 0.606 | 0.209 | 0.301 |
| Magnesium | | | – | 0.626 | 0.723* | 0.623 | -0.030 | 0.588 |
| Manganese | | | | – | 0.895** | -0.073 | -0.253 | -0.097 |
| Zinc | | | | | – | 0.224 | -0.167 | 0.058 |
| Copper | | | | | | – | 0.580 | 0.492 |
| Iron | | | | | | | – | -0.290 |
| Cobalt | | | | | | | | - |

* Significant at 5% level; ** Significant at 1% level.

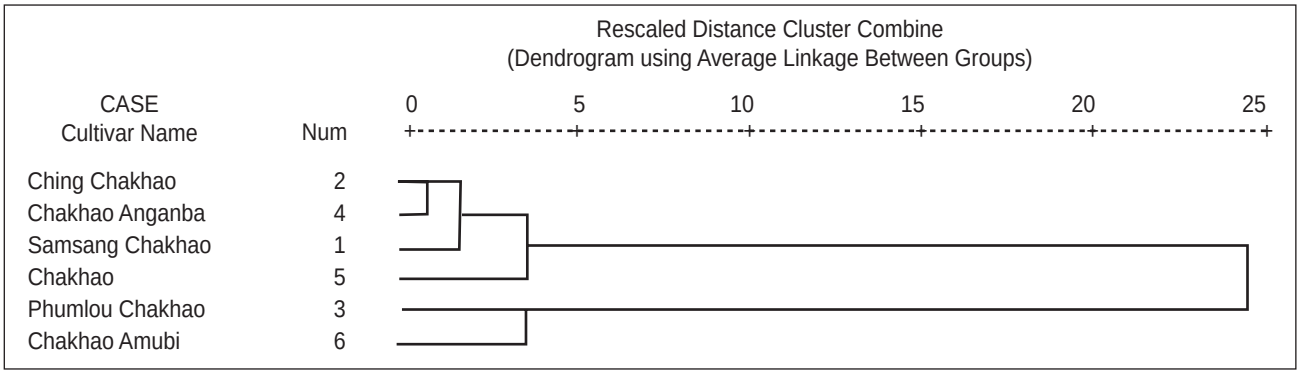


**Fig 3. Dendrogram showing relationship among varieties in respect of 8 mineral elements**

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## References

Abu-Kwarteng E, WO Ellis, I Oduro and JT Manful (2003) Rice grain quality: a comparison of local varieties with new varieties under study in Ghana. *Food Cont.* **14**: 507-514.

Anjum FM, I Pasha, MA Bugti and MS Butt (2007) Mineral composition of different rice varieties and their milling fractions. *Pakistan J. Agri. Sci.* **44**: 332-336.

Asaduzzaman Md, Md Emdadul Haque, Jiaur Rahman, SM Kamrul Hasan, MA Ali, MST Sorifa Akter and Maruf Ahmed (2013) Comparisons of physiochemical, total phenol, flavanoid content and functional properties in six cultivars of aromatic rice in Bangladesh. *African J. Food Sc.* **7**:198-203.

Basu S, A Roychoudhury, S Sanyal and DN Sengupta (2012) Carbohydrate and Antioxidative potential of the seed of three edible indica rice cultivars. *Indian J. Biochem,* **49**: 115-123.

Bhattacharjee P, RS Singhal and PR Kulkarni (2002) Basmati rice: A review. *Int J. Food Biophys.* **49**:115-123.

Bray HG and Thorpe WV (1954) Analysis of phenolic compounds of interest in metabolism. *Meth Biochem Anal.* **1**: 27-52.

Buresova I, I Sedlackova, O Famera and J Lipavsky (2010) Effect of growing conditions on starch and protein content in triticale grain and amylose content in starch. *Plant Soil Environs.* **56**: 99–104.

Capar SG, JT Tanner, MH Friedman and KW Boyer (1978) Multielement analysis of animal feed, animal waste and srwage sludge. *Environ Sci Technol.* **12**:785.

Eggum BO (1979) The Nutritional Value of Rice in Comparison with Other cereals. In: *Proceedings, Workshop on Chemical Aspects of rice Grain Quality*, Los Baños, Laguna, Philippines, IRRI. pp 91-11.

Fresco L (2005) Rice is life. *J. Food Comp Anal.* **18**: 249-253.

Hedge JE and Hofreiter BT (1962) In: Carbohydrates Chemistry, Whistler, RL and BeMiller, JN (eds), Academic Press, New York.

Humphries EC (1956) Mineral Composition and Ash analysis In: Peach K and Tracy MV (Ed.) *Modern methods of Plant Analysis.* Volume-1, Springer, Berlin. pp 468-502.

Morris DL (1948) Quantitative determination of carbohydrates with drywood's anthrone reagent. *Science* **107**: 254-255.

Oko AO, BE Ubi, AA Efisue and N Dambaba (2012) Comparative Analysis of the Chemical Nutrient Composition of Selected Local and Newly Introduced Rice Varieties Grown in Ebonyi State of Nigeria. *Intl. J. Agric. Forestry* **2**: 16-23.

Pederson B and BO Eggum (1983) The influence of milling on the nutritive value of flour from cereal grains. IV. Rice. *Plant Foods Hum. Nutr.* **33**: 267-278.

Saikia S, D Himjyoti, S Daizi and LM Charu (2012) Quality characterization and estimination of phytochemical content capacity of aromatic pigmented and non-pigmented rice varieties. *Food Res. Int.* **46**: 334-340.

Sompong R, S Ehn, L Martin and E Berghofer (2011) Physicochemical and antioxidant properties of red and black rice varieties from Thailand, China and Sri Lanka. *Food Chem.* **124**:132-140.

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# Genetic Divergence Analysis among Sunflower (*Helianthus annuus* L.) Inbred Lines for Yield and Component Traits

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Sunflower holds a great promise because of its short duration, wider adaptability and superior quality oil. Ninety sunflower inbred lines from different agro-ecological origins were evaluated to study the genetic divergence for seed yield and its components. Based on $D^2$ values, the 90 inbred lines were grouped into 8 clusters indicating considerable amount of genetic diversity. The character, seed filling percentage contributed maximum towards genetic divergence, followed by hull content and seed yield per plant. The genotype, AKSFI-54-3 exhibited the highest value of genotypic worth followed by EC-601957, RHA-3, RHA-859, AKSFI-33, EC-623015 and EC-601767. Mating among these genotypes shall be worthwhile to further expand genetic variability among populations and for selection of elite inbreds through convergent improvement for seed yield and its components for developing superior hybrids and/or elite populations through recurrent selection for composite varieties.

**Key Words: Convergent, Divergence, Inbreds, Recurrent, Sunflower**

## Introduction

Sunflower (*Helianthus annuus* L.), belonging to the family '*Asteraceae*' (*Compositae*) is a diploid species (2n = 2x = 34) and native to southern parts of USA and Mexico. Sunflower is an important oilseed crop and is the preferred source of oil for domestic consumption and cooking worldwide (Hu *et al*., 2010).

In the oilseed scenario, sunflower competes with soyabean, groundnut and rapeseed mustard at global level. As an oilseed crop, sunflower holds a great promise because of its short duration, wider adaptability, photo-insensitivity, drought tolerance and higher amount of superior quality oil. Due to presence of polyunsaturated fatty acids, which are known to reduce the risk of cardiac related problems, higher oil yield is an ultimate objective of sunflower researchers (Monotti, 2004).

Genetic diversity is of major interest to plant breeders for developing cultivars with high grain yield and high oil yield potential in oilseeds. Sunflower being a highly cross-pollinated crop has a great scope for increasing productivity by diversification of hybrid base. The choice of suitable parents is of paramount importance for a planned hybridization programme. It is, therefore, imperative to identify the best parents with wide genetic base for characters of economic importance to obtain heterotic expression in $F_1$ with possibility of broad spectrum of variability in segregating generations. Genetic divergence estimation between different sunflower genotypes is studied with the aim to identify best parents for hybrids constitution among divergent genotypes with complementary characteristics (Amorim *et al*., 2007).

The Mahalanobis $D^2$ statistic being independent of size of sample gives better idea about the magnitude of divergence and provides the basis for selection of parental lines for further breeding programme. Varieties from different geographical locations are generally included in the hybridization programmes by assuming genetic diversity and more likelihood of recovering promising segregants. However, Murthy and Anand (1966) and Medimagh *et al*. (2016) noted that there is no parallelism between geographical and genetical diversity. The present study was designed to quantify the magnitude of genetic divergence and using them in further breeding to evolve potential transgressive segregants and to elucidate the kind of relationship that exists between heterosis and parental diversity in sunflower.

## Material and Methods

The present study was carried out on 90 sunflower genotypes selected from sunflower germplasm maintained at the Oilseeds Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar.

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The experiment was conducted at the Research Farm of CCS HAU, Hisar during spring, 2013. The description of genotypes is given in Table 1. All the genotypes were grown in a randomized block design (RBD) with three replications in single row plots of 3 m length, keeping row to row distance of 45 cm and plant to plant distance of 30 cm for each genotype. Observations were recorded on the characteristics like days to 50% flowering, days to maturity, duration of reproductive phase, plant height at harvest (cm), stem girth (cm), head diameter (cm), 100-seed weight (g), seed filling percentage, hull content (%), protein content (%), oil content (%) and seed yield/plant (g). Mahalanobis $D^2$ statistics was applied to assess genetic diversity among the genotypes and genotypes were grouped on the basis of minimum genetic distance using Tocher's method as described by Rao (1952).

## Results and Discussion

Based on the divergence, 90 sunflower genotypes involved in the present study were grouped into 8 clusters. Clustering pattern revealed the presence of considerable amount of genetic diversity in this material. In general, intercluster distances were relatively greater than intracluster distances showing that genotypes included in different clusters were genetically more diverse than the genotypes included within a cluster. Highest number of genotypes were grouped in clusters-I and IV each having 21genotypes, followed by cluster-II with 14, clusters III and VII each with 12, cluster-V with 8 and clusters VI and VIII each containing only 1 genotype as seen from Table 2. Genotypes from different sources were grouped in the same cluster thereby, indicating that geographical diversity does not necessarily represent genetic diversity and there was little association of genetic divergence with place of origin of genotypes. Murthy and Anand (1966), Reddy *et al*. (2012) and Kumari and Sheoran (2012) also reported the same. However, in some clusters like, clusters III and V, the genotypes related to their place of origin have shown their tendency to group together in the same cluster.

Intra cluster distance was maximum for cluster VII, followed by clusters IV, V, III and II and minimum for cluster I which indicates the existence of maximum variability within cluster VII. Inter cluster distance was maximum in case of Cluster IV and VIII and minimum in case of clusters I and II as shown in Table 3. The higher intercluster distances exhibited the presence of more diversity among the genotypes involved in these clusters. So, it is desirable to select accessions from the clusters having high inter-cluster distance in the recombination breeding programmes.

**Table 1. List of 90 genotypes selected for the study**

| | | | | | |
|---|---|---|---|---|---|
| 1 | ACGIP-1436 | 31 | EC-601801 | 61 | GPB-07 |
| 2 | AKSFI-33 | 32 | EC-601806 | 62 | GPB-18 |
| 3 | AKSFI-52-4 | 33 | EC-601820 | 63 | GPB-50 |
| 4 | AKSFI-54-3 | 34 | EC-601871 | 64 | GPB-61 |
| 5 | AKSFI-58-3 | 35 | EC-601875 | 65 | GPB-67 |
| 6 | AKSFI-71 | 36 | EC-601885 | 66 | GPB-07-1 |
| 7 | AKSFI-78 | 37 | EC-601889 | 67 | GPN-145 |
| 8 | AKSFI-186 | 38 | EC-601896 | 68 | GPN-215 |
| 9 | AKSFI-190 | 39 | EC-601906 | 69 | LSF-902 |
| 10 | AKSFI-197 | 40 | EC-601926 | 70 | MR-6 |
| 11 | CGP-17 | 41 | EC-601935 | 71 | NDR-2 |
| 12 | CGP-39-1 | 42 | EC-601953 | 72 | P35R-PAU |
| 13 | CGP-112 | 43 | EC-601957 | 73 | RCR-22-2 |
| 14 | CSF1-5311 | 44 | EC-601963 | 74 | RCR-24-11 |
| 15 | CSF1-5313 | 45 | EC-601971 | 75 | RCR-39 |
| 16 | CSF1-5317 | 46 | EC-601974 | 76 | RCR-72 |
| 17 | DRSF-106 | 47 | EC-623009 | 77 | RHA-271 |
| 18 | DRSF-120 | 48 | EC-623013 | 78 | RHA-859 |
| 19 | EC-512673 | 49 | EC-623015 | 79 | RHA-298 |
| 20 | EC-512674 | 50 | EC-623016 | 80 | RHA-2 |
| 21 | EC-512676 | 51 | EC-623017 | 81 | RHA-3 |
| 22 | EC-512684 | 52 | EC-623019 | 82 | R-101 |
| 23 | EC-512687 | 53 | EC-623020 | 83 | R-102 |
| 24 | EC-601746 | 54 | EC-623024 | 84 | R-103 |
| 25 | EC-601747 | 55 | EC-623025 | 85 | R-105 |
| 26 | EC-601748 | 56 | EC-623026 | 86 | R-107 |
| 27 | EC-601755 | 57 | EC-623028 | 87 | 1-OH-07-8 |
| 28 | EC-601758 | 58 | EC-623031 | 88 | 1-OH-07-62 |
| 29 | EC-601767 | 59 | EC-623032 | 89 | 1-OH-07-65 |
| 30 | EC-601769 | 60 | GPB-02 | 90 | 1-OH-07-108 |

**Table 2. Clustering of 90 genotypes of sunflower on the basis of $D^2$ statistics**

| Cluster | No. of genotype(s) | Name of genotype(s) |
|---|---|---|
| I | 21 | GPB-07-1, RCR-39, GPB-67, 1-OH-07-108, R-101, GPB-18, EC-601871, R-103, MR-6, GPN-145, R-102, EC-601885, EC-623031, RHA-271, AKSFI-197, GPB-61, R-105, EC-623009, R-107, EC-512684, EC-601758 |
| II | 14 | 1-OH-07-8, 1-OH-07-62, LSF-902, DRSF-106, RHA-3, AKSFI-58-3, AKSFI-54-3, ACGIP-1436, EC-623017, EC-623016, RHA-859, EC-623015, DRSF-120, CGP-112 |
| III | 12 | EC-601889, EC-601896, EC-512673, EC-601748, EC-623028, EC-601926, EC-601906, EC-601820, EC-623013, EC-623024, EC-512676, EC-601935 |
| IV | 21 | RCR-22-2, RHA-2, AKSFI-78, AKSFI-33, CSF1-5317, 1-OH-07-65, AKSFI-52-4, CGP-17, CSF1-5311, CGP-39-1, AKSFI-186, RCR-24-11, AKSFI-71, CSF1-5313, GPB-07, RCR-72, GPB-50, GPB-02, GPN-215, AKSFI-190, EC-623019 |
| V | 8 | EC-512687, EC-601746, EC-623020, EC-623026, EC-601974, EC-601769, EC-601806, EC-601963 |
| VI | 1 | EC-601957 |
| VII | 12 | EC-601755, EC-623025, EC-601801, EC-601747, RHA298, EC-601971, EC-601953, NDR-2, EC-601875, EC-623032, EC-512674, P35R-PAU |
| VIII | 1 | EC-601767 |

**Table 3. Average intra (diagonal) and inter (above diagonal) cluster $D^2$ values in 90 genotypes of sunflower**

| Cluster | I | II | III | IV | V | VI | VII | VIII |
|---|---|---|---|---|---|---|---|---|
| I | 10.45 | 13.67 | 14.77 | 21.26 | 16.14 | 20.97 | 16.55 | 18.14 |
| II | | 12.13 | 19.77 | 20.53 | 20.56 | 17.66 | 16.88 | 24.16 |
| III | | | 13.51 | 24.34 | 17.26 | 24.80 | 20.37 | 16.17 |
| IV | | | | 14.96 | 25.58 | 22.26 | 24.17 | 32.66 |
| V | | | | | 13.94 | 30.14 | 24.43 | 21.10 |
| VI | | | | | | 0.00 | 16.73 | 28.55 |
| VII | | | | | | | 16.68 | 22.16 |
| VIII | | | | | | | | 0.00 |

To get more heterotic $F_1$'s and large number of desirable transgressive segergants, selection of parents for hybridization should be properly based on genetic diversity rather than geographic diversity. An effective hybridization programme may be initiated involving the genotypes belonging to diverse clusters with high mean for almost all component characters. The cluster means for seed yield and its component characters revealed considerable differences among all the clusters for most of the characters studied.

In the present study, days to 50% flowering had the highest mean value in cluster III and lowest mean value in cluster IV as shown in Table 4. For days to maturity, cluster VIII exhibited the highest mean value and cluster II showed the lowest mean value. Cluster III revealed the highest mean value for plant height, whereas cluster VI had the lowest mean value. For stem girth, cluster VIII had the highest mean value, while cluster V had the lowest mean value. Cluster VI showed the maximum mean value for head diameter and cluster III showed the lowest mean value. For 100-seed weight, the highest mean value was possessed by cluster VI and the lowest was possessed by cluster VIII. Seed filling percentage was the highest in cluster VIII and the lowest in cluster IV. Cluster V recorded the highest mean value of hull content, while cluster VI recorded the lowest. Protein content exhibited its highest and lowest mean values in cluster VIII and cluster V, respectively. Cluster II

**Table 4. Mean values of different clusters for 12 characters in sunflower**

| Cluster | Days to 50% flowering | Days to maturity | Duration of reproductive phase (days) | Plant height (cm) | Stem girth (cm) | Head diameter (cm) | 100-seed wt (g) | Seed filling per cent | Hull content (%) | Protein content (%) | Oil content (%) | Seed yield / plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 60.95 | 94.44 | 32.97 | 127.39 | 5.61 | 11.85 | 3.74 | 66.49 | 31.29 | 22.23 | 38.56 | 19.67 |
| II | 59.52 | 91.86 | 32.07 | 123.38 | 5.66 | 13.50 | 5.63 | 68.03 | 30.03 | 21.95 | 38.95 | 34.67 |
| III | 67.64 | 102.44 | 32.53 | 142.22 | 6.11 | 10.87 | 3.71 | 61.50 | 32.96 | 24.27 | 38.18 | 12.24 |
| IV | 57.89 | 92.40 | 32.87 | 132.44 | 5.90 | 12.06 | 4.14 | 32.28 | 31.13 | 21.83 | 37.85 | 22.56 |
| V | 62.92 | 98.29 | 33.21 | 140.02 | 5.41 | 11.05 | 3.71 | 64.53 | 37.40 | 17.81 | 37.83 | 14.94 |
| VI | 67.00 | 98.00 | 31.00 | 121.57 | 5.93 | 15.87 | 5.73 | 56.42 | 21.05 | 24.31 | 38.33 | 37.07 |
| VII | 62.44 | 95.08 | 31.83 | 135.66 | 6.03 | 11.79 | 4.49 | 66.99 | 24.73 | 23.51 | 37.76 | 21.99 |
| VIII | 62.33 | 104.33 | 30.67 | 129.77 | 6.88 | 12.73 | 1.90 | 79.67 | 30.35 | 24.93 | 37.52 | 5.42 |
| GM | 62.59 | 97.11 | 32.14 | 131.56 | 5.94 | 12.47 | 4.13 | 61.99 | 29.87 | 22.61 | 38.12 | 21.07 |

revealed the highest mean value for oil content, whereas cluster VIII had the lowest mean value. The highest seed yield per plant was recorded in cluster VI and the lowest in cluster VIII for mean values.

Comparative evaluation of cluster means suggested that for improving specific characters, select the genotypes from the cluster having high mean value for that character. This comparison indicates that clusters II, IV, VI and VIII had better cluster means for most of the characters, therefore, these clusters might be considered better for selecting genotypes.

From Table 5, it was observed that out of 12 characters studied, the contribution of seed filling percentage was maximum (33.61%) towards genetic divergence, followed by hull content (25.24%), seed yield per plant (15.66%) and days to maturity (11.69%) whereas the remaining characters like, days to 50% flowering (0.12%), duration of reproductive phase (0.40%), plant height (2.75%), stem girth (0.07%), head diameter (0.42%), 100-seed weight (1.30%), protein content (7.37%) and oil content (1.37%) contributed very little for divergence. Similar results for one or more characters have been reported by Pandya *et al*. (2014), Manivannan *et al*. (2003) and Ravi *et al*. (2006).

**Table 5. Contribution of different characters towards divergence**

| S.No. | Character | Times ranked 1st | Contribution towards divergence (%) |
|---|---|---|---|
| 1. | Days to 50 % flowering | 5 | 0.12 |
| 2. | Days to maturity | 468 | 11.69 |
| 3. | Duration of reproductive phase (days) | 16 | 0.40 |
| 4. | Plant height (cm) | 110 | 2.75 |
| 5. | Stem girth (cm) | 3 | 0.07 |
| 6. | Head diameter (cm) | 17 | 0.42 |
| 7. | 100-seed weight (g) | 52 | 1.30 |
| 8. | Seed filling per cent | 1346 | 33.61 |
| 9. | Hull content (%) | 1011 | 25.24 |
| 10. | Protein content (%) | 295 | 7.37 |
| 11. | Oil content (%) | 55 | 1.37 |
| 12. | Seed yield plant-1 (g) | 627 | 15.66 |

Table 6 shows diverse and promising genotypes namely, AKSFI-33, AKSFI-54-3, EC-601767, EC-601957, EC-623015, RHA-3 and RHA-859 which were selected on the basis of $D^2$ ( intercluster distance) values and cluster means from different clusters including clusters II, IV, VI and VIII along with the list of characters for which they attributed superior performance, so these clusters may be used for selecting parents in future breeding programmes. Genotypic worth was then calculated for these genotypes on the basis of range of all the characters. AKSFI-71 has highest value of seed yield/ plant (g), *i.e*., 39.0g, ACGIP-1436 has highest value of oil content (%), 42.10% and EC-601935 has highest value of protein content (%), 29.64%. The genotype, AKSFI-54-3 exhibited the highest value of genotypic worth (17), and therefore, was adjudged the most superior, followed by EC-601957 (16), RHA-3 (15), RHA-859 (14), AKSFI-33 (14), EC-623015 (12) and EC-601767 (11).

These genotypes figured important to be included in crossing programme to further expand genetic variability among populations, to effect selection of elite inbreds for hybridization programme and/or elite populations for composite varieties.

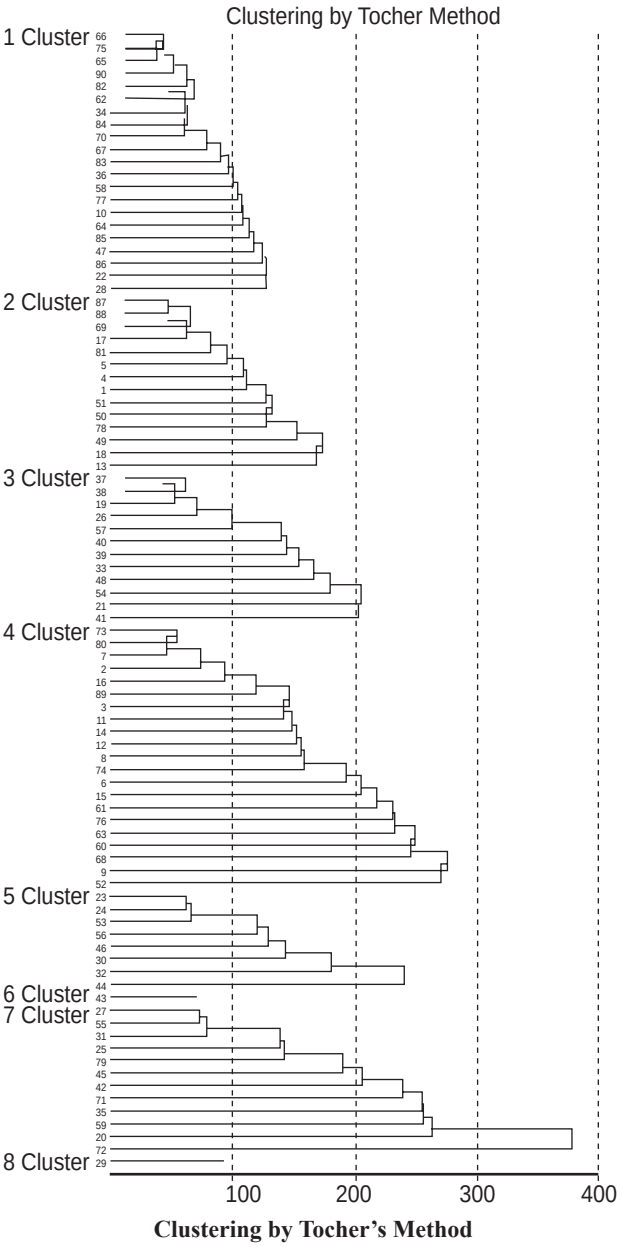
Table 7 shows the distribution of genotypes based on their values for individual traits. With the help of convergent improvement of these inbreds for a particular trait, the performance of these inbreds can be improved. Good general combiner inbreds can be utilized for development of synthetic varieties. The so developed synthetic varieties can be used as source populations for isolation of inbreds which are superior for several traits or show heterosis for several traits. As a result of this, the genetic variability will be further widened.

**Table 6. Diverse and promising genotypes selected from different clusters in sunflower**

| Genotype | Cluster | Characters | Genotypic worth |
|---|---|---|---|
| AKSFI-33 | IV | Days to 50% flowering, days to maturity, duration of reproductive phase, plant height, seed yield plant-1 | 3+3+3+2+3=14 |
| AKSFI-54-3 | II | Days to 50% flowering, days to maturity, plant height, seed filling percentage, oil content, seed yield plant-1 | 3+3+2+3+3+3=17 |
| EC-601767 | VIII | Plant height, seed filling percentage, stem girth, protein content | 2+3+3+3=11 |
| EC-601957 | VI | Plant height, stem girth, head diameter, 100-seed weight, hull content, seed yield plant-1 | 2+2+3+3+3+3=16 |
| EC-623015 | II | Duration of reproductive phase, plant height, seed filling percentage, oil content, head diameter | 2+2+3+3+2=12 |
| RHA-3 | II | Days to 50% flowering, days to maturity, seed filling percentage, oil content, seed yield plant-1 | 3+3+3+3+3=15 |
| RHA-859 | II | Duration of reproductive phase, plant height, seed filling percentage, head diameter, seed yield plant-1 | 3+2+3+3+3=14 |

**Table 7. Distribution of genotypes based on value for each trait in sunflower**

| Characters | Number of genotypes | | | |
|---|---|---|---|---|
| | Low | Medium | High | Total |
| Days to 50% flowering | 36 | 35 | 19 | 90 |
| Days to maturity | 19 | 44 | 27 | 90 |
| Duration of reproductive phase (days) | 34 | 20 | 36 | 90 |
| Plant height (cm) | 18 | 47 | 25 | 90 |
| Stem girth (cm) | 26 | 50 | 14 | 90 |
| Head diameter (cm) | 27 | 49 | 14 | 90 |
| 100 seed wt (g) | 20 | 43 | 27 | 90 |
| Seed filling percent | 11 | 26 | 53 | 90 |
| Hull content (%) | 17 | 49 | 24 | 90 |
| Protein content (%) | 15 | 63 | 12 | 90 |
| Oil content (%) | 11 | 55 | 24 | 90 |
| Seed yield (g/plant) | 26 | 37 | 27 | 90 |




## Conclusion

The present study has led to improve the understanding of many interrelated processes involved in the genetic control of variation in the seed yield. Based on genetic divergence and *per se* performance/genotypic worth for various traits some sort of inter-mating among diverse and promising genotypes namely, AKSFI-33, AKSFI-54-3, EC-601767, EC-601957, EC-623015, RHA-3 and RHA-859 figured important to further expand genetic variation for important yield attributing traits to build either improved populations or draw improved inbred lines for developing heterotic hybrids. Also the improved sunflower populations must combine high seed yield with high percentage of good quality oil for human health. For that matter, selection in segregating populations as evident from present studies, can be based on 100-seed weight, seed filling per cent, head diameter and oil per cent along with seed yield.

The results, thus, obtained in the present study would provide some guidelines in selection of parents and in the prediction of possible merits for genetic recombination and would also be of value in formulating model plant type for selection in segregating generations.

## References

Amorim EP, NP Ramos, MRG Ungaro and AMT Kiihl (2007) Genetic divergence in sunflower genotypes. *Sci. Agrotechnologia* **31**: 1637-1644.

Hu J, G Seiler and C Kole (2010) Genetics, genomics and breeding of sunflower. *Routledge*, USA, 342 p.

Kumari S and RK Sheoran (2012) Genetic divergence in sunflower (*Helianthus annuus* L). Crop science and technology for food security, bioenergy and sustainability. AGROBIOS (INTERNATIONAL) Publication, Jodhpur, India. pp 219-223.

Manivannan N, V Muralidharan and B Subbalakshmi (2003) Genetic divergence in sunflower. *Agric. Sci. Digest* **23**: 125-127.

Medimagh S, M Mastouri, B Bargaoui, HB Salah and IBE Ali (2016) Agro-morphological diversity of tunisian sunflower (*Helianthus annuus* L.). 19th International sunflower conference, 29th April-3rd May. Edirne, Turkey, 614 p.

Monotti M (2004) Growing non-food sunflower in dry land conditions. *Italian J. Agronomy* **8**: 3-8.

Murthy BR and IJ Anand (1966) Combining ability and genetic diversity in some varieties of *Linum usitatissimum*. *Indian J. Genet.* **26:** 21-26.

Pandya MM, PB Patel, AV Narwade and GB Vaidya (2014) Genetic divergence studies in sunflower [*Helianthus annuus* (L.)]. *Trends Biosci.* **7**: 167-169.

Rao CR (1952) Advanced statistical methods in biometrical research. John Wiley and Sons, New York, 389 p.

Ravi E, M Bharathi, AV Reddy and K Madhvilatha (2006) Analysis of genetic divergence in sunflower (*Helianthus annuus* L.). *J. Oilseeds Res.* **23**: 165-167.

Reddy SM, TD Reddy and MY Dudhe (2012) Analysis of genetic diversity in germplasm accessions of sunflower (*Helianthus annuus* L.). *Madras Agric. J.* **99**: 457-460.

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SHORT COMMUNICATION

# *Saccharum edule* Hassk. an Under-exploited Germplasm Resource of Sugarcane

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The genus *Saccharum* L. has six species of which *S. edule* Hassk. is being cultivated from New Guinea to Fiji for its edible aborted inflorescence. The germplasm maintained at Sugarcane Breeding Institute- Research Centre, Kannur, Kerala houses 17 accessions of *S. edule* and these accessions were characterized for 30 qualitative and 10 quantitative morphological traits. There was considerable variability among these accessions for the characters studied. The yield evaluation of regularly flowering clones in a replicated trial showed significant variation for yield attributes of edible inflorescence and the clones, namely, IJ 76-338, IJ 76-360 and IJ 76-552 were identified with potential for commercial cultivation.

**Key Words: Edible Inflorescence, Germplasm resource, *Saccharum edule*, Sugarcane**

The genus *Saccharum* L. belongs to the family *Poacea* and has six species *S. officinarum, S. barberi*, *S. sinense*, *S. edule*, *S. robustum* and *S. spontaneum*. The first four of the species are domesticated and the remaining two are wild. All the species of the *Saccharum* except *S.edule* are utilized in breeding programme to develop superior commercial hybrids of sugarcane. The modern varieties of sugarcane are complex hybrids involving these species and even allied genera like *Erianthus*, *Miscanthus* etc. *S. edule* Hassk is a species with aborted inflorescence which is being cultivated from New Guinea to Fiji for its edible inflorescence (Massal and Barrau, 1956). Daniel and Roach (1987) cited that Rumphius listed *S. edule* as *Ova piscium* in his herbarium Amboinense (Vol. 5) in 1747, as to the Indonesians the inflorescence resembled a mass of fish egg. It has many common names in the place of its cultivation, Coastal pitpit, duruka, dule in Fiji and Fiji asparagus, naviso, pit-pit in Melanesia. The unopened flower heads of *S. edule* are gathered and used as a vegetable, eaten either raw or cooked. The world collection of sugarcane germplasm located at Sugarcane Breeding Institute-Research Centre, Kannur houses 17 accessions of *S. edule*. Warner and Grassl (1958) reported large number of distinct clones of *S. edule in* Melanesia. Berding and Koike (1980) noticed a large number of clones in the western highlands of Irian Java. Later Grassl (1967) suggested that *S.edule* consists of two groups, the New guinea type where *S.robustum* × *Miscanthus* introgression was most probable and the Fijian type where *S. officinarum* × *Miscanthus* introgression has operated *S. edule* has a polyploid series 2n= 60, 70, and 80 with aneuploid forms. Now it is strongly believed that *S.edule* is regarded as a product of introgression in *S. officinarum* and *S. robustum* with other genera (Daniel and Roach, 1987). This species remains unexploited in India for its edible inflorescence by want of detailed information on production potential/suitable cultural practices and in other parts of the world it is still under-utilized. The present study was done to characterize the collection for various agro-morphological traits to understand the extent of variability and to assess the potential of edible inflorescence and biomass yield in the local environment.

The world collection of sugarcane germplasm is maintained at Sugarcane Breeding Institute-Research Centre, located at Kannur, Kerala, India (11°52 N, 75°25 E, 11m MSL, mean annual rainfall 3350 mm). Each of the 17 accessions (28 NG 82, 28 NG 201, 28 NG 272, 57 NG 27, 57 NG 234, NG 77-1, IJ 76-312, IJ 76-329, IJ 76-336, IJ 76-337, IJ 76-338, IJ 76-360, IJ 76-375, IJ 76-552, IS 76-119, NG 77-10, NG 77-235) was planted in one row of 2 m length during 2013-14 and the recommended packages and practices followed for sugarcane were adopted. Total 30 qualitative and 10 quantitative traits were recorded during the crop season. The morphological characters were recorded

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after 8th month of the crop and cane characters after 10th month. Non- parametric analysis was done using SAS 9.0 software package with qualitative and quantitative data after converting the later into binary data to find the relationship between the accessions. The dendrogram was constructed based on UPGMA using Squared Euclidean distance as distance measure. To assess the yield potential of edible inflorescence and total biomass yield a replicated trial was conducted with nine regularly flowering accessions during 2014-15. The plants were grown in a two meter row in three replications. The inflorescence data were collected as and when it was ready for harvest from 10 shoots/accessions. Biomass yield was calculated by harvesting the shoots growing in one meter long rows. ANOVA was calculated for yield and yield related traits. For multi-factorial comparison, Principal Component Analysis (PCA) was done using SAS, JMP version 9.0. The correlations between the various parameters among the accessions were also displayed using the same software package.

Morphological traits showed considerable variation between accessions. The rind colour and internode surface are generally used for identifying a genotype in *Saccharum species*. In the accessions studied, the exposed rind colour ranged from green to brownish green. Similarly all bud traits viz., shape of bud, bud size, bud germ pore, bud cushion and bud groove, bud hair and bud extension were also highly variable. Variation for lamina surface was categorized into three viz., hairy on either side of the lamina, only at dorsal side or in some cases totally glabrous. In seven accessions the hairs were not observed on lamina, three accessions had hairs only on dorsal side and seven accessions had hairs on either side of the lamina. Other leaf traits like leaf sheath colour, leaf sheath hairiness, leaf sheath clasping, dewlap colour, ligule shape and ligular process also showed variation between accessions. With the canopy character the plants can be easily distinguished into compact erect, open tip droopy, open semi droopy or open droopy type. Most of the accession were open droopy (12 accessions) followed by open tip droopy (3), compact erect type (1) and open semi droopy (1). The culms had HR brix which ranged from 8.9% in IJ 76-329 to 14.0% in IS 76-119. Red rot is a major disease of sugarcane and all the accessions were screened against COC 671 isolate of the red rot pathogen. The study revealed that most of the clones were either susceptible or highly susceptible to red rot disease but one clone IJ 76-336 was moderately resistant.

Only nine out of 17 clones flowered regularly at the site of evaluation and the percentage of flowering shoots and the size and fresh weight of the edible inflorescence also varied between the accessions. The edible inflorescence after removing the leaf sheath was creamy yellow in color (Fig 1) except in IJ 76-375 where it was yellowish orange. Waqaniu-Rogers (1986) reported that the red *duruka* or *minimanu* has only one variety, whereas, the white *duruka* has at least six named varieties which are distinguished by size of stem, length of edible portion when mature and period when they are ready to harvest in Viti Levu, FIJI.

The combined cluster analysis of 30 qualitative and 10 quantitative traits showed that most of the accession behaved as independent units with high dissimilarity coefficient. Between two accessions IJ 76-329 and IJ 76-312 more than 75% similarity was observed indicating that these accessions may be a minor variant collected from same locality. The accession 28 NG 82 showed very high dissimilarity with other accessions and remained as a distant node in the dendrogram (Fig. 2) and the remaining accessions were grouped into two distinct major clusters. Similar observations with respect to diversity were recorded by Saraswathi *et al*. (2013) in the *S. edule* collection from Papua, Indonesia collected from the population growing from lowland to highland (0-175 MSL). The cluster analysis done by them based on morphological traits showed two distinct clusters from

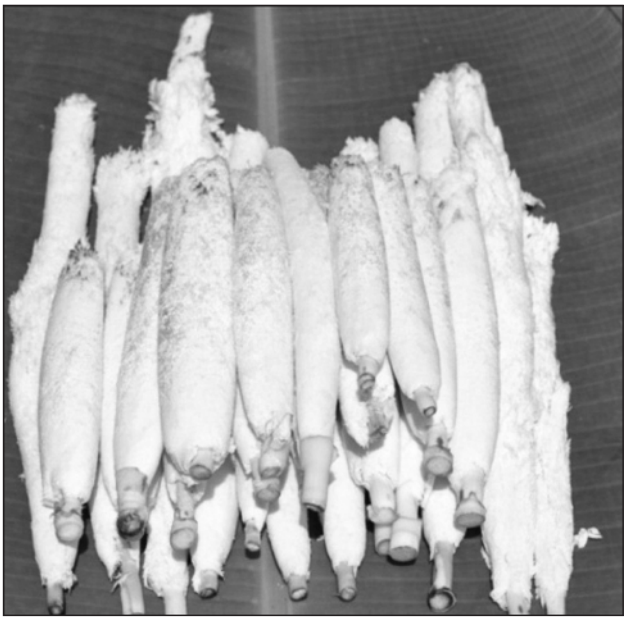

**Fig 1. Edible inflorescence of IJ 76-368**

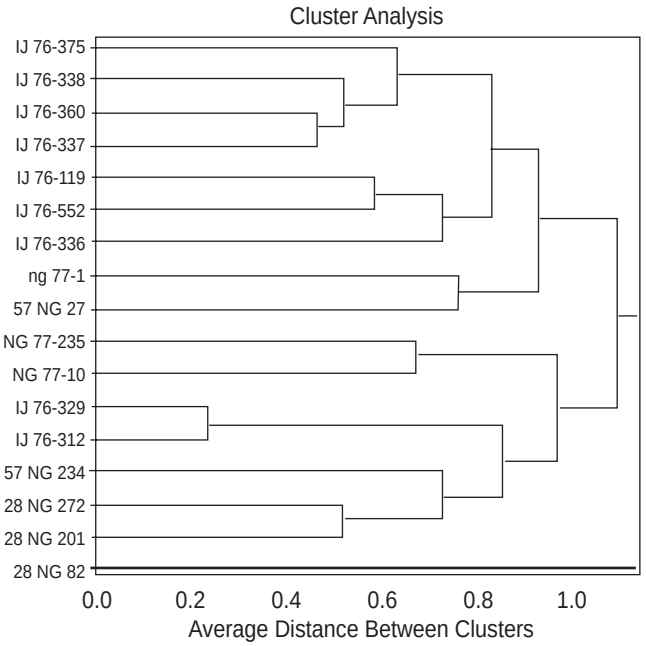


**Fig. 2. Dendrogram based on 30 qualitative and 10 quantitative traits of *S.edule* collection**

two geographical region and closer relatedness between populations growing in adjacent area. They also observed that each location had a unique plant characters which is explained by the geographical isolation and subsequent adaptation to the specific niche. The distinct grouping can also be explained as a result of independent origin of different groups as suggested by Grassl (1967), wherein the New Guinea type originated as a result of *S. robustum* × *Miscanthus* introgression and the Fijian type by S. *officinarum* × *Miscanthus* introgression. The populations developed by such intergeneric crosses resulted in aborted inflorescence in the progenies and further introgression was not possible. Such group continues to remain as discrete population and adapted to the specific geographical location. Premachandran (2006) suggested that the aborted inflorescence in *S. edule* may be due to *cal* and *ap1* mutants of the flowering gene as in the case of *Arabidopsis*, cauliflower, maize, rice etc., or its orthologs in *S. robustum*. He also suggested the possibility of transferring this gene to sugarcane to add one more economic product from sugarcane.

The ANOVA for nine accessions revealed that out of the 14 yield and yield related characters studied, all of the traits showed significant (1% level) variations except for tillering at 30 days after planting and cane thickness. The mean and standard error of the yield related traits are given in Table 1. The harvesting date of edible inflorescence extended from 2$^{nd}$ week of October to 2$^{nd}$ week of December indicate that it will be available only during this period as fresh vegetable and suitable preservation technique needs to be standardized for ensuring the year-around availability. Suitable preservation and packing techniques are also

**Table1. Mean value of yield and yield related traits of nine *S.edule* accessions**

| clone | 30d | 90d | NMC | %F | CTK (cm) | CL (cm) | LL (cm) | LW (cm) | UOL (cm) | UOW (cm) | OL (cm) | OW (cm) | FW (g) | NC | YLD (g) | BIO (Kg) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| IJ 76-312 | 10.0 | 18.3 | 15.7 | 83.8 | 1.7 | 287.8 | 136.0 | 4.7 | 65.4 | 2.0 | 18.6 | 1.7 | 29.0 | 13.0 | 377.3 | 2.1 |
| IJ 76-329 | 11.7 | 15.0 | 13.3 | 89.8 | 1.6 | 285.6 | 134.7 | 4.6 | 60.6 | 2.0 | 19.2 | 1.8 | 26.8 | 12.0 | 318.3 | 2.0 |
| IJ 76-337 | 16.7 | 32.7 | 29.0 | 24.3 | 1.3 | 290.0 | 111.8 | 3.9 | 66.1 | 1.3 | 16.1 | 1.2 | 26.1 | 7.0 | 180.4 | 2.5 |
| IJ 76-338 | 17.3 | 32.7 | 30.3 | 98.1 | 1.2 | 279.4 | 109.3 | 3.1 | 48.4 | 1.4 | 22.2 | 1.3 | 15.0 | 32.3 | 487.0 | 1.7 |
| IJ 76-360 | 13.7 | 35.0 | 32.3 | 57.5 | 1.3 | 295.6 | 109.6 | 4.1 | 54.1 | 1.9 | 31.4 | 2.0 | 25.3 | 18.3 | 464.5 | 2.2 |
| IJ 76-375 | 14.0 | 26.3 | 24.3 | 64.3 | 1.2 | 258.3 | 117.3 | 3.8 | 57.0 | 1.6 | 17.6 | 1.6 | 21.1 | 15.7 | 334.3 | 1.9 |
| IJ 76-552 | 18.7 | 23.7 | 20.7 | 77.0 | 1.5 | 267.8 | 110.4 | 4.1 | 47.9 | 2.1 | 15.8 | 2.0 | 26.9 | 15.7 | 421.1 | 1.8 |
| NG 77-10 | 6.7 | 11.3 | 9.7 | 77.0 | 1.8 | 273.3 | 97.2 | 5.0 | 36.0 | 2.3 | 20.8 | 2.2 | 48.0 | 7.0 | 337.8 | 2.1 |
| NG 77-235 | 15.7 | 27.7 | 23.3 | 77.4 | 1.5 | 272.2 | 129.7 | 4.5 | 89.9 | 1.7 | 22.9 | 1.5 | 23.0 | 17.7 | 406.4 | 2.9 |
| SE | 1.90 | 1.97 | 1.79 | 5.12 | 0.04 | 5.6 | 3.41 | 0.12 | 2.14 | 0.09 | 1.42 | 0.07 | 0.60 | 1.82 | 26.9 | 0.19 |

30d=Tillering at 30 days after planting; 90d= Tillering at 90 DAP; NMC= Number of mature canes ; %F=Percentage of flowering shoots; CTK= Cane thickness; CL= Cane length; LL= Lamina length; LW=Lamina width; UOL= Length of edible inflorescence with leaf sheath; UOW=Width of edible inflorescence with leaf sheath; OL= Length of edible inflorescence without leaf sheath ; OW= width of edible inflorescence without leaf sheath; FW= Fresh weight of edible inflorescence; NC= Number of edible inflorescence /plot; YLD= total yield of edible inflorescence/2m plot; BIO= Total biomass yield/1m plot.

needed to exploit the export market as the edible part is highly perishable owing to its high water content. The accessions IJ 76-552, NG 77-235 and IJ 76-330 flower early (2nd week of October) and the remaining started flowering from 2nd week of November. The maximum duration of flowering (two months) was recorded in IJ 76-330 which makes it suitable for prolonged availability of the fresh edible inflorescence. The highest yield of edible inflorescence/plot was recorded by IJ 76-338 followed by IJ 76-330 and IJ 76-552. The percentage of flowering stalk was highest in IJ 76-338 (98.1%).

PCA is a valuable statistical technique which has found application in reduction of original variables to a smaller number of underlying variables (Principal Components) in order to reveal the interrelationships between the different variables and to determine the optimum number of extracted principal components. The first principal component (PC1) had the highest eigen value of 6.8 and accounted for 43 per cent of the total variation in the data set, while the second principal component (PC2) with eigen value of 3.2 explained 19.8 per cent of the variation. The percentage of flowering shoots (%F), width of inflorescence with leaf sheath (UOW) and without leaf sheath (OW) were observed on the right upper side of the biplot with high positive loading for both PC1 and PC2, while fresh weight (FW), cane thickness (CTK), leaf width (LW) and leaf length (LL) were grouped together on the right lower side of the biplot with positive loadings for PC1 and negative loadings for PC2. Significant positive correlation was observed between Number of mature canes (NMC), tillers at 30 days after planting (30DAP) and tiller at 90 days after planting (90DAP) and they were found in a group at left side of biplot. Number of edible inflorescence (NEI) had a significant positive correlation (r=0.784*) with total yield of edible inflorescence (YLD). Also the cane thickness showed significant positive correlation (r=0.909**) with leaf width and this explains that higher the leaf area plausibly more photosynthesis and dry matter production by partitioning more towards shoot growth occurs.

The present study revealed that the *S.edule* can be directly exploited for edible inflorescence by commercial cultivation and the biomass for complimenting in energy production to sugar factories. Though the sugar content is varying from 8 to 14% (Ramana Rao *et al*., 1985) the extractable juice is very less and hence sugar recovery from the culms may not be economically viable. Premachandran (2006) referred the edible inflorescence as ‘‘cane flower’ owing to its similar origin to cauliflower by mutation in the floral gene. However, in gross morphology it looks more similar to a maize cob and can be named as ‘Cane Cob’. The study revealed that the accessions IJ 76-368, IJ 76-360 and IJ 76-552 are better yielder for edible inflorescence on account of fresh weight of edible inflorescence, good tillering, good flowering percentage of stalks and also for biomass yield. It has been reported that *S. edule* is suitable for intercropping with soybean and rotation with early flowering red duruka with late flowering white types for better commercial exploitation (Saraswati *et al*., 2013). They also observed that wider spacing (200x200cm) improved the growth and yield, as shown by greater plant height, number of suckers, flower number and flower weight, compared to the traditional planting of 150×150 and 100×150 cm distances. The purple duruka variety which flowers twice a year introduced to Viti Levu, Fiji become popular and it is proposed to have a canning unit in Fiji to sell this as “Fijian asparagus” (Waqaniu-Rogers, 1986).

The adaptation of *S. edule* to marginal land and its ability to check soil erosion (Waqaniu-Rogers, 1986) makes it suitable for the area where sugarcane is not commercially viable. Since it has a short flowering period of nine weeks (from October 2nd week to December 2nd week) there is a need to identify suitable genotypes which are early flowering, late flowering and that flower twice in a year to make the availability of fresh vegetable for longer duration in the market. There is also a need to develop suitable packing/canning of this vegetable on account of quick perishable nature and to extend its availability in the export market.

## References

Berding N and H Koike (1980) Germplasm conservation of the *Saccharum* complex: A collection from the Indonesian Archipelago, *Hawaiian Planters Record* **59**:87-176.

Daniels J and BT Roach (1987) Taxonomy and evolution. In: DJ Heinz (ed.) *Sugarcane Improvement through Breeding*, Amsterdam, Elsevier, pp 7-84.

Grassl CO (1967) Introgression between *Saccharum* and *Miscanthus* in New Guinea and Pacific Area. *Proc.Int.Soc. Sugar Cane Technol*.**12**: 995-1003.

Massal E and J Barrau (1956) Food plants of the South Sea Islands. *South Pac. Comm. Tech. Paper*, 1956 (94): 51p.

Premachandran MN (2006) Cauliflower gene in sugarcane? *Current Science* **91**: 750-751.

Roach BT (1972) Chromosome Numbers in *Saccharum edule*. *Cytologia* **37**: 155-161.

Ramana RO TC, Srenivasan TV and Palanichami K (1985) *Catalogue on sugarcane genetic resources-II*. Sugarcane Breeding Institute (ICAR), Coimbatore, India. Pp 81.

Saraswati P, NL Mawikere, IAF Djuuna and F Pakiding (2013) The diversity and cultivation system of *Saccharum edule* L. and its role as an edible plant source in Papua, Indonesia. *Acta Hort. (ISHS)* **979***:373-380.*

Waqaniu-Rogers (1986) Some observations on duruka, *Saccharum edule*, in Viti Levu, Fiji, *The Journal of the Polynesian Society* **95**: 475-478.

Warner JN and CO Grassl (1958) The 1957 sugarcane expedition to Melanesia. *Hawaiian Planters Record* **55**: 209-236.

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SHORT COMMUNICATION

# PGR-Clim: Climate Atlas of Genetic Resources of Five Crops

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PGR-Clim is a web-based tool that provides an easy interface to access climate change (temperature and rainfall) atlases relevant to plant genetic resources management. The online tool combines climatic data with information on germplasm collection sites of five crops (sorghum, pearl millet, wheat, chickpea and pigeon pea) to predict future (2020 and 2050) climatic situations at germplasm occurrence sites. The tool allows users to choose a crop and visualize how climate is predicted to change over time and stimulate them to assess impacts and plan for measures of mitigation and adaptation.

**Key Words: Climate change, Climate maps, PGR, web-based tool**

Identification and utilization of plant genetic resources (PGR) with excellent adaptation potential is a prerequisite to facilitate development of climate smart crop varieties. Genebanks, major repositories of *ex situ* collections worldwide are expected to take measures to be climate-ready. Identification of pre-adapted germplasm for immediate direct use in varietal development and vulnerable areas for collection and conservation in the Indian context in five selected crops – wheat, pearl millet, chickpea, pigeon pea and sorghum has been reported (Archak *et al.,* 2014). However, climate maps in printed forms may not be accessible to everyone easily. In order to make the climate maps, for current and future, available to PGR researchers and policy makers, an online software tool called PGR-Clim was developed. Here we report development and utility of PGR-Clim.

For the purpose of easy designation of climate periods, *current* means years spanning 1950-2000; *2020* means years spanning 2010-2039 and *2050* means years spanning 2020-2049. Climatic data were obtained from the Worldclim database for current climate (1950-2000) and from UKMO HADCM3 Climate Model for near future (2010-2039). In order to find out areas most vulnerable to changing climate, the collection sites as putative sites for occurrence of diversity were mapped on current and future climate. Information on indigenous collections belonging to five target crops was mined from ICAR-NBPGR databases as well as documentations of Bioversity International collection missions (IBPGR database) or accessed via either ICRISAT database or GENESYS portal to obtain information on international collections of the target crops sourced from India and being conserved at locations other than National Genebank, NBPGR. Search resulted in a total of 38,126 accessions that had information on collection site. In all, spatial information was manually geocoded and was brought into GIS to prepare a geo-database for 10947 sorghum, 9499 wheat, 8220 pearl millet, 6167 pigeon pea and 3293 chickpea accessions.

The information at every stage of analysis was mapped employing the geospatial processing program ArcMap 10.1 (ESRI 2010). Indian map (2001 census) and soil map (National Atlas and Thematic Mapping Organization) were procured from a commercial source. Physiographical divisions were as per NBSS&LUP and soil taxonomy classification was as per USDA. Agro-ecological zones (AEZ) were as per National Institute of Hydrology, Roorkee. The web-based tool for visualizing the climate maps was developed following three-tier system architecture. The database was placed at bottom layer and was developed by using MSSQL Server 2012. The server side application layer was developed by using C# and the client side application layer was developed by using HTML, CSS and ASP.NET. Dynamic map viewing was established by employing Google maps.

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PGR-Clim is accessible at http://www.nbpgr.ernet.in:8080/climate/arcMap.aspx. The generic process of querying for maps is given below:

1. Select crop → Click on Get Map → View collection sites on India terrain map
2. Select crop → Select map variable (AEZ or Soil) → Click on Get Map → View collection sites on India AEZ or Soil map
3. Select crop → Select climate variable (Temperature or Rainfall) → Select time period (Current or 2020s or 2050s) → Click on Get Map → View collection sites on India temperature or rainfall map for Current or 2020s or 2050s

The map output (Fig. 1) provides a quick look at the changes in the areas covered by different temperature and rainfall patterns at different points of time. Climate

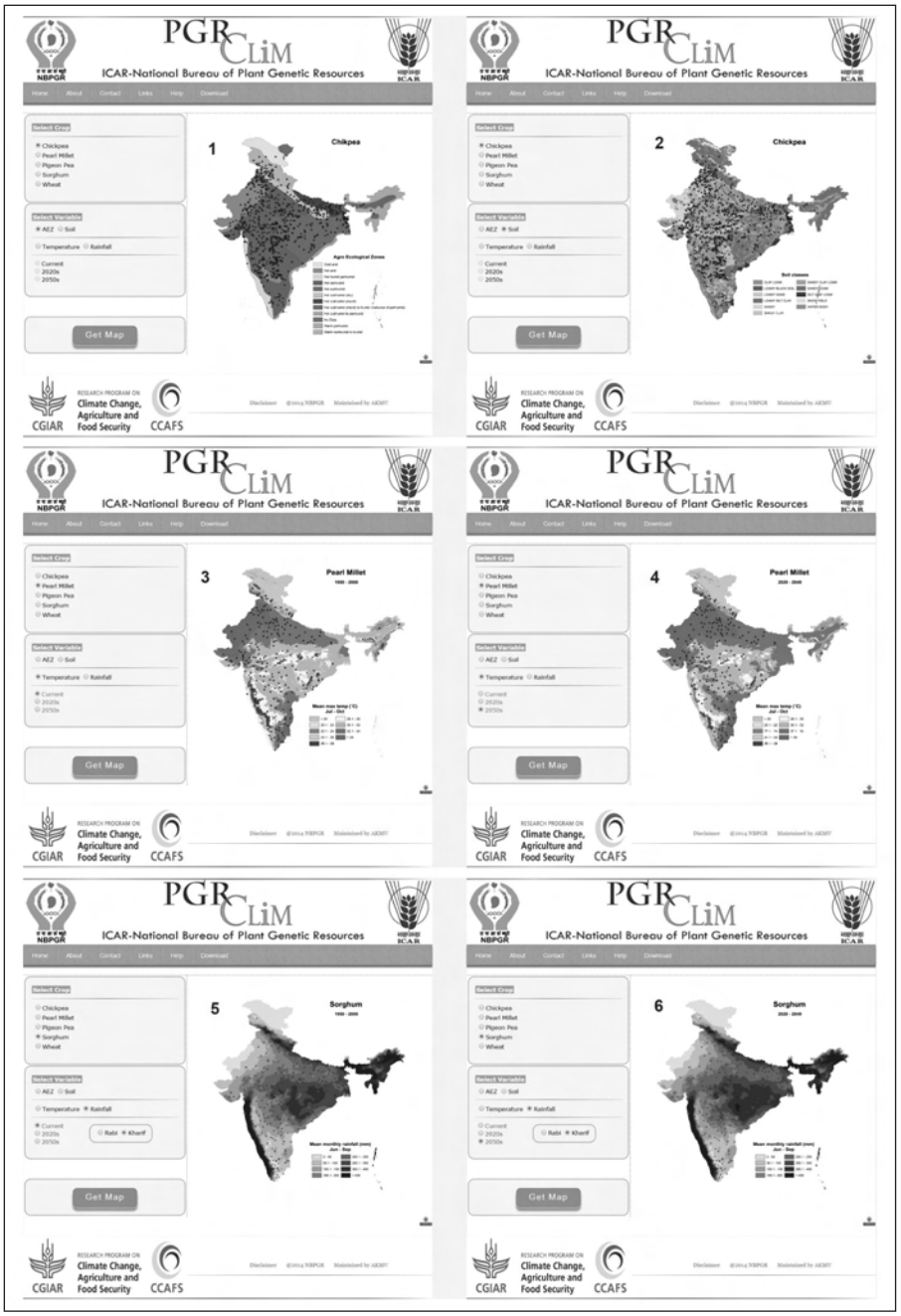


**Fig. 1. Climate atlases generated by PGR-Clim. (1) Chickpea germplasm occurrence data on AEZ map; (2) Chickpea germplasm occurrence data on soil map; (3) Pearl millet current temperature atlas; (4) Pearl millet 2050 temperature atlas; (5) Sorghum current rainfall atlas; (6) Sorghum 2050 rainfall atlas**

maps obtained on the PGR-Clim interface are only for visualization purpose. Users can download large (~2MB size) high resolution (5950×7700) jpeg images by clicking on the link at the right hand bottom of the maps.

PGR-Clim is interactive only at the level of accession map. This means by clicking on the points, genebank ID is displayed. However, the climate maps are not yet interactive. Users may have to download the high resolution climate atlases and mark the genebank IDs based on accession level map (first option) for further interpretation. It is expected that PGR researchers would make use of this tool in order to identify accessions that are climate resilient or areas that may go vulnerable due to changed climate. Addition of more crops and making the tool more interactive are future prospects of PGR-Clim.

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## Reference

Archak S, DP Semwal, S Pandey and BS Phogat (2014). *Utilization of ex situ collections and climate analogues for enhancing adaptive capacity to climate change: Final Report.* National Bureau of Plant Genetic Resources, New Delhi. India. 47 p.

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SHORT COMMUNICATION

# High Kernel Weight Genotypes of Indian Bread Wheat (*Triticum aestivum* L.)

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In an experiments on assessment and identification of elite Indian wheat genotypes, IC138896, IC138893, IC28664, IC35069, IC532841, IC534435, IC534777, IC534787, IC82197, and IC82198, showed high kernel weight compared to 'Moti (HD-1949)'. These can be gainfully used as parental lines in breeding for increasing grain weight, both for hybridization and selection.

**Key Words: Indian wheat, High kernel weight, Parental lines, Phenological characteristics, *Triticum aestivum***

Wheat (*Triticum* spp. L.) is one of the most important cereal crops that was crucial in the rise of famous civilizations and has been the chief vehicle of green revolution across the world. It has been playing the key role in India's food security and self-sufficiency.

India's rate of gain in wheat production has declined during the last two years due to adverse weather conditions (Singh, 2016). On the other hand, strong selection pressure for yield under high input conditions during and after green revolution has eliminated considerable genetic diversity in the breeding pools of major crops, including wheat, causing erosion of genetic potential for adaptation to emerging challenges of climate change (Voss-Fels *et al*., 2015). In addition, the bottlenecks of hexaploidisation followed by breeding have considerably narrowed down the bread wheat (*Triticum aestivum* L.) diversity to the extent that yields in many regions appear to be unexpectedly stagnating (Voss-Fels *et al*., 2015). Genetic diversity analyses and identification of elite genotypes can address this dilemma by providing detailed knowledge to characterize and utilize the available genetic diversity in the germplasm collections.

As compared to modern high yielding varieties, local cultivars and landraces have higher genetic variability and adaptation to the different local stress conditions and, therefore, are valuable tools for identifying genes for achieving high grain yield in arid and semi-arid areas (Lammerts-van-Bueren *et al*., 2005). Worldwide efforts are on to assess the phenotypic diversity of local landraces in order to mine useful genes and to assess the exploitable diversity, in wheat and other crops to utilize this untapped diversity: for instance, Dikshit *et al*. (2004) and Routray *et al.* (2007) reported on rice landraces and Uttaranchal wheat landraces, respectively. While genetic diversity can be estimated based on various criteria, agro-morphological characterization is a primary step for conservation and utilization of plant genetic resources (Zarkti *et al*., 2012).

In order to generate information, useful for wheat crop improvement through breeding and/or biotechnology, six hundred and eighteen Indian wheat collections, supplied with thanks by Late Dr SK Mishra, ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi, were assessed for morphological and phenological characteristics. These were grown at the experimental farm of ICAR-Indian Agricultural Research Institute, New Delhi (latitude: 80°38'23"N, longitude:77°09'27"E, and with an elevation of 228.61m above msl) for two consecutive cropping seasons (2011-12 and 2012-13), in two replicates using randomized block (RBD) design, following standard agronomic practices. Data were recorded on five randomly tagged plants in each plot. Recorded value of each trait was averaged over 5 individuals, two replications, and two cropping seasons. Data were analyzed using statistical software SAS, version 9.3 (SAS Institute Inc., USA, 2011).

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Statistical parameters such as standard error mean (SEm), critical difference (CD) and coefficient of variation (CV, %) were estimated for the entire set of 618 genotypes and were used for the comparison. In the present study, as presented in Table 1, performances of these ten genotypes were compared with that of commercial cultivar HD-1949 (IC73210). Selection of superior wheat genotypes regarding high grain yield would be as effective as selection for its components, including thousand seed weight (Peltonen-Saino *et al*., 2007). The relation of these traits with grain yield and the interrelationships have special importance as the basis for selecting high yielding genotypes (Sabaghnia *et al*., 2014). In the set of 618 Indian wheat accessions, IC73210 was a commercial cultivar Moti (HD-1949), which is a triple dwarf wheat with grain color amber and medium bold, good for chapati making (www.dacnet.nic.in) and, therefore, ten high kernel weight genotypes identified in the present study were compared with HD-1949.

The genotype IC5344777, as shown in Table 1, registered the highest thousand kernel weight (65.5 g in 2011-12, and 69.99 g in 2012-13) amounting to more than the double of the commercial cultivar HD-1949 (32.5 g in 2011-12, and 30.5 g in 2012-13) during both the years followed by genotypes IC534787 (58.6 g in 2011-12, and 56.37 g in 2012-13), IC82197 (48.2 g in 2011-12, and 46.54 g in 2012-13), IC35069 (45.8 g in 2011-12, and 44.6 g in 2012-13), IC138893 (45.05 g in 2011-12, and 44.52 g in 2012-13), IC532841 (43.3 g in 2011-12, and 41.84 g in 2012-13), IC82198 (41.5 g in 2011-12, and 41.88 g in 2012-13), IC138896 (41.23 g in 2011-12, and 42.84 g in 2012-13), IC534435 (40.25 g in 2011-12, and 42.05 g in 2012-13), and IC28664 (40 g in 2011-12, and 41.08 g in 2012-13). Our result showed higher values than those of previous reports for bread wheat (Sabaghnia *et al*., 2014). In terms of days to head emergence, days to 50% flowering, and days to physiological maturity; most of these genotypes were comparable to the HD-1949, except IC534787 that showed the longest duration for physiological maturity (155 days in 2011-12 and 150 days in 2012-13) followed by IC534777 (140 days in 2011-12, and 145 days in 2012-13), and IC82198 (100 days in both the years). IC28664, IC534435, IC82197, and IC82198 produced 50% flowers in 5 days after head emergence, while the other genotypes took 10 to 15 days. Our results were congruent with the report of Zarkti *et al.* (2012). In case of average spike length, as depicted in Fig. 1,

**Table 1. Comparative performance of twelve high-kernel-weight genotypes of Indian bread wheat (*Triticum aestivum* L.)**

| Genotypes | Thousand kernel weight (g) | | Days to physiological maturity | | Days to 50% flowering | | Days to head emergence | | Plant height (cm) | | Spike length (cm) | | Number of seeds per spike | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 2011-12 | 2012-13 | 2011-12 | 2012-13 | 2011-12 | 2012-13 | 2011-12 | 2012-13 | 2011-12 | 2012-13 | 2011-12 | 2012-13 | 2011-12 | 2012-13 |
| IC_73210 (Moti/ HD-1949) | 32.5 | 30.5 | 90 | 90 | 70 | 70 | 55 | 60 | 53.25 | 55.6 | 8.3 | 8.5 | 35 | 33 |
| IC_138896 | 41.23 | 42.84 | 90 | 90 | 70 | 70 | 60 | 65 | 92.5 | 90.3 | 10.7 | 9.5 | 39 | 37 |
| IC_138893 | 45.05 | 44.52 | 100 | 95 | 75 | 70 | 60 | 60 | 95.25 | 95.55 | 9.8 | 9..5 | 44 | 43 |
| IC_28664 | 40 | 41.08 | 90 | 90 | 70 | 70 | 65 | 65 | 80 | 82.1 | 12 | 12.5 | 49 | 47 |
| IC_35069 | 45.8 | 44.6 | 95 | 90 | 75 | 70 | 60 | 65 | 110.4 | 109.1 | 12.5 | 12 | 45 | 43 |
| IC_532841 | 43.5 | 41.84 | 95 | 90 | 70 | 70 | 60 | 60 | 91.5 | 89.05 | 8 | 8.5 | 25 | 27 |
| IC_534435 | 40.25 | 42.05 | 95 | 95 | 70 | 70 | 65 | 65 | 106 | 106.05 | 10.5 | 10 | 56 | 57 |
| IC_534777 | 65.5 | 69.99 | 140 | 145 | 110 | 120 | 110 | 110 | 102.6 | 103.6 | 10.5 | 10.5 | 42 | 38 |
| IC_534787 | 58.6 | 56.37 | 155 | 150 | 115 | 120 | 110 | 110 | 98.07 | 99.85 | 12.8 | 12.5 | 30 | 42 |
| IC_82197 | 48.2 | 46.54 | 100 | 95 | 75 | 70 | 65 | 65 | 91.5 | 91.85 | 11.2 | 11.5 | 55 | 53 |
| IC_82198 | 41.5 | 41.88 | 100 | 100 | 75 | 70 | 65 | 65 | 80.04 | 78.95 | 10.3 | 9.5 | 58 | 61 |
| SE(m) | 0.13 | 0.12 | 0.38 | 0.35 | 0.06 | 0.05 | 0.04 | 0.04 | 0.03 | 0.03 | 0.04 | 0.05 | 0.9 | 0.87 |
| CD (0.05%) | 0.36 | 0.33 | 1.05 | 0.97 | 0.17 | 0.14 | 0.11 | 0.11 | 0.08 | 0.08 | 0.11 | 0.14 | 2.49 | 2.41 |
| CD (0.01%) | 0.47 | 0.44 | 1.38 | 1.27 | 0.22 | 0.18 | 0.15 | 0.15 | 0.11 | 0.11 | 0.15 | 0.18 | 3.28 | 3.17 |
| CV (%) | 25.92 | 28.37 | 19.21 | 19.36 | 23.01 | 24.67 | 25.61 | 27.28 | 8.56 | 9.02 | 16.95 | 18.58 | 37.94 | 39.27 |

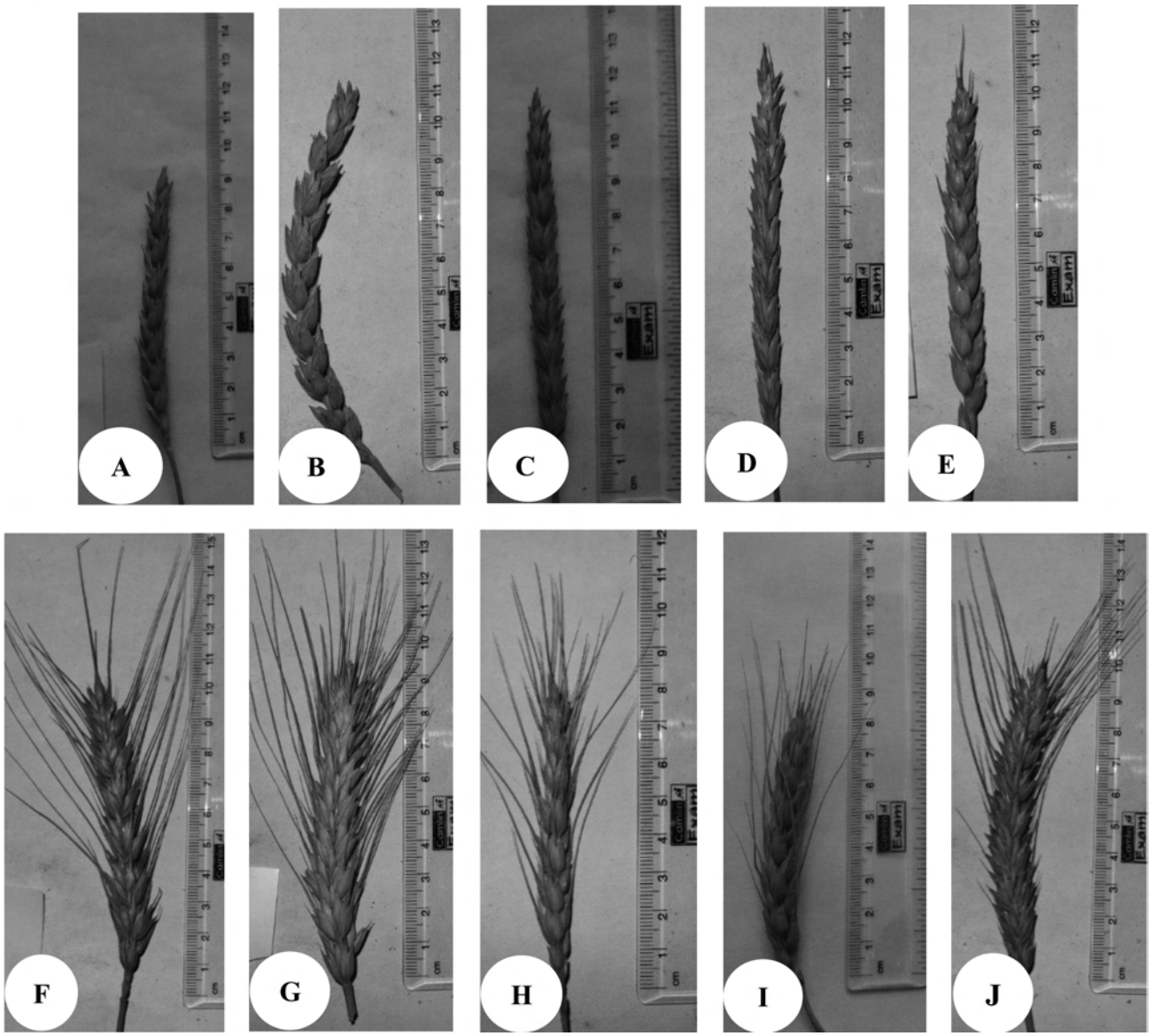


**Fig. 1. Spike characteristics of high kernel weight genotypes of Indian bread wheat: A, IC82198; B, IC534787; C, IC82197; D, IC28664; E, IC534777; F, IC534435; G, IC138893; H, IC138896; I, IC532841; and J, IC35069.**

and presented in Table 1, longer spikes ranging from 12 to 12.8 cm were recorded in genotypes IC28664, IC35069, and IC534787; whereas, the shorter spikes were observed in genotype IC532841 (8 cm in 2011-12, and 8.5 cm in 2012-13) similar to those of commercial cultivar HD-1949 (8.3 cm in 2011-12 and 8.5 cm in 2012-13). Number of seeds per spike is another important component of grain yield. As shown in Table 1, the highest number of seeds per spike was registered in IC82198 (58 in 2011-12 and 61 in 2012-13) and the lowest (25 in 2011-12 and 27 in 2012-13) values that were below those of commercial cultivar HD-1949 (35 in 2011-12 and 33 in 2012-13) were registered in IC532841. According to Subedi *et al*. (2000), when wheat is stressed during reproductive development, the grain number in fertile florets is reduced. This explains the reason for variation in number of seeds per spike within each genotype between the two cropping seasons (2011-12 and 2012-13).

Figure 1 illustrates, further, visual/qualitative characteristics of spikes of these high kernel weight genotypes. Five genotypes were awnless and the other five were awned; spike density was compact in most of the genotypes except IC534787 which exhibited lax

type; most of them were yellow in glume color except IC534787 which was brown; and, five (IC82198, IC534787, IC82197, IC534777, IC532847, and 35069) were pubescent and the other five lacked glume hairiness. Glume hairiness is another important trait of breeding value as it influences reaction of plant, particularly spike portion, to fungal infection such as powdery mildew.

In wheat breeding, thousand seed weight is one of the important parameters in that it increases seed germination percent, seedling emergence, tillering capacity, spike and yield (Sabaghnia *et al*., 2014). The results of this study will support efforts of conservation and utilization of Indian wheat landraces in wheat genetic improvement programmes as these high kernel weight genotypes of Indian bread wheat, which are already adapted to local condition due to continuous cultivation and selection for long time by farmers, can be gainfully used by breeders and biotechnologists as parental lines in breeding for increasing grain weight, both for hybridization and selection, as well as in developing mapping population to tag genomic regions for high seed weight.

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## References

Dikshit N, N Sivaraj and AB Das (2014) Genotypic variations in agro-morphological and physico-chemical traits in ethnic rice (*Oryza sativa*) landracs of orissa. *Indian J. Agric. Sci.* **84(8):** 987-992.

Lammerts-van-Bueren ET, LJM Van-Soest, EC De-Groot, IW Boukema and AM Osman (2005) Broadening the genetic base of onion to develop better-adapted varities for organic farming systems. *Euphytica* **146:** 125-132.

Peltonen-Sainioa P, A Kangas, Y Salo and L Jauhiainen (2007) Grain number dominates grain weight in temperate cereal yield determination: Evidence based on 30 years of multilocation trials. *Field Crop Res.* **100:** 179-188.

Routray P, O Basha, M Garg, NK Singh and HS Dhalikal (2007) Genetic diversity of landraces of wheat (*Triticum aestivum* L.) from hilly areas of Uttaranchal, India. *Genet. Resour. Crop Evol.* **54:** 1315-1326.

Sabaghnia N, M Janmohammadi and AB Segherloo (2014) Evaluation of some agro-morphological traits diversity in Iranian bread wheat genotypes. *Ann. Univ. Mariae Curie-sklodovska* **69(1):** 79-92.

Singh, SK (2016) India: Grain and feed annual (Grin report numer, IN6033). www.gain.fas.usda.gov. (Accessed on May 13, 2016, Please see the URL, http:// gain.fas.usda.gov/Recent%20GAIN%20Publications/Grain%20and%20Feed%20Annual_New%20 Delhi_India_2-26-2016.pdf).

Subedi, KD., PJ Gregory, RJ Summerfield and MJ Goodig (2000) Pattern of grain set in boron-deficient and cold-stressed wheat (*Triticum aestivum* L.). *J. Agric.Sci., Cambridge*, **134**: 25-31.

Voss-Fels K, M Frisch, L Qian, S Kontowski, W Friedt, S Gottwald and RJ Snowdon (2015) Subgenomic diversity patterns caused by directional selection in bread wheat gene pools. *Pl. Gen.* **8(2):** 1-13.

Zarkti H, H Quabbou, SM Udupa, F Gaboun and A Hilali (2012) Agro-morphological variability in durum wheat landraces of Morocco. *Aust. J. Crop Sci.***6(7):** 1172-1178.

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SHORT COMMUNICATION

# Genetic Divergence Studies in Winged Bean (*Psophocarpus tetragonolobus* (L.) DC.)

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Twenty-one genotypes of winged bean [*Psophocarpus tetragonolobus* (L.) DC.] were studied to understand the extent of genetic diversity based on 12 quantitative traits. Mahalanobis $D^2$ analysis revealed the presence of high amount of genetic diversity among 21 genotypes, which formed five clusters. Cluster-I had the maximum (7) and cluster-III had the minimum (1) number of genotypes. Intra cluster distance analysis revealed that the Cluster-II had highest intra-cluster distance followed by cluster-I. The inter-cluster divergence (D) was the maximum between the clusters-II and V and the minimum between clusters-I and III. The results indicated that days to first flowering contributed maximum to the total divergence followed by pod weight and days to edible maturity. The Cluster-IV had highest mean value for yield per plant and 100 seed weight and the cluster cluster-V has the highest mean value for number of primary branches per plant. The diverse parents identified could be used for genetic improvement in winged bean.

**Key Words: Character association, Cluster analysis, Genetic divergence, Genotypes, Winged bean**

A large number of leguminous species, which have not yet been fully exploited are of great potential as a nutritive food. Hence, there is a need to exploit such legume vegetables for better health and nutrition. Among the under-exploited legume vegetables, winged bean (*Psophocarpus tetragonolobus* (L.) DC) is the most important. Since nearly every portion of the plant is edible or can be profitably utilized, several superlatives like 'soya's rival', 'God-sent vegetable' and 'vegetable of twentieth century' have often been used for winged bean. Presently, it is cultivated only for its tender green pods and seeds.

Although it is a highly nutritive summer vegetable, until now no proper research thrust has been given for the genetic improvement of this vegetable, therefore, there is an urgent need to design breeding programme to identify and develop suitable genotypes for specific purposes. The knowledge on genetic diversity or similarity could help to get long term selection gain in plants (Chowdhury *et al*., 2003). Genetic divergence is crucial for the crop improvement programme. Mahalanobis's $D^2$ statistics is an ideal tool for estimating genetic divergence in crop plants and to choose the parents without making crosses before the initiation of hybridization programme (Bhatt, 1970). Despite the importance of this vegetable crop, only limited breeding work has been done for its genetic improvement in the past, in order to enhance the productivity levels. Therefore, the present investigation was undertaken to study the nature and magnitude of genetic divergence in winged bean genotypes collected from different geographical regions.

The experimental materials comprised of 21 genotypes of winged bean, which were collected from different parts of the country (Table 1). The experiment was laid out in a randomized block design (RBD) with three replications during April, 2013–March, 2014 at Department of Olericulture, College of Agriculture, Vellayani, Thiruvananthapuram. The experimental site was located at $8^{o}$ 5' N latitude and $77^{o}$ 1' E longitude

**Table 1. Source and place of collection of winged bean genotypes used in the study**

| Source | Number of genotypes | Genotypes |
|---|---|---|
| College of Agriculture, Vellayani | 7 | PT 1, PT2, PT 3, PT 4, PT 5, PT 20, PT 21 |
| Idukki, Kerala | 1 | PT 6 |
| Palakkad, Kerala | 1 | PT 7 |
| College of Horticulture, Vellanikkara | 12 | PT 8 (Revathy), PT 9, PT 10, PT 11, PT 12, PT 13, PT 14, PT 15, PT 16, PT 17, PT 18, PT 19 |

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at an altitude of 29 m above mean sea level. Soil type of the experimental site was red sandy clay loam with a pH of 5.2 and warm humid tropical climate. Seeds of each genotype were sown in rows at spacing of 125 cm between rows and 50 cm between plants. Recommended agronomic practices were followed to raise a good crop. Observations were taken on five randomly selected plants for 12 quantitative characters *viz.*, vine length (cm), number of primary branches per plant, days to first flowering, days to first harvest, days to edible maturity, pod length (cm), pod girth (cm), pod weight (g), number of pods per plant, yield per plant (g), number of seeds per pod and 100 seed weight (g). Analysis of variance (ANOVA) was carried out as suggested by Panse and Sukhatme (1964). Genetic divergence was estimated using $D^2$ statistics of Mahalanobis (1936) and clustering of genotypes was done according to Tocher's method as described by Rao (1952). The per cent contribution of characters towards genetic divergence was calculated according to Singh and Chaudhary (1985).

ANOVA for yield and its contributing traits revealed that the genotypes differed significantly for these traits (Table 2). This indicates that there is ample scope for selection of promising lines from the present gene pool aimed at enhancing genetic yield potential of winged bean. The $D^2$ value varied widely and principal component scores also revealed a good degree of genetic diversity among the genotypes.

Variation was accessed using principal component analysis by taking in to account every variable at once. First four principal components accounted for a total of 86.14 % variability among the accessions using quantitative traits (Table 3). A total of 48.22 per cent of variance of the total variation was observed in the first principal component, PC 2 depicted per cent of variance as 20.17, PC 3 accounted for 11.62 per cent of the total variation and PC 4 contributed 6.11 percent to the total variation. PC 1 showed predominantly the variation in days to first flowering, days to first harvest, primary branches per plant and 100-seed weight. PC 2 was mostly correlated with seeds per pod, yield per plant, vine length and days to first flowering. PC 3 was associated with vine length and days to edible maturity, where as vine length, pod girth and yield per plant made positive contribution to PC 4. Similar findings were also reported by Maria sultan *et al.* (2012) in cluster bean.

All the 21 genotypes were grouped into five clusters following Tocher's methods (Table 4). Cluster I constitutes of seven genotypes, forming the largest cluster followed by cluster IV and cluster V with five genotypes each. Cluster II consist of three genotypes and clusters III was comprised of single genotype. The pattern of group constellation proved the existence of significant amount of variability. There are forces other than geographical separation such as natural and artificial selection, exchange of breeding material, genetic drift,

**Table 2. Analysis of variance for different quantitative traits in winged bean**

| Characters | Treatments (df= 20) | CV % |
|---|---|---|
| Vine length (cm) | 14152.800** | 10.14 |
| Primary branches/plant | 19.882** | 22.46 |
| Days to first flowering | 2453.884** | 25.20 |
| Days to first harvest | 2101.975** | 19.32 |
| Days to edible maturity | 15.949** | 15.86 |
| Pod length (cm) | 12.333** | 10.72 |
| Pod girth (cm) | 1.982** | 10.69 |
| Pod weight (g) | 28.975** | 16.24 |
| Pods/plant | 2660.800** | 34.39 |
| Yield/plant (g) | 906210.000** | 35.30 |
| Seeds/pod | 13.543** | 17.60 |
| 100 seed weight (g) | 104.930** | 18.27 |

** Significant at P= 0.01

**Table 3. Principal components for 12 quantitative traits in winged bean**

| Trait | PC 1 | PC 2 | PC 3 | PC 4 |
|---|---|---|---|---|
| Eigen value | 5.786 | 2.421 | 1.394 | 0.734 |
| percentage variance | 48.22 | 20.17 | 11.62 | 6.11 |
| Cumulative variance | 48.22 | 68.40 | 80.02 | 86.14 |
| Eigenvectors | | | | |
| Vine length | 0.028 | 0.399 | 0.364 | 0.691 |
| Primary branches/plant | 0.294 | 0.301 | -0.202 | -0.305 |
| Days to first flowering | 0.332 | 0.326 | -0.065 | -0.030 |
| Days to first harvest | 0.315 | 0.295 | -0.233 | 0.040 |
| Days to edible maturity | -0.244 | 0.333 | 0.224 | -0.398 |
| Pod length | -0.346 | 0.279 | 0.028 | -0.035 |
| Pod girth | -0.275 | -0.149 | -0.495 | 0.353 |
| Pod weight | -0.395 | -0.043 | -0.163 | -0.143 |
| Pods/plant | -0.350 | -0.066 | -0.060 | -0.030 |
| Yield/plant | -0.279 | 0.358 | -0.220 | 0.267 |
| Seeds/pod | -0.211 | 0.455 | -0.236 | -0.198 |
| 100-seed weight | 0.214 | -0.042 | -0.579 | 0.093 |

**Table 4. Distribution of 21 winged bean genotypes in five different clusters**

| Cluster | Number of genotypes | Genotypes included |
|---|---|---|
| I | 7 | PT 1, PT 4, PT 8, PT 14, PT 15, PT 20, PT21 |
| II | 3 | PT 5, PT 10, PT 19 |
| III | 1 | PT 18 |
| IV | 5 | PT 7, PT 9, PT 11, PT 12, PT 17 |
| V | 5 | PT 2, PT 3, PT 6, PT13, PT 16 |

environmental variation, etc., which are responsible for diversity in winged bean. Therefore, choice of the parents for hybridization should be decided on the basis of genetic diversity rather than geographic diversity. Many earlier studies on $D^2$ statistics in various crops already showed the lack of parallelism between genetic and geographic diversities. Similar results were also reported by Singh and Singh (2006) in field pea, Dahiya *et al.* (2007) and Pandey (2007) in cowpea, and Mahto and Dua (2009) and Kushwaha *et al.* (2013) in winged bean.

The intra-cluster $D^2$ value ranged from 0.00 to 46.37, while inter-cluster $D^2$ value ranged from 44.77 to 269.17 which indicated that the selected genotypes were highly divergent (Table 5). The maximum intra cluster distance was recorded for cluster-II followed by cluster-I and cluster-III, IV and V showed no intra-cluster distance values indicating comparatively homogenous nature of the genotype within the cluster. The high intra-cluster distance in cluster-II indicated the presence of wide genetic diversity among the genotypes in this cluster. The maximum inter-cluster $D^2$ value was observed between cluster-II and V followed by cluster-I and V, cluster-II and IV and cluster-III and V suggesting that the genotypes belonging to these clusters may be used as parents for hybridization programme to develop desirable type because for a successful breeding programme, selection of genetically diverse parents is an important prerequisite so as to obtain better and desirable recombinants (Rai and Dharmatti, 2013). Similar results were reported by Venkatesan *et al.* (2004), Naher *et al*. (2005) in cowpea Arora *et al.* (2005) in cluster bean, and Mahto and Dua (2009) and Kushwaha *et al*. (2013) in winged bean.

**Table 5. Average intra (bold face) and inter-cluster distance ($D^2$) for 21 winged bean genotypes**

| Clusters | I | II | III | IV | V |
|---|---|---|---|---|---|
| I | 25.56 | 54.07 | 44.77 | 53.96 | 169.62 |
| II | | 46.37 | 83.32 | 127.66 | 269.17 |
| III | | | 0.00 | 53.53 | 105.44 |
| IV | | | | 0.00 | 89.16 |
| V | | | | | 0.00 |

**Table 6. Relative contribution of 12 characters towards genetic divergence in 21 winged bean germplasm**

| S. No. | Characters | Number of times ranked first | % contribution |
|---|---|---|---|
| 1 | Vine length (cm) | 6 | 2.86 |
| 2 | Primary branches / plant | 1 | 0.48 |
| 3 | Days to first flowering | 65 | 30.95 |
| 4 | Days to first harvest | 20 | 9.52 |
| 5 | Days to edible maturity | 28 | 13.33 |
| 6 | Pod length (cm) | 7 | 3.33 |
| 7 | Pod girth (cm) | 10 | 4.76 |
| 8 | Pod weight (g) | 31 | 14.76 |
| 9 | Pods / plant | 2 | 0.95 |
| 10 | Yield / plant (g) | 2 | 0.95 |
| 11 | Seeds / pod | 17 | 8.10 |
| 12 | 100 seed weight (g) | 21 | 10.00 |
| | Total | 110 | 100 |

The knowledge of the characters contributing to divergence is an important factor and the contribution of an individual character to the total divergence has been worked out in terms of number of times it ranked first (Table 6). This study helps in identifying the diversity in different proportion which ultimately helps in deciding the utilization of genetic material for the improvement of specific character. The maximum contribution to genetic divergence by days to first flowering followed by pod weight, days to edible maturity and 100-seed weight, therefore necessary attention is required to be focused on these characters. There is always difference in opinion in specifying the trait that is contributing high or low towards the genetic diversity. The contribution mainly depends upon the genotypes included in the study and the environment influences over the character. Regarding the least contribution, number of primary branches per plant and pods per plant contributed the least. The minimum contribution by this trait reveals that this trait was least affected in course of evolution.

The comparison of cluster means revealed considerable differences among the clusters of different quantitative characters (Table 7). Cluster-I showed the high mean values for days to edible maturity and number of seeds per pod. Cluster-IV showed highest mean value for pod length, pod girth, pod weight, number of pods per plant, yield per plant and 100-seed weight. The maximum value of cluster mean for vine length, primary branches per plant, days to first flowering and days to first harvest was recorded in cluster-V.

It has been well established that greater the genetic variability in the population higher will be the chances of obtaining desirable gene combination. In the present study, the possibility of choice of highly divergent and desirable types based on $D^2$ cluster means was also examined. The cluster-IV had the highest cluster mean values for number of pods per plant and yield per plant

**Table 7. Cluster mean values for different quantitative characters in winged bean**

| Cluster Characters | I | II | III | IV | V |
|---|---|---|---|---|---|
| Vine length (cm) | 668.45 | 675.90 | 553.33 | 767.67 | 813.33 |
| Primary branches / plant | 12.91 | 8.57 | 11.33 | 11.67 | 15.67 |
| Days to first flowering | 117.32 | 89.00 | 119.26 | 175.22 | 178.83 |
| Days to first harvest | 142.59 | 111.29 | 146.24 | 190.35 | 192.67 |
| Days to edible maturity | 15.15 | 14.57 | 11.67 | 11.33 | 13.67 |
| Pod length (cm) | 19.06 | 19.24 | 17.58 | 20.16 | 14.84 |
| Pod girth (cm) | 7.80 | 7.65 | 6.76 | 8.32 | 5.03 |
| Pod weight (g) | 19.61 | 20.14 | 14.30 | 20.76 | 10.13 |
| Pods / plant | 84.73 | 99.18 | 47.43 | 99.42 | 44.98 |
| Yield / plant (g) | 1493.33 | 1819.52 | 696.67 | 2083.33 | 750.00 |
| Seeds / pod | 12.79 | 11.82 | 10.75 | 11.22 | 8.05 |
| 100 seed weight (g) | 34.42 | 29.83 | 26.96 | 37.52 | 27.76 |

and cluster-V has the highest mean value for number of primary branches per plant. The genotypes in the two clusters may be utilized in crossing programme which may yield in a wide spectrum of variability and for selection for pod yield in the subsequent generations. The lines fall into same cluster having lowest degree of divergence from each other (Fig. 1) and crosses among these lines of the same cluster unable to produce any transgressive segregants. While, the lines belonging to different clusters having maximum divergence. Similarly

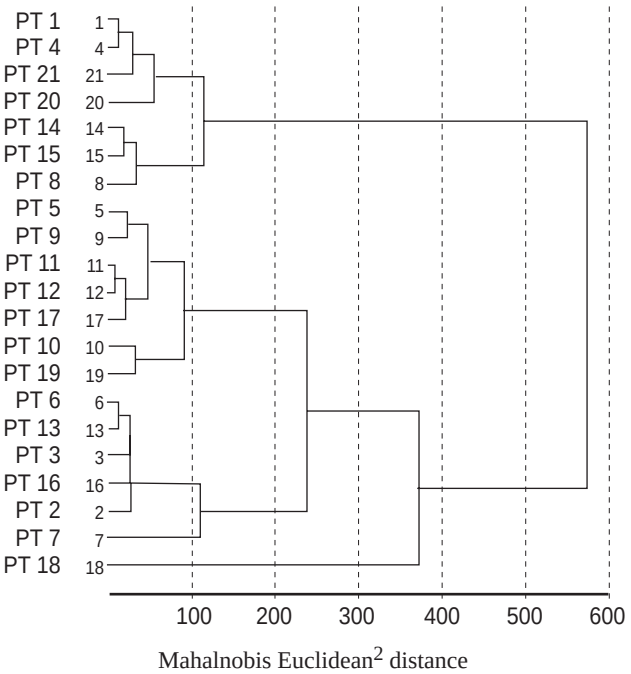


**Fig. 1. Euclidean average linkage dendrogram**

the cluster-I which had highest cluster mean value for number of seeds per pod and may be selected for crossing with the cluster-IV for obtaining desirable segregants with higher yield.

## References


Arora D, NPS Dhillon and AS Sidhu (2005) Genetic diversity studies in cluster bean (*Cyamopsis tetragonoloba* (L.) Taub) germplasm collection. *Crop Improv*. **32:**86-91.

Bhatt GM (1970) Multivariate analysis approach to selection of parents for hybridization aiming at yield improvement in self-pollinated crops. *Australian J. Agric. Res.* **21**: 1-7.

Chaudhary SPS, AK Choudhary, SS Shekhawat and NP Singh (2003) Quantitative genetic analysis in some genotypes of cluster bean. *Adv. Arid Leg. Res.* pp. 9-13.

Dahiya OP, D Singh and SK Mishra (2007) Genetic divergence in cowpea (*Vigna ungiculata* (L.) Walp). *Arid legumes* **4**: 62-65.

Indradeo Pandey (2007) Genetic diversity in grain cowpea. *Legume Res.* **30**: 92-97.

Kushwaha, RK, Rajeshwar Nandan and GE Reddy (2013) Genetic divergence for morphological and qualitative characters in winged bean. *Progressive Res.* **8**: 200-202.

Mahalanobis PC (1936) On generalized distance in statistics. *In*: *Proceed. National Institute of Sci. India* **2**: 49-55.

Mahto CS and RP Dua (2009) Genetic divergence for yield contributing traits in winged bean (*Psophocarpus tetragonolobus* L. (DC)). *Indian J. Plant Genet. Resour.* **22**: 239-242.

Maria Sultan, M Ashiq Rabbani, ZK Shinwari and M Shahid Masood (2012) Phenotypic divergence in guar (*Cyamopsis tetragonoloba*) landrace genotypes of Pakistan. *Pakistan J. Bot*. **44**: 203-210.

Naher Z, MG Rabbani and EHMS Rahaman (2005) Study on genetic diversity for quantitative characters in cowpea (*Vigna unguiculata* (L.) Walp.). *Bangladesh J. Training Development* **18**: 135-140.

Panse VG and PV Sukhatme (1964) Statistical Methods for Agricultural Workers, ICAR, New Delhi pp. 235-247.

Rai PS and PR Dharmatti (2013) Genetic divergence studies in clusterbean genotypes (*Cyamopsis tetragonoloba* (L.) Taub.). *Global J. Sci. Frontier Res. Agric. Veterinary* **13**: 45-48.

Rao CR (1952) Advanced Statistical Method in Biometrical Research, *Ed. II. New York. John Willey and Sons.*

Singh JD and IP Singh (2006) Genetic divergence in advanced genotypes for grain yield in field pea (*Pisum sativum* L.) *Legume Res.* **29**: 301-303.

Singh RK and BD Chaudhary (1985) Biometrical Methods in Quantitative Genetic Analysis, Kalyani publishers, New Delhi-Ludhiana, India. p. 318.

Venkatesan M, P Veeramani, P Thangavelu and J Ganeshan (2004) Genetic divergence in cowpea (*Vigna unguiculata* (L.) Walp.). *Legume Res.* **27**: 223-225.

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REPORT ON THE 1ST INTERNATIONAL AGROBIODIVERSITY CONGRESS, NEW DELHI

# Delhi Declaration provides a Roadmap for Agrobiodiversity Management

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First International Agrobiodiversity Congress (IAC2016) organized during 6-9 November 2016 at New Delhi was a watershed event in the field of agrobiodiversity. For the first time ever, an international scientific meeting dedicated to deliberate and discuss on conservation and use of agrobiodiversity in all its forms (plant, animal, aquatic, microbial and insect genetic resources relevant to food and agriculture) was organized. Objective of the first International Agrobiodiversity Congress (IAC2016) was to provide a platform to all the stakeholders engaged in genetic resource conservation and management to deliberate on thematic issues of global importance, with major emphasis on rational and effective use of agrobiodiversity for food, nutritional and environmental security. As many as 900 delegates belonging to 60 countries participated in Congress. For details of the program, speakers and to download publications please visit www.iac2016.in.

**Key Words: Agrobiodiversity, Delhi Declaration, IAC2016**

## Prime Minister Articulated Nation's Resolve on Agrobiodiversity

The IAC2016 was inaugurated by the Prime Minister of India who called for intensifying research in agrobiodiversity and harmonizing global laws on conservation to ensure food security. The Prime Minister elaborated on the strength of India's agrobiodiversity and the associated knowledge and invited the countries to develop a "shared vision" on the use of diversity for sustainability. More than 900 delegates representing 60 countries participated in the IAC2016. Organizers ensured adequate participation from gene-rich developing countries including from Africa, Central Asia and South Asia. Participants also included 41 genebank managers, over 100 students and more than 50 farmers and community representatives. Spanning the four days of IAC2016, there were 16 technical sessions, four satellite sessions, a genebank round table dialogue, a public forum, a farmers' forum and poster sessions. Participants witnessed eight plenary and two evening lectures, 72 invited lectures and 50 rapid oral presentations in the technical sessions and 30 presentations in the four satellite sessions. About 450 posters were displayed offering a cross-sectional view of the ongoing work in conservation and use of genetic resources of plants, animals, fishes, microbes and insects for food and agriculture.


## Thought-provoking Plenary Sessions and Panel Discussions

In the first plenary session on "Agrobiodiversity for Sustainable Development Goals (SDGs)", while M Ann Tutwiler (Bioversity International) highlighted the need to develop an Agrobiodiversity Index to help deliver the SDGs, RS Paroda (ISPGR & TAAS)

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emphasized on the enhanced use of agrobiodiversity despite changing global paradigms. In the second plenary session on "Conservation through Use", Gurdev S Khush, (University of California) illustrated the theme with use of rice germplasm to develop mega-varieties of rice. Toby Hodgkin (Platform for Agrobiodiversity Research) stressed the need for adopting systems based approach for conservation. In the ensuing panel discussion issues like preparedness for climate change (S Rajaram, RSM) and use of crop wild relatives (Marie Haga, Crop Trust), landraces (Calvin Qualset, University of California) and new technologies and tools (Usha Zehr, Mahyco) were highlighted. Third Plenary Session was on "Agrobiodiversity for Livelihood Security and Ecosystem Services" where two expositions linked livelihood security to conservation of biodiversity (Kamal Bawa, University of Massachusetts) as well as grassroots innovations and market mediated value chain development (Anil Gupta, NIF and IIMA). In the panel discussion issues raised include genetic erosion of farmers varieties and resultant vulnerability (Nikolay Dzyubenko, VIR), linkages between formal and informal seed system to strengthen ecosystem services (Coosje Hoogendoorn, Royal Tropical Institute) and the need of empirical studies (Gerry Jayawardena, SCARP). The last plenary session was about "Access and Benefit Sharing (ABS) in the Context of Regulatory Systems". While RS Rana (NBA and Ex-NBPGR) described the international treaties that regulate access to genetic resources and benefit sharing along with some Indian examples, Ronnie Coffman (Cornell University) shared the experience of the Borlaug Global Rust Initiative in germplasm exchange. Panelists (RS Hamilton, IRRI; Sudhir Kochhar, Ex-ICAR; Neeti Wilson, Anand & Anand) expressed the need to increase awareness and simplify the procedures, and called for greater clarity of ownership issues, transparency and legal certainty.

## Food, Nutrition and Environmental Security

Speakers of technical session on "Food, Nutrition and Environmental Security" brought to fore significance of effective partnerships (Martin Kropff, CIMMYT), mainstreaming agrobiodiversity (T Mohapatra, ICAR), bio-fortification (Howdy Bouis, HarvestPlus), diversified agro-ecological systems (Emile Frison, IPES-Food), synecological farming (M Funabashi, Sony Computer Science), animal genetic resources for food security (Olivier Hanotte, ILRI), insect biodiversity in ecosystem services (NK Krishna Kumar, Bioversity International), fish genetic resources for food security (JK Jena, ICAR), wealth of microbial diversity of extreme regions (Anil Kumar Saxena, NBAIM) and innovative integrated systems (Sijun Zheng, Yunnan Academy of Agricultural Sciences, China). Deliberations in the technical session on "Adaptation and Mitigation to Climate Change" focused upon use of orphan legumes (Ed Southern, Kirk House Trust), rethinking the role of science (Jacob van Etten, Bioversity International), mitigation strategies (JC Rana, NBPGR), post-disaster revival of local seed system (Devendra Gauchan, Bioversity International), diversifying rural livelihoods for climate resilience (Putri Hendrawan, ICRAF, Indonesia), policy framework (BK Joshi, Bioversity International, Nepal), and challenges to aquaculture (MP Paulton, CMFRI). Country experiences on germplasm enhancement for abiotic stresses tolerance from Nigeria (BN Motagi), Kenya (Ganga Rao), Niger (Hamidou Falalou), and Kenya (Manyasa Eo) were also presented.

## Conservation Strategies and Science-led Innovations

In the technical session on "Conservation Strategies and Methodologies" speakers on "Seed Genebanks" discussed the aspects of global system for the *ex situ* conservation (Marie Haga, Crop Trust), enhancing the genetic gains (HD Upadhyaya, ICRISAT), *in situ*/ on-farm conservation of dryland agrobiodiversity (Mariana Yazbek, ICARDA), genetic erosion in *ex situ* collections (N Murthy Anishetty, Ex-FAO) and India's prominent role in conservation and use of PGR (RK Tyagi, NBPGR). Speakers on "*In Situ* and On-farm Conservation" focused on crop landraces (Calvin Qualset, University of California), informal seed systems (Coosje Hoogendoorn, Royal Tropical Institute), strategic action plan for crop wild relatives (Nigel Maxted, University of Birmingham), tropical fruit tree diversity (V Ramanatha Rao, GRSV) and on-farm management of root and tuber crops (Stefan De Haan, CIAT). Speakers on "*In Vitro*, Cryo, and DNA Banking" highlighted scientific priorities (Hugh Pritchard, RBG), bridging the gap between gene function and phenotype (Hiroshi Abe, RIKEN), cryopreservation for perpetual conservation (Bart Panis, Bioversity International), applications of cryobanking (Rekha Chaudhary, NBPGR), and *in vitro* propagation of tropical RTBs (Badara Gueye, IITA). Concurrent sessions on genetic resources other than plants deliberated on complementary strategies and global innovation challenges (SJ Hiemstra, CGN), Indian dairy animal

biodiversity (SB Gokhale, BAIF), responsible fisheries and technologies (CN Ravishankar, CIFT), conservation of animal genetic resources in India (Arjava Sharma, NBAGR), birds and insectivory (A Verghese GPSIAM), Conservation of Fleshy Fungi (RC Upadhyay, DMR), conservation of pollinator biodiversity (VV Belvadi, UASB) and microbial conservation strategies (Sushil K Sharma, NBAIM).

Technical session on "Science-led Innovation: Trait Discovery and Enhanced Use of PGR" deliberated on global wheat breeding program (Ravi Singh, CIMMYT), value capture from PGR (Andreas Graner, IPK), trait value of Indian wild rice (NK Singh, NRCPB), introgression of biotic stress resistance genes in rice (Kuldeep Singh, NBPGR), and neglected and utilized crops (Zhang Zongwen, Bioversity International, China). Concurrent session on "PGR and Genomics" recorded the progress made in application of genomics to enhanced utilization (Robert Henry, QAAFI), deciphering the potential of wheat (Bikram Gill, Kansas State University), identification of novel genes and alleles for biotic stress resistance (TR Sharma, NRCPB) and genome sequencing of African indigenous tree species (Alice Muchugi, ICRAF). In the concurrent Session on "PGR Informatics", speakers covered wide range of topics including third global assessment on the state of PGRFA conservation and use (Stefano Diulgheroff, FAO), digital technologies for effective use of PGR (Eric Huttner, ACIAR), accessing information for discovery and deployment of PGR (Michael Mackay, University of Queensland) and India as a crucible to develop integrated information systems (Sunil Archak, NBPGR). Concurrent sessions on other genetic resources recorded presentations on genetic improvement of adaptive traits in livestock (JM Reecy, Iowa State University), aquaculture genomic resource (Vindhya Mohindra, NBFGR), advanced reproductive biotechnologies for animal conservation (AK Srivastava, NDRI), molecular traceability of spatial genetic diversity of fish genetic resources (Kuldeep K Lal, NBFGR), innovation for utilization of insect genetic resources (Chandish Ballal, NBAIR), devising strategies for salinity and drought tolerance by using microbial diversity of the Rann of Kutch (KK Pal, DGR), insect derived volatiles (Bakthavatsalam N, NBAIR), and genome based informatics of agriculturally important microorganisms (Alok Srivastava, NBAIM).

**Policies on Biosecurity, ABS and Partnership**

Technical session on "Quarantine, Biosafety and Biosecurity Issues" discussed effect of provisions of CBD and WTO (Ravi Khetrapal, CABI), invasive species and international trade (Kenza Le Mentec, STDF, WTO) on the use and exchange of germplasm (P Lava Kumar, IITA, Nigera). There was a panel discussion within the session (Panelists: GJ Randhawa, NBPGR; Vibha Ahuja, BCIL; and Neeraj Sood, NBFGR) that brought out specific recommendations on enhanced use of agrobiodiversity complying with the provisions of biosecurity and biosafety. In the technical session on "IPRs, ABS and Farmers' Rights" speakers presented the status on Indian initiatives on farmers' rights (RR Hanchinal, PPV&FRA), strategies for enhanced role of ITPGRFA in use of agrobiodiversity (Lim Engsiang, ITPGRFA), and ABS of animal genetic resources (Ilse Köhler-Rollefson, LPP). On the other hand, technical session on "Partnership, Networks and Capacity Building" witnessed talks on lessons learned and success stories from PGR networks (Stephan Weise, Bioversity International), capacity building in application of biotechnology (Darshan Brar, PAU), implementation of SUWON declaration (Raghunath Ghodake, APAARI), transforming Indian agriculture for national and global environmental benefits (GG Koppa, FAO), and plant diversity to improve food security and support the livelihoods of local communities (Tiziana Ulian, Royal Botanic Gardens).

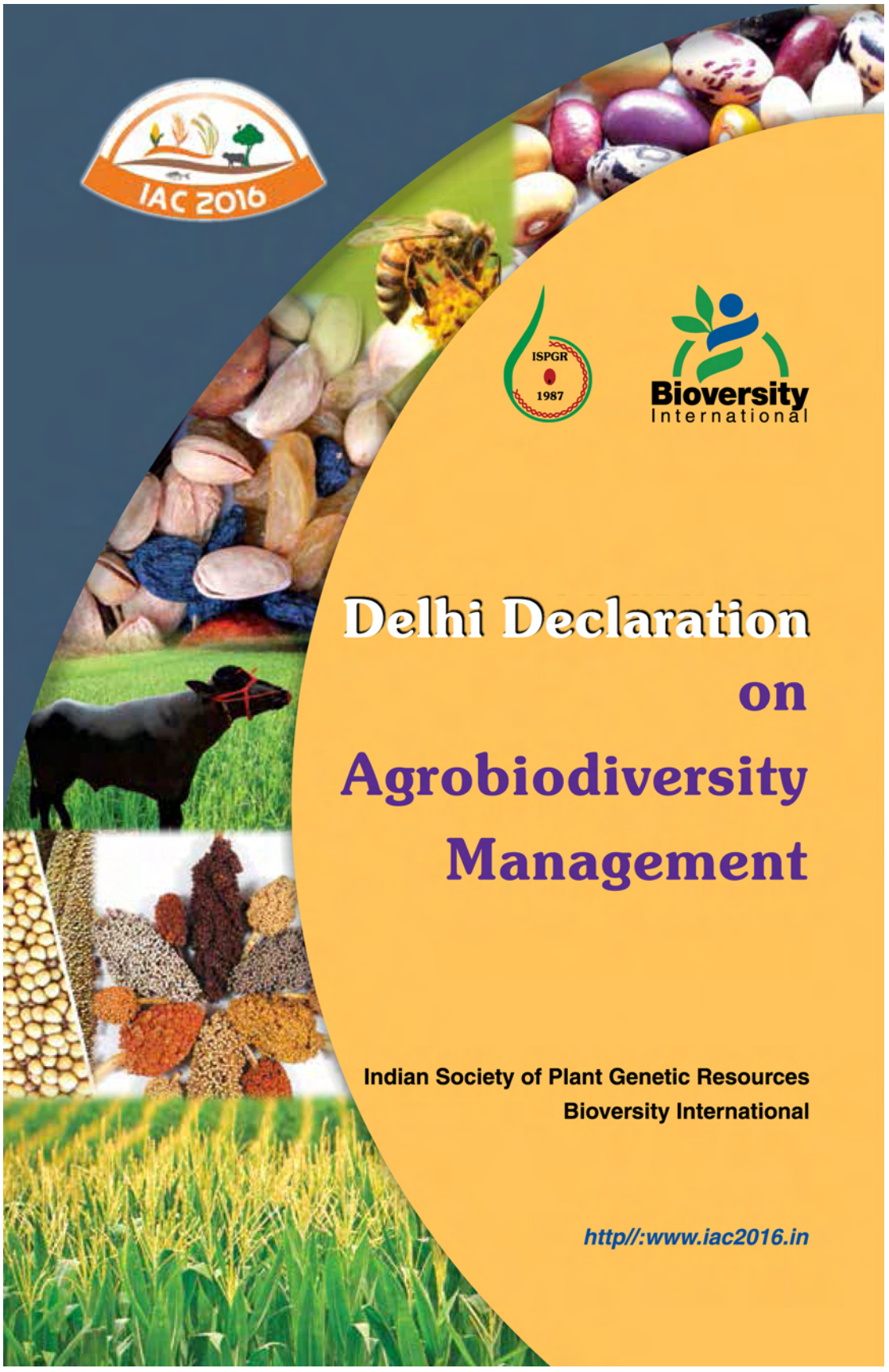
**Public Forum, Farmers' Forum, Round-table Dialogue and Satellite Sessions**

Participants were regaled by inimitable duo of MS Swaminathan (MSSRF, India) and Peter Raven (MBG, USA) in their evening lectures full of narratives where they both underlined "agrobiodiversity for huger-free world". A public forum on "Role of Stakeholders in Agrobiodiversity Management" was coordinated by MS Swaminathan and RS Paroda. Panelists represented international organization (Adel El-Beltagy, IDDC, Egypt); grass-root innovators (Anil Gupta, NIF); farmers (Ajay Jakhar, BKS) and legal fraternity (Sunita Sreedharan, SKS Law). Public forum called for urgent attention to check biodiversity loss and incentivizing stakeholders' participation. A farmers' forum was also arranged on the topic "Farmers' Role in Conservation

of Genetic Resources" and was moderated by RR Hanchinal (PPV&FRA), AK Singh (ICAR) and Vipin Kumar (NIF). Practicing on-farm conservators presented their case (in vernacular dialects helped by translation) on passion to conserve; economics of conservation activities; and need for sustained support. IAC2016 had a unique session as "Round Table Dialogue on Genebank Management: Challenges and Opportunities" where genebank managers from 41 countries participated in the discussion. Recommendations included completion, rationalization and documentation of collections, and capacity building.

IAC2016 also hosted satellite sessions on "Harnessing Biodiversity for Food Security and Sustainable Development" (Organized by CIMMYT); "Agrobiodiversity for Nutrition and Health" (Organized by Bioversity International and National Institute of Nutrition); "Climate Change as an Opportunity for Agrobiodiversity Management" (Organized by GIZ) and "Crop Wild Relatives: Back to the Wild to Save the Future" (Organized by Bioversity International and University of Birmingham). Besides all the scientific deliberations, major attraction of the IAC2016 was an agrobiodiversity exhibition. Diverse live exhibits of genetic resources representing India's agrobiodiversity hot-spots were on display by farmers and research institutes.

Based on the four-day deliberations, the delegates unanimously adopted the **Delhi Declaration on Agrobiodiversity Management**. The Declaration calls upon nations to accord top priority to the shared vision of agrobiodiversity conservation and their sustainable use towards achieving targets of SDGs relating to poverty alleviation, food and nutritional security, good health, gender equity and partnership. Participants urged for periodic organization of International Agrobiodiversity Congress starting with IAC2020 that was agreed to be facilitated by Bioversity International. A Special Issue of the Indian Journal of Plant Genetic Resources, containing extended summaries of 71 invited talks as well as a Souvenir containing messages and agrobiodiversity-related functional profile of organizing partners were also released during the Congress. Detailed information about the Congress including publications and photographs are available at www.iac2016.in.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on
Agrobiodiversity
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Indian Society of Plant Genetic Resources
Bioversity International
http//:www.iac2016.in

The **1st International Agrobiodiversity Congress** held in New Delhi, India, from 6-9 November, 2016 was attended by over 900 participants from 60 countries. Congress delegates discussed various aspects of conservation, management, access and use of agrobiodiversity in 16 technical sessions, four satellite sessions, a genebank roundtable, a public forum, a farmers' forum and poster sessions. Based on detailed deliberations, the delegates unanimously adopted the following declaration in the concluding session on November 9, 2016:

## PREAMBLE

- Agrobiodiversity includes crop varieties, livestock and fish breeds, and agriculturally useful insect and microbial species. Significant progress has been made towards the documentation, collection, conservation and use of agrobiodiversity related genetic resources, yet much more needs to be done towards their sustainable use, greater exchange and knowledge and technology transfer.

- If conserved and used sustainably, agrobiodiversity could make an important contribution towards resolving problems of hunger, food insecurity, malnutrition and climate change, thus help in attaining the Sustainable Development Goals (SDGs) and the Aichi Targets of the Convention on Biological Diversity.

- Limitations in policies, investment, infrastructure, technical capacity as well as cross-sectoral coordination and partnerships have often prevented efficient use of agrobiodiversity. This is particularly alarming since it is projected that the world, where almost 795 million people go hungry today, will need 70% more food to feed 9.6 billion people by 2050 (FAO, 2015). Hence, high priority and policy support by world leaders and organizations is warranted for enhanced use of agrobiodiversity.

- The world is also facing rapid loss and extinction of biodiversity. It is estimated that species are being lost at 1,000 to 10,000 times the rate at which natural extinction took place at any time during the past 66 million years mainly due to explosive population growth and overexploitation of natural resources. Extinction of agrobiodiversity and associated traditional knowledge is an irreversible process and hence must receive priority attention. In fact, loss of a gene is a major loss for our future generations.

## DECLARATION

1. We call upon nations to accord top priority to the shared vision of agrobiodiversity conservation and sustainable use towards achieving the Sustainable Development Goals (SDGs) and the Aichi Targets of the Convention on Biological Diversity addressing poverty alleviation, food, nutritional and health security, gender equity and global partnership.

2. We recognize the importance of traditional agrobiodiversity knowledge available with farm men and women, pastoralists, tribal and rural communities and its central role in the conservation and use for a food secure and climate resilient world. We, therefore, call upon countries to develop the necessary legal, institutional and funding mechanisms to catalyze their active participation.

3. We urge researchers and the policymakers to initiate, strengthen and promote complementary strategies to conserve agrobiodiversity through use, including greater emphasis on using crop wild relatives. We call for them to ensure a continuum between ex situ, in situ, on-farm, community-based and other conservation methods with much greater and equal emphasis on each.

4. We propose that researchers employ modern technologies including, but not limited to, genomics, biotechnology, space, computational, and nano-technologies for genetic resources characterization, evaluation and trait discovery. The aim must be to achieve efficiency, equity, economy and environmental security through diversified agricultural production systems and landscapes.

5. We reemphasize the necessity of global exchange of plant, animal, aquatic, microbial and insect genetic resources to diversify agriculture as well as our food basket and to meet the ever-growing food and nutritional needs of all countries. To ensure this, nations need to be catalysed to adopt both multi-lateral (as envisaged in the International Treaty on Plant Genetic Resources for Food and Agriculture) and bilateral (as per the Nagoya Protocol) instruments to facilitate the exchange of genetic resources, while ensuring equitable access and benefit sharing opportunities.

6. Countries are also expected to harmonize their existing biosecurity systems, including phytosanitary and quarantine, and enhance their capacities to facilitate safe trans-boundary movement of germplasm.

7. We also expect that the governments and civil societies lay much greater emphasis on public awareness and capacity enhancement programs on agrobiodiversity conservation in order to accelerate its effective and efficient use.

8. We recommend the development and implementation of an Agrobiodiversity Index to help monitor on-going genetic resource conservation and management efforts, with particular emphasis on agrobiodiversity hot spots.

9. It is also urged that public and private sectors and civil societies henceforth actively invest in and incentivize the utilization of agrobiodiversity to mitigate malnutrition, increase the resilience and productivity of farms and farming households and enhance ecosystem services. Such efforts should lead to equitable benefits and opportunities, with particular emphasis on women and youth.

10. We urge countries to reprioritize their research and extension with increased investments to support the conservation and use of agrobiodiversity. Furthermore, we strongly recommend to create an International Agrobiodiversity Fund as a mechanism to assist countries and communities in scientific *in situ* and *ex situ* conservation and enhanced use of agrobiodiversity.

11. We urge the United Nations to consider declaring a 'Year of Agrobiodiversity' in order to draw worldwide attention and catalyse urgent actions for effective management of genetic resources by the global community.

12. Finally, we recommend that the *International Agrobiodiversity Congress* be held every four years, with Bioversity International playing the facilitator's role, to maintain the momentum gained in 2016 and continue emphasizing the need to implement the 'Delhi Declaration on Agrobiodiversity Management' and monitor the progress so made by the different stakeholders and countries.

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# GUIDELINES TO AUTHORS

## GENERAL

The Indian Journal of Plant Genetic Resources (IJPGR) is the official publication of the Indian Society of Plant Genetic Resources. For publication in the journal, the authors must be a member of the Society. IJPGR publishes full-length papers or short communications of original scientific research in the field of plant genetic resources. Review articles (with prior consent or invitation only) summarizing the existing state of knowledge in topics related to plant genetic resources will also be published.

Contributions should be as concise as possible. The maximum length of the review article, full-length papers and short communications is usually restricted to 12, 6, 3 printed pages including illustrations and tables, respectively.

## ORGANIZATION OF THE MANUSCRIPT

### Full-length papers

**Title Page:** The title page of the manuscript should be the first page and should include the title, names and addresses of the authors, abstract and keywords.

**Title:** Keep the title brief, specific and informative and amendable to indexing. It should be typed in running text with first letter of word as capital and latin names in italics.

**Name and Address:** The name of authors and the address of the institution where the work was carried out should be mentioned below the title. Present address of correspondence, if different, should be given as footnote indicating by asterisk (*) the author to whom the correspondence and reprint requests are to be made. E-mail addresses should also be indicated, if any.

**Abstract:** The abstract should clearly state the rationale, objectives, methods, and important conclusions of the study. It should not exceed 150 words.

**Key Words:** The abstract should be followed by not more than five key words indicating the contents of the paper and useful for abstracting purposes.

**Main Text:** The main text of the paper should start from the second page which should contain the title of the paper followed by the text divided into following main headings which are to be typed in running text and flushed with the margin: Introduction, Materials and Methods, Results, Discussion, Acknowledgements, References. Wherever appropriate, results and discussion can be combined and acknowledgements be omitted.

**Introduction** should be brief and limited to the statement of the problem and aim of the experiment.

**Materials and Methods** should include relevant details on the nature of material, experimental design, the techniques employed and the statistical method used. For well-known methods, citation of reference will suffice.

**Results and Discussion** should be clear to readers in different disciplines. Units of measurement should be SI.

**Tables** should be typed on separate sheets, each with a heading stating its contents clearly and concisely. Numerical data and calculations should be thoroughly checked.

**Figures** of only good quality that are essential to a clear understanding of the paper shall be accepted. Legends to the illustrations should be typed on separate paper. Information in the legend should not be repeated in the text and similarly, the same data should not be represented in both graph and table form. All figures, whether photographs, maps, graphs or line drawings should be numbered consecutively. Illustration number and title of the article with authors' name should be given at the back of the plates in soft pencil.

**Line drawings** of high quality, preferable in the desired final size would be accepted. The inscriptions should be clearly legible.

**Photographs** for publication should be of high contrast, black and white, glossy print, trimmed at right angles. Magnification should be indicated with a bar scale on the photo. Authors need to indicate colour reproduction of photographs (cost of colour printing borne by the authors).

**Acknowledgements** should mention only guidance or assistance received in real terms, and financial grant provided by an agency. Acknowledgements for inspiration, typing etc., need not be mentioned.

**References** in text should be cited by author, year of publication (e.g. Joshi, 1995) and multiple citations should be in chronological order (Withers and Englemann, 1998; Rao *et al.*, 2001). References should be listed in alphabetical order under the first authors' name. The names of journals should be abbreviated according to the latest edition of the World List of Scientific Periodicals (eds. P Brown and GB Stratton), Butterworths, London. The following examples may be used for citations:

1. Bisht IS, RK Mahajan, TR Loknathan and RC Agarwal (1998) Diversity in Indian sesame collection and stratification of germplasm accessions in different diversity groups. *Genet. Resour. Crop Evol.* **45**: 325-335.
2. Withers LA and F Engelmann (1998) In vitro conservation of plant genetic resources. In: A Altman (ed.) *Agricultural Biotechnology*. Marcell Dekker Inc., New York, pp 57-58.
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.
4. Engels, JMM and V Ramanatha Rao (eds) (1988) *Regeneration of seed crop and their wild relatives*. Proceedings of a Consultation Meeting, 4-7 December 1995. ICRISAT, Hyderabad, India and IPGRI, Rome, Italy, 167 p.

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The style and format as mentioned for full-length papers should be followed for Short Communications. However, the abstract should be restricted to not more than 50 words and the remainder text should be continuous (without headings). Illustrative material should be kept at minimum, usually not more than one table or figure and only few references should be included (not more than 10).

**Submission of the Manuscript**

Submission of an article will be held to imply that it has not been previously published or submitted for publication elsewhere. A cover letter including a statement to this effect should be submitted with the manuscript. Three copies of the manuscript written in English and typed in double space on one side of A4 bond paper with the pages numbered consecutively (starting with the title page and through the text, reference list, tables and figure legends, and should be submitted (preferably in floppy or CD or through email) to:

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## CONTENTS



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