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The Society was founded in 1987 with the following objectives:

- 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

Interplay of National and International Laws on Access to Biological Resources and Benefit Sharing 165
Rai S Rana

Identification of Gaps in Pigeonpea Germplasm from East and Southern Africa Conserved at the ICRISAT Genebank 180
HD Upadhyaya, KN Reddy, M Irshad Ahmed, CLL Gowda, M Thimma Reddy and Senthil Ramachandran

Diversity Analysis among Chickpea Genetic Stock as Revealed Through STMS Marker Analysis 189
Nandakini Lahiri, Tapan Kumar, C Bharadwaj, Ashutosh Sarker, Aqeel Hasan Rizvi, SK Chauhan, AK Verma and Guru Prasad

Patterns of Genetic Variation, Correlations under Irrigated and Rainfed Conditions in Indian Mustard [*Brassica juncea* (L.) Czern. & Coss.] 198
VV Singh, ML Meena, BR Singh and Dhiraj Singh

Rice Diversity – The Genetic Resource Grid of North-East India 205
A Anna Durai, JMS Tomar, Premila Devi, A Arunachalam and H Mehta

Genetic Variability and Diversity of *Sorghum* Landraces Collected from Uttar Pradesh, India 213
M Elangovan and P Kiran Babu

Exploiting Genetic Divergence for Crop Improvement in Coriander (*Coriandrum sativum* L.): A Neglected and Underutilized Crop 222
Giridhar Kalidasu, S Suryakumari, C Sarada, A Rajani, N Hariprasada Rao, SR Pandravada and L Naram Naidu

Variability and Correlation Studies in Garlic (*Allium sativum* L.) Germplasm Collected from Different Parts of Jammu 229
Shilpi Khar, Satesh Kumar, RK Samnotra, Manoj Kumar, Sandeep Chopra, Manish Kumar and Sachin Gupta

Recent Developments for Access to Plant Genetic Resources in India and their Implications 237
Pratibha Brahmi and Vandana Tyagi

SHORT COMMUNICATIONS

Fingerprinting Based on Microsatellite Markers for the Identification of Rice Varieties in Chhattisgarh 247
Jitendra Kumar Tiwari, NK Rastogi, PK Chandrakar and SB Verulkar

"Tikdi" – A Fruit Fly Resistant Land Race of Ber (*Ziziphus mauritiana* Lamarck) 252
Om Vir, Sharmila Roy, RK Tyagi, AK Singh and PR Meghwal

Screening of *Coffea arabica* Germplasm for Caffeine Level 256
TN Gopinandhan, NS Prakash, BR Shivalingu and DR Shanmukappa

HUBR-16: A High Yielding Early Maturity Rice Line Coupled with Extra Long Kernel and High Kernel Elongation 260
HK Jaiswal, Showkat A Waza and T Sravan

Genetic Divergence of Tossa Jute (*Corchorus olitorius* L.) for Fibre Yield and its Related Component Characters Under Moisture Stress Condition 263
Ashutosh Sawarkar, Sonika Yumnam, SG Patil and S Mukherjee

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Interplay of National and International Laws on Access to Biological Resources and Benefit Sharing

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International laws, emerging often from legally binding global conventions and treaties, operate through national laws extending their jurisdiction beyond their national boundaries but may also sometime override them. When a country becomes contracting party to several such treaties, and their provisions seem to be in conflict, problems may arise in fulfilling national obligations. Provisions on intellectual property rights under the Convention on Biological Diversity (CBD) and the WTO-TRIPS Agreement over products and processes, based on biological resources, illustrate this point. Likewise, provisions on sharing of benefits arising from the use of genetic resources under CBD and the Nagoya Protocol on one side and the International Treaty on Plant Genetic Resources for Food & Agriculture and the FAO Commission on Genetic Resources for Food & Agriculture on the other, seem to differ in many ways. This paper discusses the complex interplay of governance of access to genetic resources and benefit sharing at the international and national levels.

Key Words: Biological resources; Genetic resources; Access and benefit sharing; ABS mechanisms; ABS governance; Global governance of ABS; Regulatory system for ABS in India

I. ABS Governance at the National and International Levels

Global regulation of access to biological resources and sharing of benefits arising from their commercial utilization is one of the three most discussed topics today, the other two being the multilateral trade and climate change. Negotiations under various fora in this context require a clear understanding of the complex interplay of international laws and national legislation so as to maintain a harmonious and synergistic relationship among them.

An international law, or the law of nations, is primarily a system governing the relationship among nations who have become contracting parties to legally binding international treaties and are required to adapt their national legal framework to meet their national obligations under the provisions of those treaties. However, it happens sometimes that the national obligations under some international treaties on specific topics, like access to biological resources and benefit sharing, may appear to be in conflict as seen from the relevant provisions under the Convention on Biological Diversity (CBD) and WTO-Trade Related Intellectual Property Rights (TRIPS) or even those of CBD and the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA or the Plant Treaty).

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To go a step further, perceptions on the relationship between international law and national law also differ regarding supremacy of one over the other. There are two contending concepts: monism and dualism (Park and Yanos, 2006; Muller, 2013). The idea of monism assumes that international law and national law are simply two components of a single legal system and regards 'law' as one entity. In other words, both are interrelated parts of one single legal structure and form a unity, though international law may have supremacy over the national law in cases of conflict. Monism in practice envisages that the legal institutions of a country, such as its judiciary, legislature and executive, should ensure that national rights and obligations in this context conform to international law.

Dualism, on the other hand, assumes that international law and national law of States are two separate and distinct legal systems. Being different legal orders, international law would not as such form part of the domestic law of a State. Where rules of international law apply within a State, they do so as a result of their adoption under the national law and not under the international law. Dualism refrains from any controversy as to supremacy of one legal system over the other recognizing that each one is considered supreme in one's own sphere and operates on a different level but recognizes that, ultimately, national (state) interests can override the international interests

in some situations.

There are, however, some distinctions between national law and international law. Firstly, the subjects of national law are individuals, while the subjects of international law are Nation States. Secondly, juridical origins of the two legal systems are different, *i.e.*, the source of national law is the will of the representatives of public expressed through the State while the source of international law is the common will of contracting parties (Nation States). Thirdly, national law is a law of the sovereign (national government) over individuals (citizens) whereas international law is a law, not above, but among Sovereign States.

II. Access to Biological Resources and Benefit Sharing (ABS)

Governance systems for access to genetic resources and sharing of benefits (ABS) arising from their commercial utilization may be seen from several positions such as perspectives of the primary stakeholders, provisions of the national regulatory framework and the country's legally binding obligations under international treaties to which it is a Contracting Party (Halewood *et al*., 2014). Although the CBD, adopted in 1992, recognized sovereignty of nations over their natural resources, and also on setting terms of access to them subject to their national legislation, yet the bilateral, multilateral and international treaties as well as global conventions have a way of overriding the sovereign rights of nations in view of the contractual nature of these agreements (Oberthur and Rosendal, 2014).

Regulation of genetic resources has three distinct dimensions, namely, perspectives of their developers and users, governance at the state and national levels, and national obligations under international treaties/ agreements (Rana, 2010).

The first dimension comprises local farming communities (developers, conservers and end-users of their genetic resources who are the primary stakeholders), public sector research institutions and genebanks (trustee custodians of germplasm collections and users for public good), and seed companies/corporations (users for commercial utilization meant for private benefits). They together represent the main stakeholders and key beneficiaries. The second dimension involves policy makers, legislators, managers and administrators regulating authorised access while promoting conservation with sustainable use. The third dimension relates to national obligations under multilateral environment and trade agreements. Under the last category, three major international agreements, namely, CBD, ITPGRFA and WTO-TRIPS have impacted the access to genetic resources globally and also at the national level, more so in biodiverse developing countries. The first two treaties highlight the conservation of bio-resources, their sustainable use, regulated access and fair and equitable benefit sharing while the third focuses mainly on patenting/ crop variety protection laws that grant monopolistic/ exclusive rights to IPR holders/ breeders to the exclusion of the rights of farmers and other primary beneficiaries. All the three are legally binding treaties and India is a contracting party to them. Considering that agro-biodiversity constitutes a subset of the total biological diversity, and a very important one, it is imperative that all these international agreements need to be implemented in harmony with each other, more particularly in countries like India whose national economy is primarily based on agriculture (Tvedt, 2014).

III. Global Developments on ABS

In order to understand the landscape of international governance of genetic resources, it is important to appreciate the on-going governance efforts and identify the problematic areas where more attention is required for moving forward. An overview of the global developments, bearing on access to genetic resources and benefit sharing, is presented below:

1. International Laws and the National Legal and Policy Framework

National policies describe the objectives and missions of a government indicating how it proposes to achieve those objectives by issuing relevant guidelines. Laws, on the other hand, are the standard rules and regulations that are compulsory to be followed by all the people of that country and there are provisions in those laws for punishment for those who contravene them. In other words, laws help a government in setting up legal and institutional framework to achieve the aims spelt out in its policy statements. National laws are enacted by the parliament and enforced by the national government within its national boundaries. International laws, in contrast, arise from customary laws, judiciary pronouncements, and more often, from legally binding national obligations under international agreements, treaties, conferences and conventions. In a way, they expand the jurisdiction of national laws beyond their

national boundaries but they also impact them.

2. *Impact of the UN Conference on the Human Environment, 1972*

UN Conference on the Human Environment, held in Stockholm in 1972, took some important decisions concerning environment and sustainable development and had a significant impact in India. Impact of these decisions in the Indian context may be clearly seen in the 42nd Amendment to the Indian Constitution, enacted in 1976, adopting Article 48A (one among the Directive Principles which cannot be challenged in any court of law) stating that the State shall endeavour to protect and improve the environment and to safeguard the forests and wildlife of the country. The subject of wildlife and forests was thus transferred from the state list to the concurrent list of the constitution through this decree, providing enormous powers to the Central Government in this area. In addition, Article 51A (g) (Fundamental Duties) was also introduced to protect and improve the natural environment including forests, lakes, rivers, wildlife and to have compassion for living creatures. The Wildlife (Protection) Act, 1972 (as amended in 1991), the Water (Prevention and control of pollution) Act, 1974, the Air (Prevention and control of pollution) Act, 1981 and the Environment Protection Act, 1986 were enacted to fulfill the commitments made by India during the Stockholm Conference. In addition, a separate Department of Environment was created in 1980 and a separate Union Ministry of Environment & Forests (with Climate Change added subsequently) was established in 1985.

3. *The International Undertaking on Plant Genetic Resources, 1983: A New Initiative*

In 1983, the FAO established a Commission on Plant Genetic Resources (later renamed the Commission on Genetic Resources for Food and Agriculture), the first permanent intergovernmental forum devoted to conservation and development of genetic resources. The Commission's first major action was to adopt a non-binding resolution in 1983 for setting up the International Undertaking (IU) on Plant Genetic Resources (PGR). It worked on the basic principle that PGR are common heritage of humankind and, hence, should be made available to researchers without restriction. Many commercial seed companies disliked the IU because it required that elite genetic stocks (including improved and current breeders' lines) should also be made available without restriction. Under their influence, the United States and many other developed countries declined to sign the IU and adhere to it. Efforts to conciliate the concerns of developed and developing countries resulted in two 1989 amendments to the Undertaking paving the way for the United States and Canada signing the IU but they still declined to adhere to its binding obligations. In 1993, FAO adopted the Resolution 7/93, calling for intergovernmental negotiations for revision of the IU to harmonise its contents with those of the CBD, acknowledging thereby the sovereignty of States over their natural resources. Accordingly, provisions of the IU were suitably revised to bring them in harmony with those of the CBD and the revised version was adopted in 2001 as the legally-binding International Treaty on Plant Genetic Resources for Food and Agriculture.

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

In 1992, the United Nations hosted an Earth Summit in Rio de Janeiro and it gave birth to the legally binding Convention on Biological Diversity (CBD) under UNEP besides several other treaties. The CBD has 193 Contracting Parties making it almost globally accepted treaty though the USA is the only major country that has not yet ratified it. Its objectives include the conservation of biological diversity, sustainable use of its components and fair and equitable sharing of benefits arising out of the utilization of genetic resources.

To recapitulate, the CBD marked the end of the 'common heritage' concept of genetic resources and it asserted that nations have sovereign rights over natural resources within their boundaries, and that the authority to determine access to genetic resources rests with the national governments and it is subject to national legislation.

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 under it in 2004.

5. *The Nagoya Protocol to CBD on ABS, 2010: A New Beginning*

The Nagoya Protocol to CBD on ABS is a new international treaty on ABS, adopted in October, 2010 to support implementation of the third objective of CBD, namely, the fair and equitable sharing of benefits arising from the utilization of genetic resources. It is based on the twin principles of prior informed consent (PIC) and mutually agreed terms (MAT) enshrined in the CBD. This Protocol on ABS entered into force on 9 October, 2014 prompting the Parties to CBD to prepare for its implementation by taking appropriate policy, legislative and administrative measures. Sixty nations have already ratified this legally binding Protocol and many more are in the process of doing so. India signed the Protocol on 11 May, 2011 and ratified it on 9 October, 2012. This Protocol requires that Provider Parties adopt measures that need to:

- Create legal certainty, clarity and transparency for access to genetic resources
- Provide fair and non-arbitrary rules and procedures
- Establish clear rules and procedures for prior informed consent and mutually agreed terms
- Provide for issuance of an internationally recognized certificate of compliance when access is granted.

The Nagoya Protocol establishes clear rules for accessing, trading, sharing and monitoring the use of the world's genetic resources that can be used for pharmaceutical, agricultural, industrial, cosmetic and other purposes. By establishing this framework, it seeks to ensure that genetic resources are not used without prior consent of the countries that provide them, and that the communities, that possess the traditional knowledge associated with the use of these resources, also share the benefits arising from its commercial utilization. The Protocol seeks to increase transparency in transfer of genetic resources through its Access Benefit-Sharing Clearing House (ABS-CH), which is an online platform for exchanging relevant information (Morgera *et al*., 2014). Its goal is to enhance clarity on procedures in provider countries for access to genetic resources and also to monitor their commercial utilization in user countries.

6. *The International Treaty on Plant Genetic Resources for Food and Agriculture: New Approach to promote Global Food Security*

Recognizing the interdependence among countries regarding crop genetic resources, representatives of 135 member-nations of FAO approved in Rome on 3 November, 2001 a new International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) to promote global food security. The FAO had revised the text of the IU on PGR to bring its provisions in harmony with those of the CBD and then adopted it as the legally binding International Treaty. Farmers' Rights were recognized under this Treaty but its realization was left to the national governments in their jurisdiction. India's legislation on Protection of Plant Varieties and Farmers' Rights, 2001has led the way in this direction but there is need to evaluate its effectiveness. It is now widely recognized that a reliable way to realize Farmers' Rights is to enable them to save, exchange and sell the seeds of improved and IPR protected varieties grown by them, and also to assist them in improving their locally adapted crop varieties through participatory breeding while paying greater attention to the needs and circumstances of resource-poor farmers who are the real guardians of much of the agricultural biodiversity [FAO, 2010].

Of the nations participating in that FAO conference, that adopted the ITPGRFA, only the United States and Japan abstained, citing concerns about a lack of clarity regarding the effect of the Treaty on intellectual property rights (IPR). The Plant Treaty, which entered into force on 29 June, 2004, provides a Multilateral System (MLS) of Access and Benefit-Sharing to facilitate exchange of PGRFA. The MLS presently applies to an initial annex of 35 food crops and 29 genera of forages. Because this list is a result of political compromises, some crops that might have been expected to be covered, such as soybean, groundnuts, and sugar cane are conspicuously missing. It is notable that the MLS covers only those PGRFA which are "in the public domain;" and those which are held in trust, in *ex situ* collections by IARCs.

The Standard Material Transfer Agreement (SMTA) provides a mechanism for overcoming potential difficulties of enforcement by empowering FAO, as the entity chosen by the Governing Body, to represent its

interests as a third party beneficiary under the SMTA, and to initiate action where necessary to resolve disputes.

The Treaty forbids recipients of PGRFA through the MLS to claim any IPR on them in the form received from the MLS as that may limit access to them or their genetic parts or components. There are, however, some hazy areas on this aspect that need to be addressed (Andersen *et al*., 2010).

The ITPGRFA differs substantially from the CBD, as this treaty as a whole applies to one specific group of organisms, *i.e.*, plant genetic resources for food and agriculture (PGRFA). The MLS for ABS has become the legal instrument for the already ongoing exchange of accessions of PGR stored in the international collections, while adding a number of national collections to the MLS [See Box 1]. It still remains to be validated whether the MLS has led to more exchange of, and better access to, PGRFA. Further, the issue of genetic resources collected from countries of their origin, prior to CBD, still hangs on though the designated accessions stored in CGIAR's International Genebanks have been brought under the jurisdiction of FAO.

The Multilateral System for ABS under the Treaty, as mentioned above, applies only to PGRFA under specific circumstances, *i.e.* when certain accessions of PGRFA are in the public domain, are accessed for specific uses, and under the condition that no IPRs hinder the further exchange and access of the material received from the MLS. These limitations in the scope of the MLS need to be better understood if we are to clarify the legal relationship between the two instruments.

Box 1

Benefit-sharing under the Multilateral System of ITPGRFA

Facilitated access to genetic resources, that are in public domain and are included in the Multi-lateral System, is itself recognized as a major benefit for researchers and plant breeders. Other benefits arising from the use of PGRFA that are to be shared on a 'fair and equitable' basis include:

(1) Exchange of information
This includes catalogues and inventories, information on technologies and results of technical, scientific and socio-economic research on PGRFA including data on characterization and evaluation.

(2) Access to and transfer of technology
Contracting Parties agree to provide or facilitate access to technologies for the conservation, characterization, evaluation and use of PGRFA. The Treaty points out various means by which transfer of technology is to be carried out, including participation in crop-based or thematic networks and partnerships, commercial joint ventures, human resource development and through making research facilities available. Access to technology, including that protected by IPR, is to be provided and/or facilitated under fair and most-favourable terms, including on concessional and preferential terms where mutually agreed. Access to these technologies is provided while respecting applicable property rights and access laws.

(3) Capacity building
This Treaty assigns priority to programmes for scientific education and training in the conservation and use of PGRFA, to the development of facilities for conserving and using PGRFA and to the carrying out of joint scientific research.

(4) Sharing of monetary and other benefits arising from commercialization
Monetary benefits include payment into a special Benefit-Sharing Fund of the MLS of a share of the revenues arising from the sale of PGRFA products that incorporate material accessed from the MLS. Such payment is mandatory where the product is not available for further research and breeding, for example, as a result of certain types of patent protection. In the SMTA, adopted by the Governing Body at its First Session in 2006, the payment is set at 1.1% of the gross sales generated by the product less 30% (*i.e.* 0.77%).

When the CBD was finalized, negotiating parties recognized that some important issues were left without satisfactory solutions in international law as reflected in section 4 of Resolution 3 adopted by the Nairobi conference, where the text of the CBD was agreed, which reads: 'Further recognizes the need to seek solutions to outstanding matters concerning plant genetic resources within the Global System for the Conservation and Sustainable Use of Plant Genetic Resources for Food and Sustainable Agriculture, in particular: (a) Access to *ex situ* collections not acquired in accordance with this Convention; and (b) The question of farmers' rights.' These issues were referred to the FAO in the context of suitably revising the contents of the International Understanding on PGRFA. The issue of genetic resources collected from countries of their origin, prior to CBD, still hangs on but the designated accessions stored in CGIAR's International Genebanks have been brought under the jurisdiction of FAO.

The MLS is highly relevant for ABS because it is the first sectoral approach to ABS, and could provide useful lessons for the implementation of ABS, including whether and if so, how, sectoral ABS can be dealt with to meet the objectives of the CBD (under NP Art. 4 and Art. 19). Sixth Session of the Governing Body of the ITPGRFA, scheduled to be held in Rome on 5-9 October 2015, is expected to provide further guidance on this aspect.

7. Trade Related Intellectual Property Rights (TRIPS) Agreement under WTO

The TRIPS Agreement under WTO, which came into effect on 1 January 1995, is to date the most comprehensive multilateral agreement on IPRs. It requires Member countries to make patents available for any inventions, whether products or processes, in all fields of technology without discrimination, subject to the normal tests of novelty, inventiveness and industrial applicability. The WTO now has 153 member nations and 29 others with observer status.

There are three permissible exceptions to the basic rule on patentability. One is for inventions contrary to *ordre public* or morality including inventions dangerous to human, animal or plant life or health or seriously prejudicial to the environment. The second exception is that Members may exclude from patentability the diagnostic, therapeutic and surgical methods for the treatment of humans or animals. The third exception is that Members may exclude plants and animals other than micro-organisms and essentially 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 protection. The term of protection available shall not end before the expiry of a period of 20 years counted from the filing date. Members shall require that an applicant for a patent shall disclose the invention in a manner sufficiently clear and complete for the invention to be carried out by a person skilled in the art. Compulsory licensing and the government use, without the authorization of the right holder, are allowed.

It is noteworthy that the agricultural plants sector is currently the only one where access is granted under two ABS systems operated by the CBD and the FAO. In addition, two other systems are available for securing IPRs over them, namely, patents and plant breeders' rights [See also Box 2].

Box 2

Some Notable Points

Animal genetic resources are not covered under the ITPGRFA and WTO-TRIPS whereas CBD and also its Protocol on ABS cover all genetic resources holistically. CGRFA under FAO is now engaged in developing an international treaty on animal genetic resources on the pattern of ITPGRFA.

Accessions of PGR, that are stored in the National Genebank, need to be carefully scrutinized to identify designated accessions for placing them under public domain and making them available for exchange under ITPGRFA. For the PGR, not covered under the ITPGRFA, there is need to continue regulating their access and ensure benefit sharing as provided under the Biological Diversity Act, 2002. There is also an urgent need to prepare inventory of high value traits of our genetic resources and to monitor their commercial utilization abroad.

IV. Overlapping Provisions on ABS under CBD, ITPGRFA and TRIPS

Unlike the CBD, which provides for bilateral negotiations to establish the terms of access and benefit sharing for each specific exchange of materials, all multilateral germplasm exchanges under the MLS would be subject to SMTA. Monetary benefits would be paid to the Global Crop Diversity Trust Fund to be used primarily to support farmers who conserve and sustainably use PGRFA. However, the financing of germplasm conservation activities has been addressed only in general terms, making this aspect of the treaty potentially difficult to implement.

Concerns on the relationship between ABS provisions under CBD and other international legal regimes bearing on genetic resources led to inclusion of Article 4 in the Nagoya Protocol stating that the Nagoya Protocol does not apply to Parties to the specialized instrument in respect of specific genetic resources covered by and for the purpose of that specialized instrument. The scope of other existing regimes would therefore be crucial to define which genetic resources are covered by the Nagoya Protocol. The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), for example, has been in force since 2004. It is a global instrument designed to promote conservation of PGRFA, and to help protect farmers' rights, and also to ensure fair and equitable sharing of benefits arising from the use of PGRFA. The Plant Treaty has established a Multilateral System (MLS) under which genetic resources of crops, listed in Annex-1, are exchanged without individual regulation, subject to a standard material transfer agreement (SMT). One challenge concerning this instrument is that not all parties to the CBD are members of the Plant Treaty. Another concern is that ABS in the Plant Treaty differs from the ABS regime of the CBD.

Another alarming development is that the FAO CGRFA is now discussing ABS mechanisms for six more groups of genetic resources, namely, animals; aquatic; invertebrates; plants; forest; and microbial genetic resources (FAO, 2015). Any agreement in the Commission on need for specialised regimes for ABS holds potential to exclude commercially valuable groups of ABS governed by the CBD and the Nagoya Protocol. Another international platform for regulating access and benefit sharing has also reached agreement with the World Health Organisation in 2011 giving green signal to two SMTAs concerning exchange and use of viral genetic resources with pandemic potential for humans. The question of access and benefit sharing from genetic resources in the area beyond national jurisdiction has also been on the agenda of the UN Convention on the Law of the Seas and this may include, for example, genetic resources taken from the seabed and/or the high seas, taking them out of purview of CBD. In addition, discussion under the auspices of the Antarctic Treaty is also progressing on how to regulate genetic resource material from one of the world's most remote, yet biologically unique areas. To sum up, dimensions of global governance of ABS (related to bioresources) are being expanded and there is need for increasing clarity and also convergence.

V. Regulating Access and Benefit Sharing in India: Procedures

Under CBD, the sovereign authority to determine access to genetic resources rests with the national governments and it is subject to national legislation. To fulfill national obligations under the CBD, India enacted the Biological Diversity Act in 2002 through a systematic consultation process and also framed the Biological Diversity Rules under it in 2004. 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 [See Box 3].

This Act also provides further support to other relevant national laws in force, namely, the Wildlife (Protection) Act, 1972 as amended in 1991, and the Protection of Plant Varieties & Farmers' Rights (PPVFR) Act, 2001. It also provides suitable linkage to the provision for patenting of products and processes/ technologies, based on the use of bio-resources and associated indigenous traditional knowledge (ITK), under Section 10 (4) of the Patents (Amendment) Act, 2002. The stage is thus set for developing a national movement for implementing these combined provisions for access and benefit sharing to ensure food and livelihood security based on conservation, inclusive development and sustainable use of bio-resources.

The Act provides for its implementation through a 3-tier system comprising the National Biodiversity Authority (NBA), the State Biodiversity Boards (SBBs)

Box 3

Salient Features of the Biological Diversity Act, 2002:

- Regulates access to biological resources of the country with the purpose of securing equitable and fair sharing of benefits arising out of the use of biological resources; and associated traditional knowledge (TK) relating to biological resources;
- Promotes conservation and sustainable use of all components of biological diversity;
- Aims at respecting and protecting traditional knowledge of local communities related to biodiversity;
- Provides for sharing of benefits with local people as developers and conservers of biological resources and holders of knowledge and information associated with their use;
- Promotes conservation and development of areas of importance from the standpoint of biological diversity by declaring them as biological diversity heritage sites;
- Lends support to on-going programmes on protection and rehabilitation of rare, endangered and threatened species;
- Encourages increasing involvement of institutions and state governments in the broad scheme of implementing the Biological Diversity Act, through constitution of appropriate committees.
- Recognizes four broad categories of users who are required to apply in different kinds of specified forms along with payment of prescribed fees. These categories are based on stated objectives of the applicants and include accessing biological resources for research /biosurvey & bio-utilization /commercial utilization, transferring results of research on bioresources, seeking IPR over products /innovations based on use of bioresources. And third party transfer of already accessed bioresources.

and the Biodiversity Management Committees (BMCs) at the local communities level. Functions of this system at all the three levels have been clearly defined and all the Union States have constituted SBBs.

In exercise of the powers conferred by Sub-Section (1) (4) of Section 8 of the Biological Diversity Act, 2002, the Central Government established the National Biodiversity Authority on 1st October, 2003. For major functions of NBA, see Box 4.

Recognising that the Indian citizens owe allegiance to the Indian Constitution and can be called upon by the courts in person to ensure compliance to this Act's provisions, a differentiating way has been adopted under which the following categories of persons/ body corporate / associations/ organizations are required to obtain prior approval of the 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 [Section 3 (2) and Section 19):

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

For more information, see Box 5.

Access to bioresources for research by Indian citizens, and companies registered in India and not having any foreign share in their management, is unrestricted and free. However, Section 7 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 to the concerned State Biodiversity Board which grant the required approval based on relevant rules and procedures for this purpose (Sections 23 and 24) and imposes benefit sharing terms

Box 4

Main Functions of the National Biodiversity

1. To lay down procedures and guidelines to govern the activities provided under Section 3, 4, and 6: Permission to foreigners/non-resident Indians/foreign entities.

2. To regulate activities and advise the government of India on research/commercial use of bio-resources, bio-survey and bio-utilization.

3. To grant approval under Section 3, 4 and 6 based on the following considerations:

(i) Certain persons not to undertake Biodiversity related activities without approval of National Biodiversity Authority (Section 3).

(ii) Results of research not to be transferred to certain persons without approval of National Biodiversity Authority (Section 4) (Transfer of Research Results).

(iii) Applications for seeking IPR rights not to be made without prior approval of the NBA (Section 6).

4. To grant approval to certain persons seeking transfer of already accessed biological resource/associated traditional knowledge (Third Party Transfer) (Section 20).

5. To determine and impose terms of equitable benefit sharing, arising out of the use of accessed biological resources and associated traditional knowledge (Section 21).

6. To establish and operate the National Biodiversity Fund.

7. To advise the State Governments in the selection of areas of biodiversity importance to be notified under Section 37 (1) as heritage sites and measures for their management.

8. To take any measure, on behalf of the Central Government, necessary to oppose the grant of IPR in any country outside India on any bioresource obtained from India or knowledge associated with it which is derived from India.

Box 5

The Principle of Common but Differentiated Responsibilities

1. The Biological Diversity Act differentiates between Indian citizens/Indian entities and foreign citizens/ foreign entities (including Persons of Indian Origin) requiring the latter category to obtain prior approval of NBA for accessing India's bioresources for research/commercial utilization or for undertaking biosurvey and bio-utilization. Whereas the Indian citizens are required to approach the concerned State Biodiversity Board, the foreign citizens/foreign entities need to apply to NBA.

2. The Act also requires Indian citizens to take prior approval of NBA for transferring the results of research, conducted on bioresources, to foreign citizens/foreign entities.

Box 6

Restrictions Imposed on Granting Access to Bioresources under Section 24 (2) read with Rule 16

Certain restrictions have been imposed under Rule 16 on NBA's, and also SBBs' approvals for activities related to access to bio-resources, requiring the Authority to take steps to restrict or prohibit requests for such access on considering the following reasons:

- The request for access is for any endangered taxa;
- The request for access is for any endemic and rare species;
- The request for access may result in adverse effect on the livelihoods of the local people;
- The request for access may result in adverse environmental impact which may be difficult to control and mitigate;
- The request for access may cause genetic erosion or adversely affect ecosystem functioning;
- When the use of resources is for purposes contrary to national interest and other related international agreements entered into by India.

based on the guidelines notified for this purpose in November, 2014.

See Boxes 6 and 7 for some restrictions imposed on granting access to bioresources and also some exemptions from the provisions of this Act.

However, all the users, Indian citizens as well as foreigners, are required to seek prior approval of NBA for transferring results of their research on bioresources to foreign persons/entities [Section 4), for applying for IPR on products/processes based on bioresources (Section 6) and also for third party transfer of the already accessed bioresources (Section 20), by submitting applications in specified formats along with payment of prescribed fee for each of the above mentioned purposes.

Authorised Access to Biological Resources required prior to seeking IPR

Any person seeking any kind of IPR in or outside of India for any invention/ technology/ product or process based on any biological resource (or associated information) obtained from India, is required to obtain prior permission of the NBA [Section 6]. In addition, the Patent (Amendment) Act, 2002, requires the patent applicant to disclose the source and geographical origin of the used biological material in the patent application, when used in an invention [Section 10 (4)].

Notification on Guidelines on Access and Benefit Sharing

Regulation of Access to Biological Resources (and associated TK) and Benefit Sharing: Notified under Biological Diversity Act on 21 November, 2014

These Guidelines provide:-

- legal certainty,
- clarity and transparency,
- simplified procedure for the Indian researchers/ Govt. institutes to carry out basic research outside India.
- Options of benefit sharing for different users
- Graded benefit sharing system,
- Establishing supply chain from source to manufacturer.
- Upfront payment on high economic valued bioresources (Red sanders, Sandalwood etc.)
- Apportioning accrued benefits to the local communities /BMCs.

Facilitating non-commercial research abroad by Indian researchers /Government Institutions

Through this guideline, NBA introduced a special Form for the Indian research/scientists or Government Institutes to carry/send the biological resources outside

Box 7

Exemptions Provided under the Biological Diversity 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 are exempted from provisions of this Act.
- Provisions of Section 3 (access to bio-resource) and Section 4 (transfer of research results) shall not apply to the approved collaborative research projects, conforming to the extant policy and guidelines issued by the Ministry of Environment and Forests such as the notification dared 8 November, 2006.
- Provision 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. Where any right is granted under this law, the concerned authority granting such right shall endorse a copy of such document (granting the right) to the NBA.
- Accessing biological resources 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 the 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, covered u/s 2(f), are not exempted.
- Publication of research papers or dissemination of knowledge, in any workshop exempted from provisions of Section 4 of the Act if it is in conformity with the Guidelines issued by the Central Government for this purpose.
- 'Value added products', which may contain portions or extracts of plants and animals in unrecognizable and physically inseparable form as defined u/s 2(p).
- Provisions of Section 7 (prior intimation to SBB for commercial use) shall not apply to the local people and communities including village healers/ *vaids*, farmers and other traditional growers and also to Indian users of these bio-resources for research (not when seeking intellectual property rights).
- Items such as normally traded commodities, as notified by the Central Government u/s. 40 would be exempt from purview of this Act.
- Exchange of designated accessions of genetic resources of crops listed in Annex-1 of the ITPGRFA have been exempted but cannot apply for any IPR without prior approval of the NBA.

India for doing research (like CSIR, ICAR, ZSI, BSI, Government Universities) Government institutes may send the biological resources outside to carry out studies to avert emergencies like epidemics etc.

Determination of benefit sharing; Monetary and/ or non-monetary modes, as agreed upon by the applicant and the NBA/SBB concerned in consultation with the BMC/Benefit claimer, etc.

Determination of the amount of Benefit Sharing:

a. Benefit Sharing for Commercial Utilization of Bioresources:

Annual gross ex-factory sale of the product (minus govt. taxes)	Benefit sharing component
Up to Rs. 1,00,00,000	0.1%
Rs. 1,00,00,000 To Rs. 3,00,00,000	0.2%
Above Rs. 3,00,00,000	0.5%

b. Transfer of results of research:

The benefit sharing obligation shall be 3.0 to 5.0% of the monetary consideration received.

c. Intellectual Property Rights:

Relevance	Terms of Benefit Sharing
When applicant himself commercialises the process/ product/ innovation	0.2 to 1.0 % of the annual ex-factory gross sale (minus government taxes).
When applicant assigns/ licenses the process/ product/ innovation to a third party for commercialisation	3.0 to 5.0 % of the fee received in any form and 2.0 to 5.0 % of the royalty received.

d. Alternative option for procurement of bioresources through a supply chain:

Where the trader sells the biological resource purchased by him to another trader or manufacturer, the buyer,

- if he is a trader, he is to pay @ 1.0 to 3.0% of his purchase price.
- If he is a manufacturer, he is to pay 3.0 to 5.0% of his purchase price.
- If the buyer submits proof of benefit sharing paid by the immediate seller in the supply chain, then the buyer shall pay benefit sharing on that portion of the purchase price for which the benefit has not been paid along the supply chain.

In cases of biological resources having high economic value, such as sandalwood and red sanders, the benefit sharing may include an upfront payment of not less than 5.0%, on the proceeds of the auction or sale amount, as decided by the NBA or SBB, as the case may be. If the sale is through auction, the successful bidder or the purchaser shall pay the amount to the designated fund, before accessing the biological resource.

Information on penalties for contravention of this Act or abetting such contraventions is provided in Box 8.

VI. Present Status of Implementing the Biological Diversity Act

India's 5th National Report to CBD, submitted in 2014, provides an overview of the status of implementing the provisions of CBD along with the progress made in implementing the Biological Diversity Act and the Rules framed under it. Following the establishment of NBA in 2003, SBBs have also been constituted in all the 29 states and over 38,000 BMCs set up. Nearly 1900 Peoples' Biodiversity Registers (PBRs), documenting local bioresources and associated traditional knowledge, have also been developed and validated.

NBA has provided financial assistance of over rupees 100 million towards strengthening SBBs and BMCs and developing PBRs.NBA has also set up expert committees on 'access & benefit sharing', 'agro-biodiversitty' and 'normally traded commodities. Fifteen National Designated Repositories have been recognized for safekeeping of voucher specimen/reference samples and a core expert group has also been constituted to address concerns of these repositories and develop guidelines. Another core expert group has been constituted to develop a unified model agreement deed to replace the existing four kinds of agreement forms. Effort is also on to develop on-line processing of all applications.

Guidelines on collaborative research projects were notified in 2006 for claiming exemption from the Act's provisions under Section 5. Much awaited guidelines on ABS have also been notified in November 2014 to speed up implementation of ABS provisions under the Act. NBA has already approved 633 applications out of 985 applications received by it under different categories and entered into 171 benefit sharing agreements with the users of bioresources [See Box 9].

Guidelines, exempting designated accessions of crops listed in Annex-I of the ITPGRFA from Sections 3 & 4 of the Act, have also been notified for smooth implementation of this Treaty. The expert committee on

Box 8

Penalties for Contravention of the Biological Diversity Act

Whoever contravenes or attempts to contravene or abets the contravention of the provisions of section 3 or section 4 or section 6shall be punishable with imprisonment for a term which may extend to five years, or with fine which may extend to ten lakh rupees and where the damage caused exceeds ten lakh rupees such fine may commensurate with the damage caused, or with both [Section 55 (1)].

Whoever contravenes or attempts to contravene or abets the contravention of the provisions of section 7 or any other order made under sub-section (2) of section 24 shall be punishable with imprisonment for a term which may extend to three years, or with fine which may extend to five lakh rupees, or with both. Section 55 (2)]

If any person contravenes any direction given or order made by the Central Government, the NBA or the SBB for which no punishment has been separately provided under this Act, he shall be punished with a fine which may extend to one lakh rupees and in case of a second or subsequent offence, with fine which may extend to two lakh rupees and in case of continuous contravention with additional fine which any extend to two lakh rupees everyday during which the default continues. [Section 56]

The offences under this Act shall be cognizable and non-bailable. [Section 58]

The provisions of this Act shall be in addition to, and not in derogation of, the provisions in any other law, for the time being in force, relating to forests or wildlife. [Section 59]

Box 9

Status of the processing and approval of applications as on 30 April, 2015

Items	Form I	Form II	Form III	Form IV	Total
Number of applications received	186	40	681	78	985
Number of applications approved	85	16	494	38	633
Number of applications in process	66	13	159	24	262
Number of applications closed	44	14	34	17	109
Number of BS agreements signed	40	12	93	26	171
Total	421	95	1461	183	2160

Normally Traded Commodities has now prepared a list of over 420 species for exemption under Section 40 of the Act so long as these are traded as commodities. Over 14 States have developed and notified lists of threatened species under their jurisdiction. More than 160 million rupees have already been deposited in the National Biodiversity Fund for payment to benefit claimers and to promote conservation and sustainable use of bioresources. Some SBBs, notably those of Gujarat, West Bengal and Uttarakhand, have gone ahead and signed a large number of benefit sharing agreements with the user companies in their states, securing thereby the much needed funds required for their functioning aimed at conservation of bioresources and their sustainable use at the ground level, besides ensuring fair and equitable sharing of benefits arising from their commercial utilization.

High level consultations have been held with the Council of Scientific & Industrial Research, Indian Council of Agricultural Research and the Indian Patent Office to address concerns and ensure smooth implementation of the Act. National consultations have also been held with major stakeholders, including pharmaceutical and seed sectors, to provide further clarifications on definition of some terms under Section 2 of the Act. Effort is now on to expand the list of Frequently Asked Questions displayed on NBA's website to provide the required guidance. An expert Committee is also working on developing a unified version of the four types of benefit sharing agreements, presently in vogue, with a common basic format attached with four

kinds of annexes meant for granting access for research and commercial utilization, transfer of the results of research on bioresources, IPR and third party transfer of bioresources. In another significant move forward, it has been agreed to notify 427 plant species as Normally Traded Commodities which will be exempted from provisions of the BD Act as long as they are traded as commodities.

VII. Implementing Provisions of CBD, ITPGRFA and TRIPS Agreement in India

In India, the Union Ministry of Environment, Forests & Climate Change is the nodal ministry for implementing the CBD and also the Nagoya Protocol 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 and also to provide further support to other complementary national laws in force, namely, the Wildlife (Protection) Act, 1972 (as amended in 1991), and the Protection of Plant Varieties & Farmers' Rights (PPVFR) Act, 2001. It also provides suitable linkage to the provision for patenting of products and processes/ technologies, based on the use of bio-resources and associated indigenous traditional knowledge (ITK), under Section 10 (4) of the Patents (Amendment) Act, 2002. The stage is thus set for developing a national movement for implementing these combined provisions for access and benefit sharing to ensure food and livelihood security based on conservation, inclusive development and sustainable use of bio-resources (Rana, 2012). National Biodiversity Authority (NBA) has been designated as the National Competent Authority for this purpose. Format for the Internationally Recognized Certificate of Compliance has also been approved. Efforts are now on to designate the Check Points to monitor commercial utilization of India's bioresources or patenting of their derivatives/ products in other countries. Other key provisions to make the ABS regime functional include developing user and provider country measures.

Union Ministry of Agriculture and Cooperation is the nodal ministry for implementing the ITPGRFA and the Joint Secretary (Seeds) is the National Focal Point, 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 Biological Diversity Act for research, breeding and training purposes. Germplasm exchange would be based on signing the SMTA as approved under this Treaty.

For implementing the WTO-TRIPS agreement, Union Ministry of Commerce is the nodal ministry in India. India amended its Patents Act, 1970 to permit patenting of products and also of micro-organisms, as required under the TRIPS Agreement, and also enacted the Protection of Plant Varieties and Farmers' Rights Act, 2001.

In a bid to harmonise provisions of the CBD and WTO-TRIPs, the Doha Ministerial Declaration had asked for 'Disclosure of Source and Origin' to be made mandatory in patent applications which were also required to have an International Certificate of Compliance to the CBD confirming PIC and MAT provisions. Doha Round of negotiations is, however, underway since 2001 but the progress made so far is much below the developing countries' expectations.

VIII. The Way Forward

The CBD continues to provide the overall legal and policy framework for ABS with regards to genetic resources as reflected in the mid-term assessment of the progress made towards implementing the Global Strategic Plan for Biodiversity 2011-2020 (CBD, 2014). There is now an urgent need, however, to harmonise provisions for benefit sharing under CBD and WTO-TRIPS. For implementing the two main principles of ABS mechanism under CBD, namely, "prior informed consent" and "mutually agreed terms", legal requirement of a CBD-compliant and internationally recognized certificate, to be issued by the national authority of provider country, needs to be adopted as an essential attachment with the applications submitted to patent offices for seeking patents on products or processes based on bio-resources (and associated TK).

Notwithstanding the lack of clarity on some of its Articles, the Nagoya Protocol to CBD on ABS holds much promise and its provisions need to be fully utilized towards better monitoring of the commercial utilization of India's bioresources, and associated traditional knowledge, in other countries (Morgera *et al*., 2014, Richerzhagen, 2014). However, the Nagoya Protocol's provisions are binding only on those countries who have become Contracting Parties to it and, hence, the real

advantages of this Protocol would depend upon how it is implemented at the national level. Recent notification of the Guidelines on ABS in India has galvanized this process but creating more awareness on this subject and further capacity building are required to make a real headway in this direction.

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Identification of Gaps in Pigeonpea Germplasm from East and Southern Africa Conserved at the ICRISAT Genebank

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The genebank at ICRISAT, Patancheru, India conserves 13,771 accessions of pigeonpea germplasm from 74 countries, including 1,168 accessions from 13 East and Southern African (ESA) countries: Based on availability of georeference data, 916 landraces from seven countries were considered for identifying gaps. Eighty four districts located in four East African countries and 54 districts located in three Southern African countries were identified as geographical gaps in the ICRISAT collection. A total of 25 districts in four countries; six provinces in Tanzania and Zambezia province in Mozambique were identified as gaps in phenotypic diversity for specific traits. Kitui and Machakos in Kenya were found as common districts for geographical as well as trait diversity gaps. Launching collection missions in ESA countries to fill geographical, trait-specific and taxonomical gaps in pigeonpea collection from ESA countries at ICRISAT genebank is recommended.

Key Words: Diversity, Genetic resources, Geographical gap, Germplasm, Landrace

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is a versatile food legume of the tropics and subtropics. Because of its multiple uses including food, feed, fuel, fencing, roofing, basket making and as a soil enricher and soil binder, pigeonpea is cultivated in about 82 countries as a field crop or a backyard crop. It has wide adaptability to diverse climates (Nene and Sheila, 1990) and due to high seed protein (up to 31% in the world collection), pigeonpea is an important source of protein for the vegetarian diet especially in the Indian sub-continent. FAO production statistics are available only for 21 countries. During 2010, pigeonpea as a field crop was grown on 4.8 million ha. India has the largest area under pigeonpea cultivation (3.53 m ha) followed by Myanmar (0.58 m ha), Malawi (0.19 m ha), Kenya (0.16 m ha), Uganda (0.10 m ha), Tanzania (0.08 m ha), Dominican Republic (0.02 m ha) and Nepal (0.02 m ha) (FAO, 2010).

Although, East Africa is considered as the secondary center of diversity for pigeonpea (van der Measen, 1990), East and Southern African (ESA) countries, mainly Kenya, Tanzania and Uganda in East Africa and Malawi, Mozambique and Zambia in Southern Africa have been considered as important pigeonpea growing countries (Ramanatha Rao, 1981). Upadhyaya *et al*. (2005) reported high diversity for quantitative traits in accessions from Africa. Over most of Africa, pigeonpea is grown as a vegetable near houses and farm steads, as hedges, and as a crop mostly mixed with cereals and short duration legumes (van der Maesen, 1976; Upadhyaya *et al*., 2010a). Pigeonpea landraces are widely adapted compared to green pea, and can be grown as a vegetable in backyards and on field bunds to support the economies of the landless poor. Because of the perenniality of pigeonpea coupled with the indeterminate flowering habit of most vegetable type accessions, it is possible to extend the harvest of immature pods to sell in local markets for longer period.

Geographic Information Systems (GISs), particularly FloraMap and DIVA_GIS have facilitated a better understanding of species distribution and the gaps in collections (Hijmans and Spooner, 2001; Van Treuren *et al*., 2011). The genebank at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India holds the world's largest collection of pigeonpea germplasm (13,771 accessions), sourcing from

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74 countries including 1,168 accessions from 13 ESA countries. In view of the relatively poor representation of ESA countries in the ICRISAT genebank and the fast erosion of crop diversity due to replacement of landraces, including those of pigeonpea by modern varieties, natural catastrophes such as droughts, floods, fire hazards, urbanization and industrialization and habitat loss due to irrigation projects, overgrazing, mining and climate change (Upadhyaya and Gowda, 2009), there is an urgent need for a critical assessment of the existing world collection of pigeonpea for gaps. Therefore, this study is aimed at summarizing pigeonpea germplasm assembled from East and Southern Africa and conserved at ICRISAT genebank, mapping their geographical distribution, and identifying geographical and trait-specific diversity gaps for possible exploration before potentially valuable germplasm material is lost forever.

Materials and Methods

Passport and characterization databases of the world collection of pigeonpea germplasm conserved at the ICRISAT genebank was used in the present study. Passport data of landraces from ESA countries, including Ethiopia (14), Kenya (343), Rwanda (5), Tanzania (275), Uganda (98) in East Africa and Botswana (3), Madagascar (1), Malawi (249), Mozambique (32), Namibia (5), South Africa (40), Zambia (93) and Zimbabwe (10) in Southern Africa was updated, particularly for information on precise location of collecting site and corresponding geographic coordinates. Using Microsoft Encarta®, an electronic atlas (MS Encarta® Interactive World Atlas, 2000), geographic coordinates were retrieved for landraces having location information. To verify the accuracy of coordinates, the landraces were plotted over a country level map and checked for their presence in the appropriate province/state, district, village or precise location of sampling. Landraces having latitude and longitude information (up to four decimals) were used in the present study to identify gaps in collections from these countries. Landraces from Rwanda (5) and South Africa (4) having georeference data were considered too few, therefore, not considered for identifying gaps in collections from these countries. The final set of 916 landraces from seven countries with geographic coordinates was used to identify gaps in the collections. FloraMap, a software tool developed at Centro Internacional de Agricultura Tropical (CIAT) (Jones and Gladkov, 1999) was used to map the predicted distribution of pigeonpea and DIVA-GIS software was used to identify trait-specific diversity.

The FloraMap makes precise and detailed maps that eliminate much of the guesswork from the slow, expensive process of finding and recovering species. It takes the absolute minimal data available from germplasm passport database, just latitude and longitude of the collecting site and accession number/identity. The collection sites form a calibration set to construct a climate model. This model is then mapped as a probability surface throughout the world. This has proved its worth in the analyses of a number of important species. Identification of geographical gaps in germplasm collections using FloraMap was considered as the most practical approach. Developed, tested and refined over the past two decades, this Windows based tool relies on climatic data to predict promising collection sites. FloraMap predicts on the idea that climate is a robust indicator of the environmental range of plants and other organisms.

While working with the passport dataset, depending on the country, weights ranging from 1.0 to 1.2 for rainfall and from 0.80 to 1.00 for temperature and diurnal temperature were allocated maintaining the total of the three variables to 3 and an exponential transformation with a power of 0.3 was applied to the monthly rainfall data. More than 91% of total variation was explained by first five principal components (PCs) depending on the country. To achieve higher precision in predicting the probability of pigeonpea occurrence, FloraMap was run for each country separately. Since multiple accessions with identical coordinates were considered as single collection site, the number of actual geographical sites within an area of 18 × 18 km² is less than the number of sampled sites. Collection sites were overlaid on the probability map of each country. Provinces/states (name 1) and districts/administrative units (name 2) with high probability (>50%) and with no collection and/or few collection sites were recorded as gaps. To restrict the area for exploration, the smallest administrative unit (district) was considered as a gap.

Assembled accessions were evaluated for nine quantitative characters in different years at ICRISAT (17° 25'N latitude, 78° 00'E longitude and 545 masl) in vertisols during rainy season. Accessions were sown in 3 rows of 4 m long, with a spacing of 50 cm between plants and 75 cm between rows. The crop was fertilized with 20 kg N and 40 kg P_2O_5 ha^{-1} as basal dose, managed by recommended cultural and plant protection practices, including supplementary irrigation. Observations were recorded as mean of three representative plants from

the middle row for days to 50% flowering, plant height, number of primary and secondary branches/plant, pods/plant, seeds/pod, shelling percentage, 100 seed weight and seed yield/plant, following the descriptors for pigeonpea (IBPGR and ICRISAT, 1993). Using the passport and characterization data of pigeonpea germplasm from ESA countries and DIVA-GIS software (Hijmans *et al*., 2005), gaps in diversity for traits under study were identified. Using DIVA-GIS software, Shannon-Weaver diversity index for different traits was estimated and mapped (Shannon and Weaver, 1949). Districts with high diversity and relatively fewer collection sites were identified as gaps in diversity for each trait and in each country. Due to large number, the diversity maps for important traits do not depict collection sites avoiding the possible clutter. A United States Geological Survey (USGS) land cover map for Africa was used to identify the type of vegetation and land cover in the districts selected and to exclude lakes, forests and other areas where crop cultivation is not known (USGS EROS Center, 2005).

Results

Germplasm Assembled

Initially, the pigeonpea germplasm was assembled by introducing already collected germplasm from various organizations located in different countries and then by launching systematic germplasm collection missions in ESA countries in partnership with national and international institutes, National Agricultural Research Systems (NARS), universities and Non-governmental Organizations (NGOs). The analysis of passport data of the world collection of pigeonpea germplasm assembled at the ICRISAT genebank revealed that a total of 1,168 accessions were assembled from East and Southern African countries (ESA) (Table 1). The collection is from a wide range of latitudes ranging from -26.00° (South Africa) to 8.75° (Ethiopia).

Germplasm Introduced

Eight organizations located in eight countries donated a total of 255 accessions originating in 11 ESA countries (Table 1). Commonwealth Scientific and Industrial Research Organization (CSIRO), Division of Tropical Crops and Pasture, ATFGRC, St. Lucia, Australia (49); Station De Genetique D Amdioration Des Plantes, Versailles, France (2); National Dryland Farming Research Station, Katumani, Kenya (16); Chitedze Agricultural Research Station, Lilongwe, Malawi (3); United States Department of Agriculture (USDA)/Southern Regional Plant Introduction Station, Griffin, USA (1); Agricultural Research and Extension Authority, Agricultural Research Station, Taiz, Yemen (9); Directorate of Plant and Seed Control, Pretoria, South Africa (21) and Msekera Regional Research Station, Chipata, Zambia (61) were the donors of pigeonpea germplasm to ICRISAT genebank (Table 1). ICRISAT regional center at Nairobi has also sent 82 samples

Table 1. Pigeonpea germplasm from East and Southern Africa assembled at ICRISAT genebank

Region/Country	Total accs.	Introductions	Collections		Biological status of collection			Landraces with geo-reference data
			Year of collection	No. of accs. collected	Breeding material	Wild	Landraces	
East Africa								
Ethiopia	14	-	1984	14	-	-	14	14
Kenya	343	31	1976	63	26	5	312	311
			1982	249				
Rwanda	5	-	1982	5	-	-	5	5
Tanzania	275	58	1981	217	3	13	259	257
Uganda	98	15	1991	24	1	-	97	90
			1993	34				
			1993	25				
Southern Africa								
Madagascar	1	1	-	-	1	-	-	-
Malawi	249	5	1979	21	1	4	244	133
			1983	223				
Botswana	3	3	-	-	-	3	-	-
Mozambique	32	22	1981	10	-	1	31	31
Namibia	5	5	-	-	-	5	-	-
South Africa	40	37	1982	3	21	15	4	3
Zambia	93	68	1980	20	-	7	86	80
Zimbabwe	10	10	-	-	-	10	-	-
Total	1168	255		913	53	63	1052	924

originating in Kenya (6), Mozambique (21), Tanzania (41) and Uganda (14). All accessions from Botswana (3), Madagascar (1), Namibia (5) and Zimbabwe (10) are introductions in the ICRISAT genebank in India.

Germplasm Collected

During 1976-93, ICRISAT and its partners have launched 14 collection missions in nine ESA countries (eight in East Africa and six in Southern Africa) and collected a total of 913 samples (Table 1). Maximum samples were collected in Kenya (312) followed by Malawi (244) and Tanzania (217). ICRISAT had collaboration with 15 organizations for collecting pigeonpea germplasm in nine ESA countries. Important collaborators in East Africa include, Haile Sellassie I University, Debre Zeit and Plant Genetic Resources Centre (PGRC), Addis Ababa in Ethiopia; University of Nairobi, Nairobi, Kenya and Food and Agriculture Organization (FAO)/National Dryland Farming Research Station, Katumani in Kenya (van der Maesen, 1976; Remanandan *et al*., 1982); Institut Des Sciences Agronomiques Du Rwanda (ISAR), Butare in Rwanda (Prasada Rao and Mengesha, 1982); International Institute of Tropical Agriculture (IITA)/ United States Agency for International Development (USAID), Dar-Es-Salaam/Ministry of Agriculture, Zanzibar in Tanzania (Remanandan and Mengesha, 1981) and Makerere University, Kampala in Uganda (Singh *et al*., 1991; Reddy *et al*., 1993). The collaborators in Southern Africa includes IBPGR, Italy/Ministry of Agriculture and Natural Resources in Malawi; IBPGR, Rome/University of Eduardo Mondlane, Maputo in Mozambique (Ramanatha Rao, 1981); Grain Crops Research Institute, Potchefstroom in South Africa (van der Maesen, 1982); IBPGR, Rome/Ministry of Agricultural and Water Development in Zambia.

Past collections revealed that Shewa (12) in Ethiopia; Central (20), Coast (38), Eastern (242) and Nyanza (12) in Kenya; Southern (104) in Malawi; Nampula (17) and Zambezia (13) in Mozambique; Arusha (22), Dodoma (63), Lindi (16), Morogoro (56), Mtwara (26), Pwani (15) and Ruvuma (18) in Tanzania; Northern (35) in Uganda and Eastern (61) and Northern (16) in Zambia are the important source provinces resulting in more than 10 accessions.

Biological Status of Collection

Analysis of the passport data for biological status of the collection from ESA includes 1,052 landraces, 53 breeding materials and 63 wild accessions belonging to 14 species of three genera (Table 1). Landraces were from Ethiopia (14), Kenya (312), Rwanda (5), Tanzania (259), Uganda (97), Malawi (244), Mozambique (31), South Africa (4) and Zambia (86). All accessions from Botswana (3), Namibia (5) and Zimbabwe (10) belong to genus *Rhynchosia*.

Wild Relatives

The 14 species of genus *Dunbaria, Eriosema* and *Rhynchosia* assembled from nine ESA countries includes 59 introductions and four collections. The wild species assembled from ESA countries include *Dunbaria ferruginea* (1), *Eriosema ellipticum* (1), *Rhynchosia aurea* (1), *R. cyamosperma* (1), *R. densiflora* (3), *R. edulis* (1), *R. micrantha* (5), *R. minima* (22), *R. rothii* (1), *R. sublobata* (9), *R. totta* (11), *R. velutina* (1), *R. venulosa* (1) and *R. verdcourtii* (3). Species name is not available for two accessions of genus Eriosema. All wild species assembled from ESA countries belong to the quaternary genepool (Bohra *et al*., 2010). None of them are crossable with cultivated pigeonpea.

Intensity of Collection

Accessions with geo-reference data represent 336 geographical sites of germplasm collection in Ethiopia (10), Kenya (66), Malawi (35), Mozambique (29), Rwanda (2), South Africa (3), Tanzania (88), Uganda (58) and Zambia (45). The average number of samples per collection site was three in the collection from ESA; one in Ethiopia, Mozambique and South Africa; two in Uganda and Zambia; three in Rwanda and Tanzania; four in Malawi and five in Kenya indicating the intensity of germplasm collection in these countries. FAO statistics for area of cultivation in different countries and the number of accessions in genebank from those countries indicated the representation of one accession per 463 ha in Kenya, per 275 ha in Tanzania, per 249 ha in Malawi and per 98 ha in Uganda (FAO, 2010).

Geographical Gaps

A total of 84 districts located in 35 provinces of four East African countries and 54 districts located in 18 provinces of three Southern African countries were found as the important geographical gaps (Fig. 1, Table 2 and 3). Five districts of three provinces in Ethiopia, 12 districts of three provinces in Kenya, 37 districts of 14 provinces in Tanzania, 30 districts of 15 provinces in Uganda, six districts of three provinces in Malawi, 28 districts of eight provinces in Mozambique and 20 districts of seven provinces in Zambia were identified

as the geographical gaps in the collections from ESA countries (Fig. 1, Table 2 and 3). Maximum districts (37) were identified as gaps in Tanzania. Districts of Welo in Ethiopia; Kagera, Kigoma, Mara, Mwanza, Rukwa, Shinyanga and Singida in Tanzania; Kamuli, Kibaale, Kitgum, Kotido, Moroto, Pallisa in Uganda; Central and Northern in Malawi; Inambane, Manica, Maputo, Nassa, Sofala and Tete in Mozambique and Central, Copper belt, Lusaka and Southern in Zambia were not explored during the past collection missions launched by ICRISAT.

Gaps in Trait-specific Diversity

Eight districts in Eastern, Central and Coast provinces in Kenya were identified as gaps in phenotypic diversity for all traits (Fig. 2 and Table 4). Mubende district in South Buganda province for days to 50% flowering; Hoima and Msindi districts in Western province for seeds/pod, shelling percentage and seed yield/plant and Apec and Gulu districts in Northern province for primary and secondary branches/plant and shelling percentage were the trait diversity gaps in Uganda. Coast, Dodoma, Mtwara and Tanga provinces for all traits except pods/plant, Arusha and Dodoma provinces for pods/plant were identified as gaps in Tanzania. Zambezia province in Mozambique was identified as gap for diversity of all traits. Nsanje and Thyolo for days to 50% flowering, Balantyre, Chickwawa, Chiradzulu, Machinga, Mulanje, Mwanza Nsanje, Thyolo and Zomba districts in Southern province in Malawi were identified as gaps in diversity for all traits except days to 50% flowering. Chipata district in Eastern province of Zambia was identified as gap in diversity for primary branches/plant, shelling percentage and seed yield/plant.

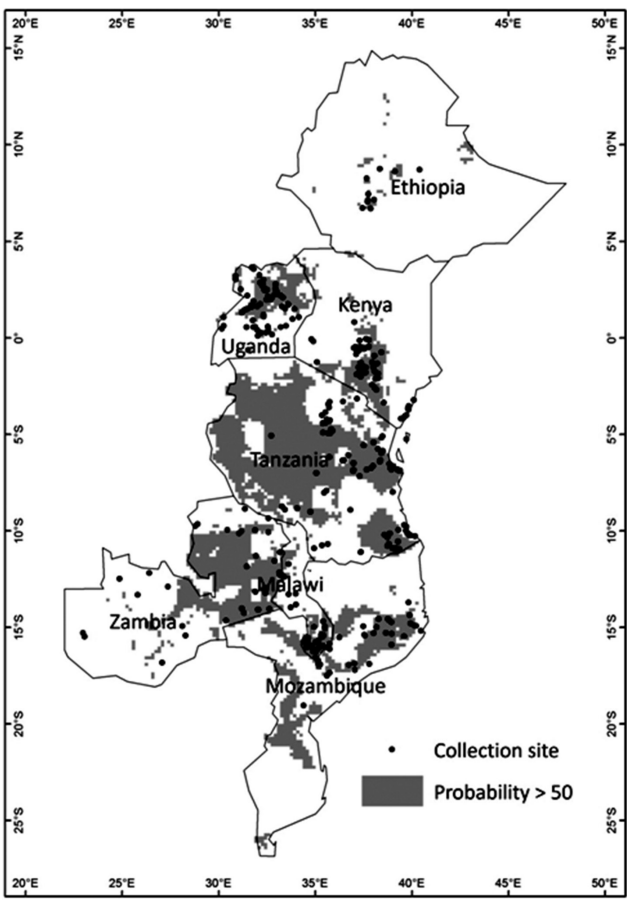

Fig. 1. Geographical distribution and the gaps (districts shaded) identified in the pigeonpea landraces collection from East and Southern African countries at ICRISAT genebank

Table 2. Geographical gaps (districts) identified in pigeonpea germplasm from East Africa, assembled at ICRISAT genebank

Country	Province	District
Ethiopia	Hararge	Dire Dawa-Isa-Gurgur, Jijiga
	Shewa	Haykoch & Butajira, Yerer & Kereyu,
	Welo	Wag
Kenya	Coast	Taita-Taveta
	Eastern	Isiolo, Kitui, Machakos, Meru, Nithi
	Rift Valley	Kajiado, Laikipia, Narok, Samburu, Turkana, West Pokot
Tanzania	Arusha	Kiteto
	Iringa	Iringa, Njombe
	Kagera	Biharamulo, Muleba, Ngara
	Kigoma	Kasulu, Kibondo, Kigoma
	Lindi	Kilwa, Lindi, Liwale, Nachingwea
	Mara	Bunda, Magu, Musoma, Serengeti
	Mbeya	Chunya, Mbeya, Mbozi
	Morogoro	Morogoro
	Mwanza	Geita, Kwimba, Sengerema
	Pwani	Kisarawe
	Rukwa	Mpanda, Nkasi, Sumbawanga
	Shinyanga	Kahama, Maswa, Shinyanga,
	Singida	Iramba, Manyoni, Singida,
	Tabora	Igunga, Nzega, Tabora
Uganda	Apac	Kwania
	Arua	Koboka, Madi-okollo,
	Gulu	Ajwa, Nwoya,
	Kamuli	Budiope, Bulamogi
	Kibaale	Bugangaizi
	Kiboga	Kiboga
	Kitgum	Agago, Aruu, Chua, Lamwo
	Kotido	Jie, Labwor,
	Kumi	Bukedea, Ngora
	Lira	Dokolo, Kiyoga, Moroto, Otuke
	Luwero	Buruli, Nakaseke
	Masandi	Kibanda
	Moroto	Bokora
	Pallisa	Pallisa
	Soroti	Amuria, Kaberamaido, Kapelebyong, Usuk

Table 3. Geographical gaps identified in pigeonpea germplasm from Southern Africa assembled at ICRISAT genebank

Country	Province	District
Malawi	Central	Ntcheu
	Northern	Karonga, Mzimba, Nkata-Bay, Rumphi
	Southern	Mangochi
Mozambique	Inambane	Govuro, Inchassaro, Mabote
	Manica	Gondola, Guro, Machaze, Macossa, Mussarize, Sussumdenga
	Maputo	Boane, Namacha,
	Nampula	Muecate
	Nassa	Cuamba, Matarica, Maua, Mecanhelas, Nipepe
	Sofala	Buzi, Chibabava, Gorongosa, Machanga, Muamza
	Tete	Chifunde, Chiuta, Moatize
	Zambezia	Gile, Ile, Morrumbal
Zambia	Central	Kabwe-rural, Mkushi, Mumbwa, Serenje
	Copper belt	Kalulishi, Kitwe, Luanshya, Ndola-rural
	Lauapula	Mansa, Mwense, Samfiya
	Lusaka	Luangwe, Lusaka-rural
	Northern	Chilubi, Chinsali, Empika, Luwingu
	North-western	Mufumbwe
	Southern	Kalomo, Namwala

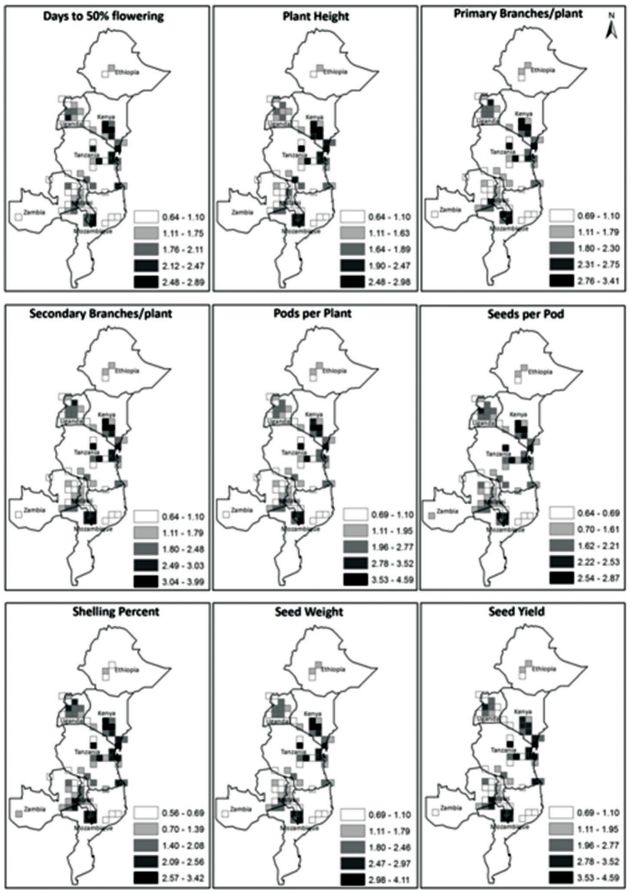

Fig. 2. High diversity areas (grids) for different agronomic traits of pigeonpea landraces from East and Southern Africa

Discussion

Success of gap analysis depends on the quality of input data. In many genebanks, most of the older germplasm collections do not have complete passport information, particularly, the georeference data (latitude and longitude) of the collection sites, which poses a problem in assessing the geographical completeness of collections (Upadhyaya *et al*., 2010b). Inaccuracy of georeference data is an additional constraint. Updating passport data for location information and geo-reference data and their validation is essential for the identification of gaps using GIS software such as FloraMap and DIVA-GIS. The gaps are more evident in legume crops including wild relatives (Khoury *et al*., 2010). The geographical gaps identified here using FloraMap and the gaps identified

Table 4. Gaps identified (districts) in diversity for different traits of pigeonpea germplasm from East and Southern Africa assembled at ICRISAT genebank

Country	Province/State	Districts	Traits*
Kenya	Coast	Kwale	DFL, PHT, PRBR, SCBR, PDPL, SDPD, SHP, SDWT, SDYLD
	Central	Kirinyaga, Muranga, Nyeri, Thika	DFL, PHT, PRBR, SCBR, PDPL, SDPD, SHP, SDWT, SDYLD
	Eastern	Imbu, Kitui, Machakos	DFL, PHT, PRBR, SCBR, PDPL, SDPD, SHP, SDWT, SDYLD
Uganda	North	Apac, Gulu	PRBR, SCBR, SHP
	South Buganda	Mubende	DFL
	Western	Hoima, Masindi	SDPD, SHP, SDYLD
Tanzania	Coast, Dodoma, Mtwara, Tanga		DFL, PHT, PRBR, SCBR, SDPD, SHP, SDWT, SDYLD
	Arusha, Dodoma		PDPL
Mozambique	Zambezia		DFL, PHT, PDPL, SDPD, SDYLD, SHP, PRBR, SCBR, SDWT
Malawi	Southern	Nsanje and Thyolo	DFL
		Balantyre, Chikwawa, Chiradzulu, Machinga, Mulanje, Mwanza, Nsanje, Thyolo, Zomba	PHT, PRBR, SCBR, PDPL, SDPD, SHP, SDWT, SDYLD
Zambia	Eastern	Chipata	PRBR, SDYLD, SHP

*DFL=Days to 50% flowering, PHT=Plant height, PDPL=Pods/plant, SDPD=Seeds/pod, PRBR=Primary branches/plant, SCBR=Secondary branches/plant, SHP=Shelling percentage, SDWT=100 seed weight, SDYLD=Seed yield/plant (g).

in trait-specific diversity using DIVA-GIS will provide valuable information such as geographical distribution of species and related traits (Marilia *et al*., 2003; Upadhyaya *et al*., 2010b).

The genetic potential of crop wild relatives (CWR) in crop improvement is now well demonstrated and are likely to contain some traits of interest including climate change adaptation (FAO, 2008). For example, *Dunbaria ferruginea* Wight and Ann. for salinity tolerance (Singh *et al*., 1990), *D. heynei* Wight & Ann as a green manure (Arora and Chandel, 1972), *Eriosema ellipticum* Wel. Ex Beker (Abbot and Lowore, 1995), *Rhynchosia minima* (L.) DC as medicinal use (Morris, 1999) and *R. rothii* Benth. Ex. Aitch, as a source for high seed protein content (>30%) (Remanandan, 1981).

When the levels of resistance to various biotic and abiotic stresses in cultivated germplasm are low or the range of genetic variability is narrow and selection pressure results in virulent biotypes of the pests and diseases, the discovery and incorporation of additional genes for resistance from wild species becomes key to sustaining crop productivity. ICRISAT had launched only a few collection missions exclusively for wild relatives and conserves only a fraction of total genetic variability that exists in wild relatives (Jarvis *et al*., 2008; Upadhyaya *et al*., 2010b). Out of 555 wild accessions belonging to 66 species of six genera conserved at ICRISAT genebank, 63 accessions of 14 species belonging to three genera are from ESA countries. Out of 33 species of *Rhynchosia*, 12 are from ESA countries indicating ESA as good source region for *Rhynchosia*. Therefore, there is a need for launching collection missions exclusively for wild relatives of pigeonpea to fill taxonomical gaps in the collection at ICRISAT genebank.

Wide variation for latitude (from -26 00^{o} in South Africa to 8.75^{o} in Ethiopia) and longitude (from 23.06^{o} in Zambia to 44.48^{o} in Mozambique) of collection sites indicates that the landraces from ESA countries are from diverse climates and show wide adaptation. Nene and Sheila (1990) reported the adaptation of pigeonpea landraces up to 32^{o} latitudes on both sides of equator. Remanandan and Mengesha (1981) reported that the main land in Tanzania has been adequately covered and fairly represented in the pigeonpea collection and the island of Zanzibar needs to be considered for collection in future. Remanandan and Mengesha (1981) reported that the collection from Tanzania is from altitudes ranging between 1000-1500 m and may be a good source for cold tolerance. Remanandan (1990) reported gaps in collection from Uganda. Collections from Tanzania and Kenya are mostly large seeded, perennial type and suitable for use as vegetable and agroforestry (Remanandan and Mengesha, 1981; Remanandan *et al*., 1982).

Pigeonpea originated in India spread around 2200-2000 BC to Africa where a secondary center of diversity developed (van der Maesen, 1980). With the slave trade, the pigeonpea was carried from Africa to the Americas. ESA being the secondary center of diversity for pigeonpea, the geographical, diversity and taxonomical gaps (all wild relatives of cultivated pigeonpea) identified in the study may be considered as the potential areas for exploration (van der Maesen, 1990) (Table 2, 3 and 4).

The gaps identified in the present study can be prioritized (Table 2, 3 and 4). Generally, prioritization will be done by the collecting team at the time of actual launch of the collection mission depending upon the threat to diversity, availability of resources and accessibility to the target region. The districts, which were found as gaps in diversity for almost all traits and those common for geographic area and diversity may be explored on priority to increase the variability in the collection. It is suggested to increase the variability not only for important agronomic traits but for new and adaptive traits also by filling gaps in the pigeonpea collection from ESA countries. Districts/provinces, the area under pigeonpea cultivation is high and per ha representation in ICRISAT genebank is low, thus require further exploration to have good representation and more variability in the world collection of pigeonpea (FAO, 2010). Uganda was under represented in the world collection of pigeonpea at ICRISAT (Upadhyaya *et al*., 2005). Because of habitat loss, changing cropping patterns and food habits in different parts of ESA, it is suggested that the area for exploration in the districts identified may be decided prior to the launch of the collection mission in consultation with local government officials, NARS scientists, extension officers and non-governmental organizations, who will have the knowledge of pigeonpea cultivation in the districts. All reports and other publications on past collections should be considered while preparing route maps for districts identified as gaps. It is especially important to collect complete passport information, including georeference data while collecting germplasm samples in order to facilitate future mapping efforts.

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Diversity Analysis among Chickpea Genetic Stock as Revealed Through STMS Marker Analysis

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Genetic diversity analysis of chickpea germplasm can provide useful information for the selection of parental material and thus help in planning breeding strategies.In the present study, a total of 57 STMS loci were analyzed to discern the variability among 87 chickpea lines consisting of released varieties and elite germplasm. A total of 87 alleles were found for the 19 STMS loci with an average of 4.57 alleles per locus. PIC value ranged from 0.94 to 0.10 and the heterozygosity ranged from 0.11 to 0.94, indicating good variability among the material as well as polymorphism generated. All the genotypes could cluster into six distinct groups with one genotype remaining unclustered. Greater gains can be obtained by crossing lines MPJG-2000-108 with SBD 377 for *Desi* and PG 0515 with ILC 212 for *Kabuli* improvement. Base broadening through *Kabuli* × *Desi* introgression with greater gains can be obtained by using ICC 4516 and ILC 212 as parents.

Key Words: Chickpea, Cluster Analysis, Molecular markers, PCR, STMS markers

Introduction

Chickpea (*Cicer arietinum* L.; Family: Fabaceae) is a self-pollinated, diploid (2n=16), cool season pulse crop with a genome size of ~738-Mb and an estimated 28,269 genes (Varshney *et al.,* 2013). It is widely grown in more than 50 countries representing all the continents (Upadhyay *et al.,* 2011). Worldwide chickpea ranks third among legumes (Food and Agricultural Organization, 2010) *i.e.* almost 15% of the total pulse production of world. In the duration of 2010, the worldwide chickpea area was about 12.0 million ha, with 10.9 million metric tons of production with the yield of 911 kg/ha (FAOSTAT, 2012). India is the world's major producer, the annual production is around 7.58 Mt, grown in the area of approximately 8.32 mha, which is the world's 68% production of total chickpea and the average yield is approximately 912 kg/ha (FAOSTAT, 2012). More than 95% of the area of production and consumption of chickpea is shared by the developing countries. Chickpea is grown mainly in South East Asian countries. *Kabuli* (white seeds) and *Desi* (brown seeds) are the two main types of cultivated chickpea, presenting two diverse gene pools (Nawroz and Hero, 2011).

Chickpea has a very narrow genetic base which is limiting the genetic improvement of chickpea through breeding efforts. The level of natural variation among cultivated chickpea and wild accessions at molecular level is greatly aids in increasing the efficiency of breeding programme (Bharadwaj *et al*., 2011). This is because the phenotypic variability is largely an account of 'G × E' interaction where as the variability at molecular level is devoid of the interference by environment. Diversity analysis is essential to understand *per se* the variability present in germplasm collection that can be practically put to use in plant breeding programmes for recombination breeding. Simple Sequence Repeats (SSRs) are the preferred markers in most areas of molecular genetics as they are highly polymorphic even between closely related lines require very low amount of DNA and are very transferable across populations. SSRs are generally co-dominant markers and are most useful for studies on population genetics and mapping (Jarne and Lagoda, 1996; Goldstein and Pollock, 1997). SSR genotypic data from a number of loci have potential to provide distinctive allelic profiles for establishing genotypes identity (Bharadwaj *et al*., 2010, 2011; Chaudhary *et al*., 2012). Keeping the above points in mind an

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investigation was planned to discern the variability of diverse chickpea lines consisting of elite germplasm and cultivated lines, so that most diverse parents for crossing programme can be identified and diversity of the material can be analyzed.

Materials and methods

A total of 87 elite chickpea genetic stock obtained from Chickpea Project, Division of Genetics, Indian Agricultural Research Institute, New Delhi 110012 were used in this study. The genotypes were designated as GS-1 to GS-87 (Table 1).

DNA Isolation and Genotyping

Isolation of DNA was carried out by as per Kumar *et al*., 2013. A total of 50 sequence tagged microsatellite site (STMS) loci were screened in the accessions of which only 19 were polymorphic (Table 2). The STMS markers were synthesized as per the sequences of (Winter *et al.,* 2000; Bharadwaj *et al*., 2010) from Bioneer, Daejeon, South Korea. BioRad MyCycler thermal cycler, Richmond, USA was used to carry out amplifications in 10 μL volume reaction mixture. This mixture contained 1 μL of 20 ng plant genomic DNA, 1.6 μL of 10×Tris buffer (15mM MgCl2 and gelatine), 1 μL of 10 mM dNTP mix, 1.0 μL each of forward and reverse primer and 0.3 μL of 3 UμL^{-1}*Taq* polymerase. PCR was performed with following conditions 50s at 90^{o}C followedby 18 cycles of denaturation at 94^{o}C for 20s, annealing for 50s at 50^{o}C (Touch down of 0.5^{o}C for every repeat cycle) and1 min elongation at 72^{o}C for 50s. Further 20 cycles of denaturationat 94^{o}C for 20s, annealing for 50s at 55^{o}C and 50s elongation at 72^{o}C were given and final extension at 72^{o}C for7 min were performed. The resolution of PCR products was done on three per cent metaphor gels (Lonza) (Fig. 1).

The polymorphic bands were scored in a spread sheet format with '0' representing absence of band and '1' representing the presence of band 'Null allele' for any specific marker in any genotype was again considered as absence of band (designated as '0'). The data was analyzed in NTSYS-PC software (version 2.21b). Bootstraps were done using Free Tree and Tree view software. For Clustering, UPGMA was used based on the similarity matrix generated on combined data. Polymorphic information content for each STMS primer pair was calculated.

Results

In the present study, a total of 57 STMS loci were analyzed, covering various bin locations on different linkage groups of which 19 were polymorphic (Table 2). A lower level of polymorphism is expected in chickpea which is having a narrow level of diversity compared to other crops and here it was 33.3%. All the 19 STMS loci, in the genetic material under study were found to be highly polymorphic. Excellent polymorphism was revealed by most of these STMS markers. Data from all the 19 STMS loci were utilized for statistical analysis. A total of 87 alleles were found with an average of 4.57 alleles per locus. The highest numbers of alleles were observed in TA194 (five alleles), TA 14, TA80, TA113, TA117 (four alleles each), TA14, TA71, TA110, CaSTMS2, CaSTMS15 and NCPGR4 (three alleles each).

Polymorphism information content (PIC) of each marker system was calculated for each marker and *locus* using the polymorphism information content (Lynch and Walsh, 1998) which gives an estimate of the discriminating power of a *locus* by taking into account not only the number of alleles that are expressed but also their relative frequencies. PIC ranged from 0.11 to 0.94. Highest PIC was observed for NCPGR7 and lowest for TA71.

Some STMS markers were found to have high discriminative power for differentiation of chickpea genetic stocks as the present study demonstrates that 19 out of 57 STMS alleles were found to be unique or rare; unique or rare allele is one with a frequency less than or equal to 0.10. The present findings also indicated instances where the STMS profiles for some of the genotypes displayed maximum variation pattern. Chickpea is highly self-pollinated and should, therefore, reveal lower polymorphism for majority of the genotypes, thus the occurrence of dialleles is also very less with a few primers only and is in concurrence with the reports (Singh *et al.,* 2008; Ahmad *et al.,* 2010; Singh *et al.,* 2014) of a narrow genetic base of chickpea. It has been The STMS data was utilized for estimating pair wise genetic similarities among various entries using Jaccard's coefficient (1908) method. The genetic similarity matrix was further analyzed using UPGMA clustering algorithm by software programme NTSYS pc version 2.21b. The dendogram derived from this analysis is depicted in Fig. 2. The dendogram clearly showed 5 large clusters, 1 small clusters and 1 genotype remained ungrouped (GS39).The

Table 1. Description of 87 elite germplasm accessions used in the present investigation.

Genetic Stock No.	Name	Source of collection	Type	Characteristics	100 SW(g)
1	MPJG-2000-108	JNKVV, Jabalpur	Desi	Improved high yielding breeding line	23.0
2	ICC 4516	ICRISAT, Hyderabad	Desi	Improved high yielding breeding line	11.6
3	KTP-1	IIPR, Kanpur	Desi	Improved high yielding breeding line	26.5
4	IPC-2000-20	IIPR, Kanpur	Desi	Improved high yielding breeding line	23.2
5	IPC-2000-37	IIPR, Kanpur	Desi	Improved high yielding breeding line	14.7
6	IPC-2004-52	IIPR, Kanpur	Desi	Improved high yielding breeding line	13.2
7	IPC-92-39	IIPR, Kanpur	Desi	Improved high yielding breeding line	20.75
8	IPCK-2002-111-2	IIPR, Kanpur	Desi	Improved high yielding breeding line	24.6
9	ICCV 6105	ICRISAT, Hyderabad	Desi	Extra bold, 100 seed weight 43.4g	40.3
10	DGS 730	IIPR, Kanpur	Desi	Improved high yielding breeding line	20.9
11	Basal Pod Mutant	JNKVV, Jabalpur	Desi	Bushy, anthocyanin, lateral spreading	16.8
12	PG0515	MPKVV, Rahuri	Kabuli	Extra bold	60.52
13	Cut ward curve mutant	JNKVV, Jabalpur	Desi	Mutant Stock	14.83
14	Double Podded	IARI, New Delhi	Desi	Very high frequency of double flower green seeded, late, axial pigmentation	17.25
15	IPC 718	IIPR, Kanpur	Desi	Desi, medium bold, multi flower, good poddy, medium tall.	13.7
16	BIO-107	NRCPB, New Delhi	Desi	Soma clonal variants	108.7
17	BIO-108	NRCPB, New Delhi	Desi	Soma clonal variants	15.64
18	BIO-110	NRCPB, New Delhi	Desi	Thick primary branches, Anthocyanin pigment rich stems	28.2
19	ILC 5498	ICARDA, Syria	Kabuli	Erect plant type	22.04
20	ILC 5598	ICARDA, Syria	Desi	Erect plant type	23.0
21	IPC-2004-46	IIPR, Kanpur	Desi	Improved high yielding breeding line	17.65
22	IPC-2006-3	IIPR, Kanpur	Desi	Erect, basal pigmentation	40.08
23	IPC-2006-11	IIPR, Kanpur	Desi	Improved high yielding breeding line	47.76
24	IPC-2006-13	IIPR, Kanpur	Desi	Improved high yielding breeding line	21.23
25	IPC-2006-129	IIPR, Kanpur	Desi	Erect type	24.73
26	IPC-2007-22	IIPR, Kanpur	Desi	Erect type	32.2
27	JGM-7	JNKVV, Jabalpur	Desi	Anthocyanin pigmentation in stem	14.85
28	DG 702	IARI New Delhi	Desi	Erect	19.92
29	DG 724	IARI New Delhi	Desi	Improved high yielding breeding line	18.8
30	DG 733	IARI New Delhi	Desi	Improved high yielding breeding line	18.32
31	DG 752	IARI New Delhi	Desi	Improved high yielding breeding line	16.54
32	HK01-36	CCSHAU, Haryana	Kabuli	Improved high yielding breeding line	12.12
33	HK01-203	CCSHAU, Haryana	Kabuli	Improved high yielding breeding line	34.08
34	HK-00-290	CCSHAU, Haryana	Kabuli	Improved high yielding breeding line	28.0
35	Double Pod High Density	IARI, New Delhi	Desi	Erect type with higher number of double flowers and double pods	10.5
36	EC565214	ICRISAT, Hyderabad	Desi	Erect type	
37	EC565211	ICRISAT, Hyderabad	Desi	Erect type	17.1
38	Kabuli Dark Brown	IARI New Delhi	Kabuli	Dark brown Kabuli seed type	18.1
39	Market Collection-1(K)	IARI New Delhi	Kabuli	Bold seeded	51.4
40	Gokcee (FLIP 87-8C)	ICARDA, Syria	Kabuli	Drought tolerant line from ICARDA	28.54
41	JG-2003-14-2	JNKVV, Jabalpur	Desi	Erect, compact	32.14
42	JG2-14-11	JNKVV, Jabalpur	Desi	High yielding, small seeded breeding line	22.44
43	BGM-408	IARI, New Delhi	Desi	Variety developed through mutation breeding	24.54
44	BGM-417	IARI, New Delhi	Desi	Variety developed through mutation breeding	12.23
45	BGM-547	IARI, New Delhi	Desi	Variety developed through mutation breeding	22.4
46	ICC-5434	ICRISAT, Hyderabad	Desi	Spreading Type	23.84

Contd.

Table 1 Contd.

Genetic Stock No.	Name	Source of collection	Type	Characteristics	100 SW(g)
47	ICC-16644	ICRISAT, Hyderabad	Kabuli	Improved breeding line	29.4
48	IPC-2006-125	IIPR, Kanpur	Desi	Erect	25.32
49	HC-5	IIPR, Kanpur	Desi	Erect	28.38
50	CSJK-25	CSKVV, Kanpur	Kabuli	Extra bold	28.27
51	IGK-I	IGKVV, Raipur	Kabuli	Extra bold	29.22
52	MNK-1	UAS, Raichur	Kabuli	Extra bold	29.21
53	PCS-10	IARI, New Delhi	Desi	Improved breeding line	34.08
54	PA-0590	IARI, New Delhi	Desi	Improved breeding line	13.98
55	Roasted Type	IARI, New Delhi	Desi	Seed suitable for parching use	30.66
56	Out warded curve	IARI, New Delhi	Desi	Mutant stock for leaflet shape	15.14
57	Pinnate leaf	IARI, New Delhi	Kabuli	Mutant stock for leaflet shape	27.91
58	Crack seed	IARI, New Delhi	Desi	Simple leaf, Mutant stock for seed type	29.9
59	Vareigata (D)	IARI, New Delhi	Desi	Mutant stock for leaflet shape	15.93
60	Fasiata Mutant	IARI, New Delhi	Desi	Mutant stock for leaflet shape	13.57
61	DG F_6-1209	IARI, New Delhi	Kabuli	Simple leaf mutant stock for leaflet shape	25.5
62	DG F_5-205	IARI, New Delhi	Kabuli	Simple leaf mutant stock for leaflet shape and white flowered	13.01
63	AKG-70	Akola, Maharashtra	Desi	Improved breeding line	15.84
64	ICC-12825	ICRISAT, Hyderabad	Kabuli	Small seed	11.76
65	ICC-17256	ICRISAT, Hyderabad	Desi	Improved breeding line	21.92
66	ICC-16341	ICRISAT, Hyderabad	Desi	Open flower	10.6
67	ICC-16129	ICRISAT, Hyderabad	Desi	Open flower	10.7
68	ICC-13925	ICRISAT, Hyderabad	Desi	Improved breeding line	11.6
69	ICC-17109	ICRISAT, Hyderabad	Kabuli	Extra large seed (100 Seed weight 65g)	44.1
70	Harigantars	IIPR, Kanpur	Desi	Black seed, erect, early, long internodes, Local land race	11.23
71	SBD-377	IARI, New Delhi	Desi	Extra bold simple leaf desi type	48.2
72	ILC-212	ICARDA, Syria	Kabuli	Small seeded	41.4
73	C-235	ICARDA, Syria	Desi	Small seeded	11.28
74	TDB	IARI, New Delhi	Desi	Tuberculated, desi, bold seeded	27.12
75	C-214	IARI, New Delhi	Desi	Improved breeding line	18.0
76	GL-769	IARI, New Delhi	Desi	Improved breeding line	14.7
77	BG-2073	IARI, New Delhi	Desi	Improved breeding line	13.96
78	K-850	Kanpur	Desi	Improved breeding line	26.72
79	CSG-8962	CSSRI, Karnal	Desi	Salinity tolerant	12.24
80	Biogreen	NRCPB, New Delhi	Pea type	Pea type kabuli with green seed coat colour	12.25
81	JG-315	JNKVV, Jabalpur	Desi	Wilt resistant donor for all the races except *foc*1	14.22
82	DG-5033	IARI, New Delhi	Desi	Extra bold desi	33.21
83	BGD-132	IARI RS Dharwad	Kabuli	Lateral spreading	23.4
84	BGD-9812	IARI RS Dharwad	Desi	Lateral spreading	13.08
85	RSG-143-1	RAU, Jodhpur	Desi	Breeding line tolerant to high temperature	26.2
86	JG-11	JNKVV, Jabalpur	Desi	Double poded high yielding line	22.1
87	DG-5066	IARI, New Delhi	Desi	Extra bold seed	21.26

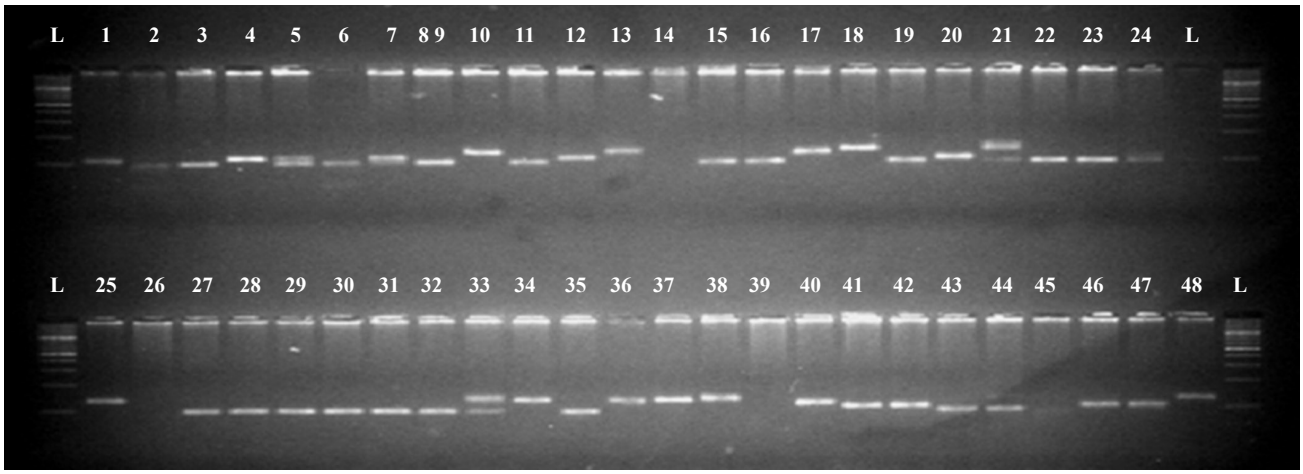

Fig. 1(a) SSR-PCR amplification products of chickpea with accessions using SSR primer TA194

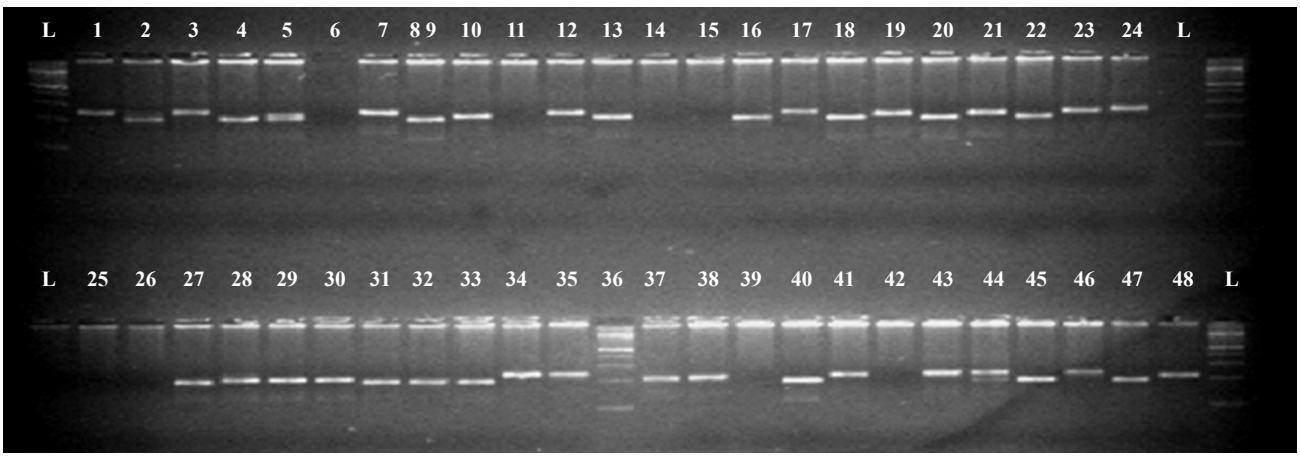

Fig. 1(b) SSR-PCR amplification products of chickpea with accessions using SSR primer TA80

Table 2. SSR primers used for chickpea germplasm analysis

S. No.	Primer name	Linkage group	PIC value	Heterozygosity
1	TA103	LG2	0.33	0.42
2	TA3	LG9	0.18	0.20
3	TA14	LG4	0.47	0.53
4	TA71	LG5	0.11	0.11
5	TA186	LG4	0.21	0.23
6	TA194	LG2	0.68	0.72
7	TA203	LG1	0.17	0.17
8	TA200	LG2	0.59	0.59
9	TA80	LG6	0.59	0.66
10	TA96	LG7	0.25	0.29
11	TA113	LG 1	0.45	0.53
12	TA117	LG2	0.47	0.56
13	TA110	LG2	0.40	0.52
14	CaSTMS2	a	0.10	0.11
15	CaSTMS15	a	0.51	0.60
16	NCPGR4	LG6	0.44	0.52
17	NCPGR6	LG6	0.84	0.84
18	NCPGR7	LG4	0.94	0.94
19	NCPGR12	LG7	0.27	0.32

Source: Bharadwaj *et al.,* 2010, 2011; a – from Huttel *et al*.; Varshney *et al.,* 2013.

cluster I, II, III, IV, V and VI comprised of 36, 5, 13, 11, 19 and 2 genotypes respectively. Maximum Jaccard's correlation was seen for the genotypes IPC-2000-20 (GS4) and IPC-2000-37 (GS5) while the genotypes BGD-132 (GS83) and BGD-9812(GS84) were having highest similarity index, while the genotypes SBD377 (GS71) and ILC-212(GS72) have shown the highest dissimilarity with all the other genotypes and distinctly formed a separate cluster (cluster VI) (Fig. 2).

Discussions

Among the various DNA based markers, microsatellite or STMS markers are highly accepted and have been used in the diverse crop plants owing to their abundance in the genome (Powell *et al.,* 1996). The application of STMS markers in genetic analysis of chickpea, started with an initial study of (Huttel *et al.,* 1999) and after that, the power and potential of SSR markers for a broad

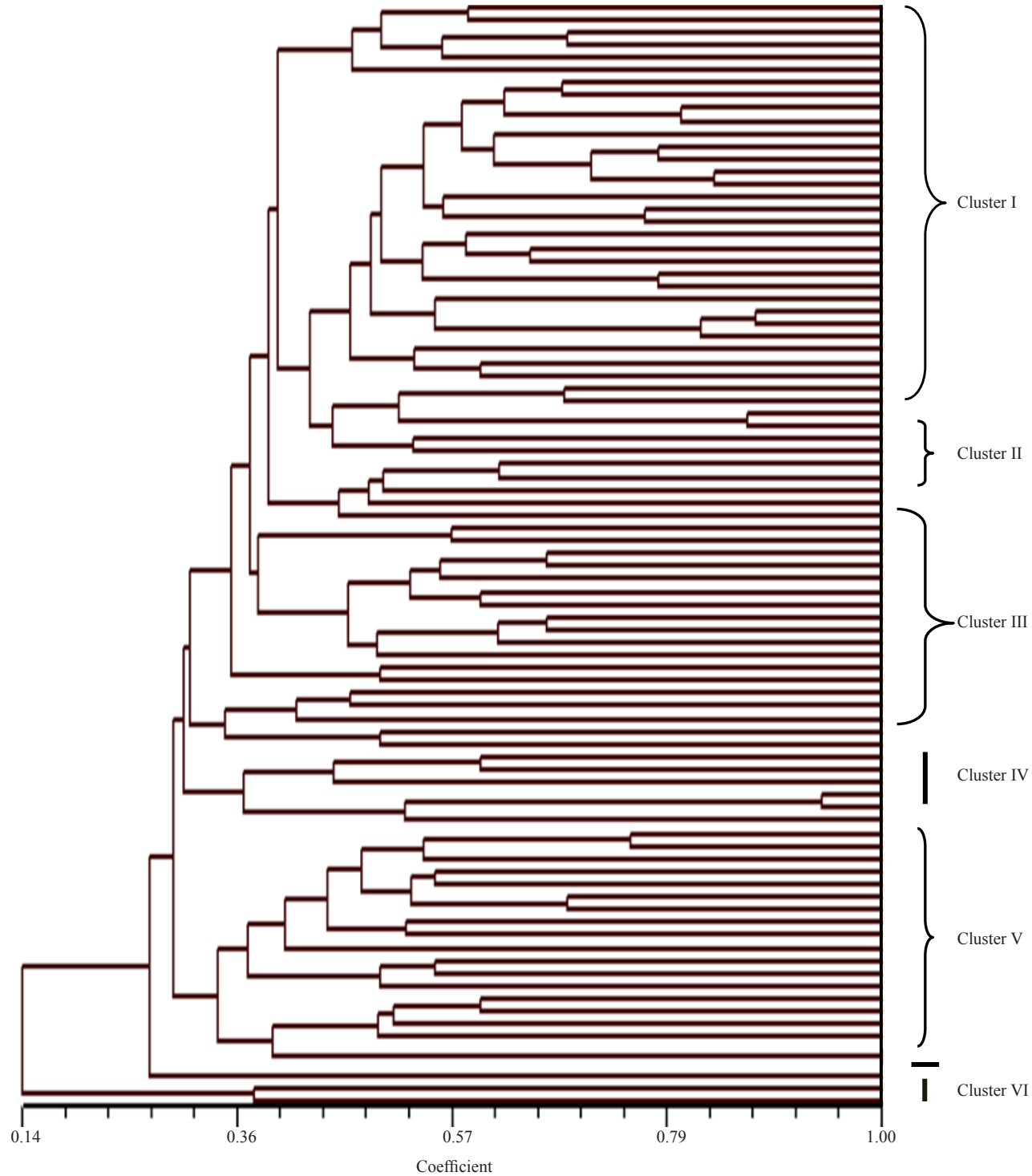

Fig. 2. Jaccard's similarity grouping of 87 chickpea genotypes

range of applications in genetic and breeding of chickpea has been well demonstrated by a number of researchers (Huttel *et al.,* 1999; Winter *et al*., 2000; Flandez-galvez *et al*., 2003; Choumane *et al*., 2000). Microsatellite genotypic data from a number of loci have potential to give unique allelic profiles or DNA fingerprints for establishing genotypes identity (Bharadwaj *et al*., 2010). A narrow genetic base in chickpea warrants immediate base broadening efforts. Though morphological diversity is generally used by the breeders as a criteria in making

Table 3. Clustering of genotypes based on UPGMA analysis of 87 genetic stocks of chickpea using SSR markers

S. No.	Cluster No.	No. of genotypes	Names of genotypes
1.	I	36	GS1, GS2, GS3, GS4, GS5, GS6, GS7, GS8, GS10, GS11, GS13, GS14, GS15, GS16, GS18, GS19, GS20, GS23, GS24, GS25, GS26, GS27, GS28, GS29, GS30, GS31, GS41, GS42, GS43, GS44, GS45, GS49, GS59, GS75, GS85, GS86.
2.	II	5	GS9, GS12, GS21, GS37, GS40.
3.	III	13	GS17, GS22, GS32, GS36, GS35, GS38, GS46, GS48, GS55, GS56, GS61, GS68, GS70.
4.	IV	11	GS57, GS69, GS65, GS58, GS60, GS47, GS52, GS87, GS50, GS51, GS53.
5.	V	19	GS33, GS34, GS67, GS64, GS66, GS79, GS80, GS73, GS78, GS74, GS63, GS77, GS76, GS54, GS81, GS82, GS62, GS83, GS84.
6.	VI	2	GS71, GS72.

crosses, it is clearly known that the manifestations of 'G × E' interactions make closely related individuals to appear diverse and thus there are greater chances of these being used in crossing programmes. Knowledge of molecular diversity in the material helps discern this diversity and in identification of parents for crossing programme (Bharadwaj *et al.,* 2010).

For acceleration and optimizing the long process of creating new chickpea cultivars molecular markers are included as analyzing tools. Molecular markers are considered as good candidates for classifying genotypes in different groups and thus assessing genetic distances as well as genetic expected gains. RAPD were earlier used. However owing to greater reliability and repeatability, SSR markers are now being increasingly used for discerning genetic diversity.

Nineteen STMS primer pairs could amplify 1-4 loci per primer pair generating 4.57allels per locus on an average. Contrary to the fact that chickpea is a self pollinated crop and should generate lower polymorphism. World chickpea germplasm has a narrow genetic base (Nguyen *et al.*, 2004) and lacks the desirable traits needed for ready utilization in varietal improvement programs. A narrow genetic base and sexual incompatibility with other *Cicer* wild types, which carry the sources for various desirable traits, contribute to the limited progress in the improvement of chickpea yield (Chaudhary *et al*., 2012). The presence of multiple alleles may have occurred to the fact that there is a very high residual heterozygotic balance conserved due to *Desi* × *Kabuli* introgression that played a major role in chickpea evolution. This may be one of the causes for obtaining multiple bands using SSR markers (Singh *et al.,* 2008). A high degree of molecular polymorphism was exhibited by all the markers studied indicates the markers that have been used for diversity analysis were sound. The PIC ranged from 0.10 to 0.94 and heterozygosity ranged from 0.11 to 0.94. The Jacards similarity matrix dendogram constructed using the UPGMA method showed that all the clusters were dissimilar and grouped into seven major clusters. A critical examination of these clusters with indicates that the grouping was primarily based on seed size. Cluster VI has SBD 377 and ILC 212. SBD 377, a simple leaf mutant developed at IARI had an ICARDA line in its pedigree PRR1, a derivative from FLIP 90-166, an ICARDA line and thus would have got clustered in proximity with GS72 *i.e*. ILC 212. The market collection GS39, a bold seeded *kabuli* type remained un-grouped as it was very bold in its size and does not represent a released cultivar but market collection obtained under the ISOPOM trial. Cluster two comprised mostly either bold seeded or erect types. Thus plant architecture also played an important role. However, contrary to earlier workers reports, it is clearly noticed that the place where the cultivars were developed did not play a major role in grouping. This may be due to the fact that, the elite breeding lines included in this study obtained from different centers were developed from germplasm either obtained from ICRISAT or ICARDA. In the previous study of Bharadwaj *et al*. (2011) specific lines of ICARDA, ICRISAT and IARI were used where all the lines from ICARDA and wild species were grouped as a distinct cluster. The breeder's generally use diverse sources selected based on morphological traits and their observation in making crosses. Similar results were obtained by Choudhary *et al*. (2012).

Results from the present study support the observations of several workers about the potential utility of STMS in characterizing asparagus lines (Huttel *et al.,* 1999; Winter *et al*., 2000; Flandez-galvez *et al*., 2003; Choumane *et al*., 2000). There was reasonably high rate of polymorphism for at least ten markers namely TA194, TA80, TA113, TA117, TA14, TA110, NC6, NC7, CaSTMS15 and NCPGR4 out of 19 STMS markers loci in the present study. This pointed towards the scope for further utilization of these markers for characterization of different cultivars of chickpea. The STMS polymorphism were assayed using a DNA pooling

strategy, although it is not supposed to do as all the genotypes under study are pure lines (Flandez-Galvez *et al*., 2003) demonstrated the power and potential of SSR markers for a wide range of applications in genetic and breeding of chickpea. Molecular markers being easily reproducible they have become favourite tools with breeders and biotechnologists to discern the traits as well as to study diversity among cultivars (Satyavathi *et al*., 2005). However, no correlation could be derived from PIC and allele numbers in this study. Further, Greater gains can be obtained by crossing lines MPJG-2000-108 with SBD 377 for *desi* improvement and PG 0515 with ILC 212 for *kabuli* improvement. These genotypes have been identified as most diverse in the present study. Pre-breeding and Base broadening through *kabuli* × *desi* introgression for greater gains is an important activity of the breeders. This increases the diversity obtained in the succeeding generations to carry out further selections as there is enormous amount of variation that is seen in these generations for seed size, seed type and other traits. In the present study greater base broadening can be achieved by using ICC 4516 and ILC 212 as parents in the breeding programme.

This study helped to determine the genetic relationship between elite genetic stock of chickpea based on STMS marker data, and these results greatly contribute to germplasm bank management, conservation programs, and breeding purposes. The occurrence of unique alleles or rare STMS alleles provides an immense opportunity for generation of comprehensive fingerprint database. The present investigation also gives an idea of the interrelationship among the genotypes and highlights the need for helpful supplementation of pedigree data and other morphological data with the database generated by STMS marker to efficiently discover the genetic inter-relationship among the genotypes, fingerprint the varieties for their protection and most importantly select parents for a sound breeding programme.

Acknowledgements

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Patterns of Genetic Variation, Correlations under Irrigated and Rainfed Conditions in Indian Mustard [*Brassica juncea* (L.) Czern. & Coss.]

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An experiment was conducted on 77 advanced progenies (F_6) of Indian mustard in augmented block design under irrigated (E_1) and water stressed (E_2) conditions to know the patterns of genetic variability and correlations under irrigated and rainfed conditions. Observations were recorded on 12 morphological characters. The estimates of heritability under irrigated conditions were of higher magnitude (>50%) for main shoot length, siliquae on main shoot, siliquae length, seed yield/plant and 1000 seed weight, whereas under rainfed conditions, secondary branches/plant, siliquae on main shoot, siliquae length and 1000 seed weight recorded higher estimates of heritability. For other characters (siliquae/plant, main shoot length and seed yield/plant) moderate estimates of heritability were observed. Under irrigated conditions, seed yield/plant was positively and significantly correlated with plant height (0.241), primary branches/plant (0.381), secondary branches/plant (0.493), fruiting zone length (0.295), siliquae/plant (0.562), biological yield (0.852) and harvest index (0.613) while under rainfed conditions, seed yield/plant was significantly and positively correlated with plant height (0.445), primary branches/plant (0.443), secondary branches/plant (0.611), fruiting zone length (0.505), siliqua/plant (0.729), main shoot length (0.410), seeds/siliqua (0.283), biological yield (0.774) and harvest index (0.482).

Key Words: Correlations, Heritability, Indian mustard, Rainfed

Introduction

Indian mustard [*Brassica juncea* (L) Czern. & Coss. 2n=4x=36] is a natural amphidiploids between *Brassica campestris* (2n=20) and *Brassica nigra* (2n=16). In India, *Brassica juncea* is a predominant species which accounts for nearly 80% of the oilseed brassicas. Central Asia- Himalayas is a primary center of diversity for this species with migration to China, India and Caucasus (Hemingway, 1976). The crop is mainly grown for its oil which is largely used in cooking and for frying purposes. Oilseed cake or meal which is a byproduct during the extraction of oil from the seeds, is an important source of protein feed for animals while the leaves of the plant are used as vegetable as well as fodder for cattle. In spite of all the efforts made over past decades, the productivity has remained almost constant, may be due to lack of high yielding genotypes with stable performance over the environment. There is lack of adequate genetic variability for morphological traits and high degree of genotype x environment interaction.

Concerted breeding efforts are required to bring out favorable change in yielding ability of this crop. The low yield and stability are ascribed to lack of genetic variability for some important yield components, non-availability of short duration, disease and pest resistant genotypes, even the limited world germplasm collections have been attributed to the limited success achieved so far.

The knowledge of the magnitude of genetic parameters of seed yield and its component traits for different conditions is essential for an effective breeding programme. Moreover, association and interaction of different component characters with seed yield may help in selection of superior lines under different environments. Considering the above facts, present study reports the pattern of variability and character association in advanced lines of Indian mustard under irrigated and rainfed conditions.

Materials and Methods

The material for present investigation consisted of 77 advanced progenies (F_6) of Indian mustard (Table 1) selected on the basis of high yield under rainfed conditions in previous generation. These progenies were derived from 49 different crosses involving Exotic × Indian and Indian × Indian genotypes. The experiment was carried out at research farm of Directorate of Rapeseed Mustard Research, Sewar, Bharatpur during 2011-12.

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Table 1. Details of progenies used in experimentation along with their mean values

S. No.	Progeny	Characters																							
		PH (cm)		PB		SB		FZL (cm)		S/P		MSL (cm)		S/MS		SL (cm)		BY(g)		SY (g)		HI (%)		1000 SW (g)	
		IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF
1	BPR-583-1	177.7	168.6	4.6	4.1	6.0	2.8	81.5	72.4	140.4	129.3	77.8	71.4	43.6	43.0	4.2	4.8	45.8	33.7	10.6	9.4	21.0	28.7	5.7	5.6
2	BPR-577-2	187.7	181.0	5.0	4.1	5.4	2.2	77.7	87.4	142.6	104.9	59.0	77.2	49.0	41.6	3.9	4.3	28.3	36.2	5.6	8.0	20.2	21.0	5.6	5.7
3	BPR-686-3	177.1	171.2	3.8	4.5	1.8	3.6	71.7	78.8	100.6	127.9	70.4	78.0	41.0	42.8	3.9	4.1	23.3	38.7	4.6	8.3	21.0	20.1	5.4	6.3
4	BPR-674-4	174.9	175.2	5.6	3.9	8.2	2.4	67.7	67.4	186.0	49.3	59.0	68.8	27.0	36.6	3.7	4.7	38.3	31.2	9.6	6.6	23.3	19.5	5.0	5.4
5	BPR-694-6	164.5	169.8	5.4	4.1	8.4	3.6	71.7	73.0	229.8	166.3	67.6	71.6	41.4	44.6	4.1	4.6	40.8	33.7	7.1	8.4	16.1	24.7	6.3	5.8
6	BPR-682-7	181.1	175.4	4.8	3.9	3.8	3.2	71.3	74.2	158.2	116.1	57.0	72.6	32.4	38.8	3.9	4.5	40.8	23.7	8.7	8.3	19.8	40.5	4.9	5.6
7	BPR-667-8	164.5	165.6	4.4	4.3	6.4	15.0	68.3	72.2	100.8	128.9	67.8	65.4	33.2	40.2	3.9	4.5	35.8	33.7	7.7	8.4	20.4	24.8	6.2	6.3
8	BPR-639-9	178.5	165.0	4.4	3.1	5.4	1.2	77.9	68.4	135.2	88.1	69.0	69.8	40.6	36.4	4.1	4.5	35.8	38.7	7.0	7.6	18.6	17.7	5.1	5.8
9	BPR-691-10	166.3	176.4	4.0	3.3	4.2	2.4	74.5	75.6	157.8	120.7	187.2	84.0	45.4	39.2	4.3	5.0	35.8	36.2	7.9	7.4	21.0	19.0	5.0	6.2
10	BPR-669-12	174.7	163.8	4.8	4.1	4.4	3.8	73.1	74.2	161.0	178.3	63.8	69.8	42.0	38.2	4.0	5.0	35.8	48.7	6.9	8.5	18.4	15.5	4.0	6.9
11	BPR-1299-18	159.9	156.4	4.8	3.9	4.0	2.0	53.1	62.0	105.2	107.1	55.6	57.6	31.8	31.2	3.7	4.3	35.8	38.7	10.2	8.0	26.7	19.3	5.0	6.7
12	BPR-1292-22	167.2	141.2	3.5	3.4	1.7	2.2	62.2	63.6	166.8	120.5	65.2	62.8	37.6	39.2	4.6	4.4	33.8	19.4	9.3	3.3	26.8	17.9	6.8	5.4
13	BPR-1307-250	188.0	148.8	5.7	4.0	2.1	1.6	69.8	68.4	276.0	104.3	88.0	73.6	47.2	44.0	4.4	4.2	38.8	19.4	10.2	5.5	25.7	30.4	6.2	5.7
14	BPR583-26	174.4	143.0	5.3	3.6	3.3	2.2	71.6	65.8	214.2	81.7	65.4	63.2	45.0	35.6	4.2	4.9	41.3	19.4	11.8	4.1	27.9	21.9	6.7	6.4
15	BPR-645-30	185.6	156.0	2.9	3.6	3.5	0.8	88.6	69.4	183.0	114.3	93.8	67.6	35.6	35.4	4.6	4.1	38.8	11.4	9.0	4.4	22.9	37.5	5.7	6.1
16	BPR-669-31	196.8	158.0	3.9	5.4	4.5	2.0	77.8	77.8	214.4	109.1	81.6	64.4	46.6	39.4	4.3	4.7	43.8	24.4	11.2	5.3	25.2	22.0	5.6	5.4
17	BPR-1293-32	202.2	145.2	3.5	3.4	2.3	2.6	77.4	70.6	170.8	95.1	86.6	73.6	48.6	35.8	3.8	4.7	38.8	29.4	9.7	5.7	24.5	19.9	5.1	6.8
18	BPR-1293-33	178.8	158.4	5.3	3.0	2.3	2.2	73.6	69.6	186.6	104.7	128.0	73.0	49.8	35.6	3.9	3.8	41.3	29.4	9.9	9.4	23.5	38.8	5.9	6.0
19	BPR-1300-35	177.6	150.2	3.5	4.6	0.7	0.8	81.2	69.2	135.4	125.1	78.8	73.0	41.6	35.2	3.7	3.9	28.8	20.9	5.0	4.4	17.6	21.9	5.7	6.3
20	BPR-625-36	162.8	156.8	3.5	4.0	3.5	3.8	71.2	82.6	154.2	134.3	84.8	73.8	42.8	42.6	4.4	4.0	31.3	24.4	4.9	4.2	16.1	18.0	5.5	6.1
21	BPR-625-36	176.2	153.8	3.7	3.8	1.7	2.2	88.0	71.8	169.2	106.1	89.2	72.6	47.2	36.4	4.8	3.7	43.8	24.4	9.0	3.7	20.0	15.9	5.9	5.2
22	BPR-625-39	183.0	151.0	4.1	4.4	0.8	1.6	72.4	66.4	156.6	103.9	65.8	64.0	43.0	39.4	4.1	4.1	31.3	16.9	7.5	3.8	23.7	23.3	5.9	5.5
23	BPR-1294-42	181.2	174.4	5.5	3.4	10.8	1.5	86.4	71.6	219.6	184.6	90.9	75.7	48.0	39.4	3.9	4.4	55.2	22.9	13.5	4.7	26.6	21.2	4.6	5.4
24	BPR-625-37	194.6	182.4	5.1	4.2	9.0	0.5	80.0	76.0	166.8	119.8	76.7	68.9	47.4	37.4	4.0	4.6	50.2	30.4	12.4	6.2	26.5	20.5	3.9	6.6
25	BPR-669-1	194.8	153.8	4.5	3.6	8.2	3.9	85.4	67.2	242.8	124.0	84.7	70.3	43.0	39.4	5.1	4.7	65.2	22.9	15.5	4.1	26.3	18.4	5.0	5.3
26	BPR-669-2	172.8	156.4	4.3	3.2	11.2	2.7	85.2	65.2	130.6	106.2	85.7	66.5	39.4	35.0	4.0	4.8	47.7	20.4	10.7	3.8	23.9	19.5	4.9	6.1
27	BPR-694-4	168.0	164.4	5.7	3.8	12.4	2.9	70.4	70.8	235.0	127.2	67.3	68.3	40.2	35.8	4.0	4.6	57.7	25.4	14.2	5.3	26.9	21.3	4.6	5.6
28	BPR-694-5	184.6	155.8	6.5	3.0	15.4	2.1	90.8	59.0	251.2	87.6	75.5	65.1	45.6	30.6	3.6	4.8	75.2	25.4	18.6	5.0	27.6	20.1	4.0	6.2
29	BPR-1304-6	179.8	173.2	3.5	3.4	13.2	4.5	84.4	80.8	218.4	182.4	81.3	87.1	37.0	50.2	4.1	4.5	67.7	40.4	17.3	10.1	28.3	24.6	4.0	6.0
30	BPR-139-7	178.8	172.4	4.5	3.8	10.2	5.7	83.2	75.2	245.8	193.0	76.7	77.5	40.0	39.4	3.8	3.7	62.7	32.9	13.5	11.7	23.7	35.8	3.4	5.0
31	BPR-606-11	178.0	170.0	5.9	4.4	13.0	5.5	78.5	76.8	226.0	191.2	75.1	74.7	44.0	47.2	3.8	4.4	55.2	45.4	15.3	10.8	30.1	23.4	3.4	5.3
32	BPR-639-16	171.0	178.0	5.1	4.6	8.4	7.3	73.2	80.4	199.0	214.8	65.9	81.5	35.8	40.4	3.9	4.2	41.7	57.9	11.9	15.0	30.2	25.2	5.2	6.6
33	BPR-639-18	180.4	177.8	4.7	3.4	12.8	5.1	73.6	78.4	204.2	139.6	79.1	80.1	49.4	30.4	4.1	4.2	52.7	37.9	14.9	9.6	30.6	25.1	5.1	7.0
34	BPR-1298-26	167.0	157.2	5.3	3.5	11.0	5.6	74.4	71.2	232.4	167.8	58.3	64.1	36.8	40.8	3.8	3.5	64.2	45.7	17.4	5.9	29.9	15.4	4.5	4.8
35	BPR-141-36	166.6	143.4	4.5	2.9	8.8	0.6	72.0	55.2	194.6	80.0	72.3	58.5	41.8	38.4	3.4	4.1	40.2	20.7	10.4	4.9	27.2	24.7	4.8	5.7
36	BPR-578-43	166.6	158.0	3.7	2.5	10.2	2.8	63.4	68.2	111.2	125.6	43.5	73.3	37.8	36.2	3.9	3.5	37.7	38.2	9.0	7.7	24.5	21.4	4.1	4.8
37	BPR-675-44	171.6	155.4	3.9	2.9	7.4	3.6	78.0	70.2	206.0	131.0	79.9	65.5	39.8	44.0	3.9	3.1	45.2	38.2	12.0	10.3	28.3	26.7	4.0	4.1
38	BPR-683-45	170.4	149.0	4.5	2.9	5.8	0.4	67.4	64.6	164.6	51.4	70.7	68.1	43.4	39.8	3.9	5.0	47.7	14.2	13.0	4.3	29.3	28.3	5.6	6.1
39	BPR-675-46	167.0	155.6	4.3	3.7	6.8	1.0	62.4	64.0	158.6	59.2	63.1	58.7	42.0	36.8	3.7	3.7	39.2	20.7	11.5	5.2	31.0	25.6	4.2	6.0
40	BPR-656-47	176.0	141.4	2.5	2.5	7.0	3.0	77.0	62.2	177.4	94.0	71.1	64.7	40.8	40.6	4.1	3.8	40.2	22.2	12.6	6.1	33.2	26.9	4.4	4.9
41	BPR-670-48	175.4	164.4	2.9	3.3	4.8	0.8	75.8	63.0	146.4	104.2	79.1	60.1	39.4	40	3.3	3.4	29.7	18.2	7.7	5.1	25.6	27.4	4.4	4.6
42	BPR-156-52	140.4	163.2	4.1	3.9	7.4	6.0	71.6	66.6	188.2	145.8	69.7	64.9	44.8	42.2	5.7	3.5	37.7	23.2	10.5	8.4	29.1	32.7	4.8	5.1
43	BPR-172-53	187.6	153.8	4.5	3.9	10.4	7.8	76.4	72.8	221.0	265.4	71.7	61.7	42.6	48.4	3.8	3.66	42.7	40.7	12.5	12.7	31.2	30.0	4.4	4.3
44	BPR-181-54	110.2	152.6	4.1	3.3	5.4	2.4	80.2	66.0	206.0	64.6	65.5	61.9	47.0	35.2	4.0	4.1	39.2	20.7	11.1	1.8	29.8	15.0	3.7	4.3
45	BPR-150-58	169.8	149.5	4.5	3.1	5.6	1.0	72.7	57.0	196.8	106.7	64.4	65.7	37.0	40.1	4.6	3.8	30.0	35.0	7.5	10.3	24.7	29.4	4.8	5.4

Table 1 Contd.

S. No.	Progeny	Characters																							
		PH (cm)		PB		SB		FZL (cm)		S/P		MSL (cm)		S/MS		SL (cm)		BY(g)		SY (g)		HI (%)		1000 SW (g)	
		IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF
46	BPR-783-60	209.2	155.3	4.7	3.9	5.4	3.8	78.5	62.0	150.8	131.7	74.6	61.9	45.6	38.7	3.8	3.9	45.0	25.0	10.3	10.5	23.6	38.8	3.3	5.4
47	BPR-1669-44	177.2	140.9	5.7	3.3	7.2	2.8	72.9	48.4	146.0	123.5	65.2	53.7	37.4	35.9	4.3	4.2	42.5	25.0	11.0	9.7	26.9	36.4	4.9	6.3
48	BPR-671-45	191.8	129.7	4.1	2.9	3.4	1.8	84.3	42.8	155.2	97.1	82.8	57.5	48.8	30.9	4.3	4.5	35.0	25.0	8.6	9.0	24.8	33.9	5.1	5.5
49	BPR-645-50	197.8	156.7	5.3	3.3	7.2	3.4	78.7	67.8	166.4	130.3	69.8	66.9	39.4	35.3	3.9	4.2	50.0	35.0	13.9	12.3	29.2	35.3	5.4	6.4
50	BPR-565-52	191.6	155.1	5.5	4.7	5.8	10.2	77.7	60.4	198.2	230.7	67.0	63.1	46.4	41.5	3.2	3.4	35.0	45.0	7.8	16.1	22.2	35.7	4.1	5.8
51	BPR-587-56	189.8	168.9	4.9	4.3	10.4	5.2	78.5	68.2	243.0	223.5	79.2	77.3	46.2	34.5	4.6	3.8	45.0	50.0	11.9	13.9	27.5	28.6	3.7	6.0
52	BPR-630-62	194.8	153.3	5.1	4.7	3.8	0.4	76.9	60.8	127.0	137.1	65.2	71.1	35.0	31.9	5.0	3.8	40.0	42.5	8.1	10.6	20. 2	25.8	5.0	5.6
53	BPR-583-63	208.6	158.9	4.1	3.3	6.2	4.4	69.9	63.6	171.2	168.7	61.6	75.5	43.0	44.5	3.7	3.6	45.0	45.0	10.3	11.6	23.7	26.7	4.8	5.8
54	BPR-606-62	198.2	147.5	4.1	2.9	5.0	2.8	85.9	60.6	169.2	131.1	82.4	66.7	46.2	35.9	4.0	4.5	37.4	42.5	10.6	12.8	29.4	30.5	5.4	6.8
55	BPR-645-68	172.2	148.1	5.9	3.5	6.4	6.4	66.9	65.4	132.6	212.7	61.2	69.9	32.2	34.7	4.7	4.2	47.5	42.5	11.2	10.0	24.4	24.6	4.6	5.4
56	BPR-648-69	172.7	173.8	3.8	3.3	2.2	6.8	62.1	78.4	130.4	181.7	64.2	87.8	37.0	56.8	3.5	4.3	33.8	43.7	5.7	10.3	16.6	23.1	6.0	5.7
57	BPR-667-70	170.5	172.4	3.0	5.3	0.8	7.0	66.5	84.4	75.0	190.5	66.8	79.0	33.6	44.0	4.1	4.3	23.3	51.2	3.5	11.0	17.3	20.4	5.6	5.9
58	BPR-671-71	163.7	158.2	4.8	4.5	4.0	6.2	71.5	73.2	143.0	177.9	61.0	76.4	39.8	47.4	4.3	4.5	25.8	38.7	4.4	9.9	18.1	25.6	4.6	5.8
59	BPR-671-72	146.1	166.6	4.2	3.6	4.8	5.4	72.3	102.2	104.4	178.9	76.4	90.4	41.6	44.4	3.7	4.6	27.3	56.2	4.7	12.8	17.9	22.1	5.8	6.3
60	BPR-671-73	180.3	147.2	3.2	4.3	2.4	7.4	77.7	75.4	86.6	158.7	72.8	84.6	42.2	45.6	3.8	4.3	25.8	53.7	3.1	8.2	14.1	13.1	5.3	5.6
61	BPR-682-74	179.1	185.2	5.2	4.7	3.4	8.0	83.1	90.2	140.4	232.5	78.2	89.8	40.0	53.0	4.1	5.0	35.8	56.2	6.7	13.3	17.9	23.2	4.1	5.1
62	BPR-1309-75	172.5	182.8	4.6	3.9	7.0	6.0	70.5	90.4	125.0	210.9	67.2	90.6	37.2	56.6	4.3	4.9	35.8	51.2	5.5	12.4	14.7	23.8	4.5	5.3
63	BPR-645-76	160.3	178.2	4.0	3.9	2.4	6.6	72.9	86.4	113.0	166.5	69.6	85.8	32.0	50.6	4.6	5.2	35.8	41.2	7.2	10.3	19.2	24.8	5.6	6.7
64	BPR-565-24	161.1	175.6	3.2	7.3	2.4	7.0	73.7	82.6	69.6	200.1	77.8	84.6	38.4	48.2	4.3	4.4	28.3	45.7	5.1	13.6	18.5	30.5	4.7	5.4
65	BPR-572-78	167.5	162.8	3.8	4.5	4.2	4.8	67.1	82.8	66.2	148.9	58.4	85.0	30.0	43.0	4.0	4.4	30.8	38.7	3.4	9.1	12.0	22.9	4.5	6.7
66	BPR-575-79	176.1	155.4	4.0	4.1	2.6	3.8	67.9	82.2	111.2	145.3	66.0	76.4	42.2	42.8	4.5	4.3	38.3	45.2	6.8	7.1	16.9	13.2	4.2	5.1
67	BPR-599-80	158.0	160.8	3.1	5.2	1.2	5.8	69.2	76.4	85.0	166.9	72.0	69.6	39.2	40.8	4.5	4.1	23.8	25.4	5.5	6.6	22.9	26.5	6.1	5.9
68	BPR-605-81	179.0	166.0	4.1	4.8	2.9	6.2	57.0	75.6	165.0	195.1	79.0	71.6	44.0	48.4	4.9	3.8	33.8	36.9	4.8	9.5	14.7	25.9	5.3	5.1
69	BPR-611-82	181.0	160.8	4.1	5.0	4.5	5.8	77.2	76.4	183.1	168.0	80.8	68.8	42.8	41.2	5.4	3.9	51.3	39.4	12.6	10.3	24.1	26.3	5.9	5.3
70	BPR-620-83	185.0	173.6	3.7	4.4	4.3	4.8	82.6	80.8	229.4	187.7	86.6	78.0	54.0	56.0	4.9	3.7	48.8	29.4	12.2	7.2	24.5	24.8	5.8	6.2
71	BPR-624-84	178.6	166.0	5.1	5.0	1.7	6.2	85.2	77.2	163.6	157.3	72.6	74.4	41.6	49.8	4.7	3.8	56.3	24.4	14.5	10.4	25.3	42.7	6.3	5.3
72	BPR-659-85	176.4	174.8	3.9	4.2	1.5	5.8	74.8	93.8	144.4	190.3	75.8	91.2	41.8	54.6	4.8	3.7	38.8	23.9	8.3	8.7	21.3	36.7	5.8	6.0
73	BPR-606-12	181.8	184.2	4.1	4.2	4.9	6.8	73.6	87.6	157.4	203.5	74.4	85.6	45.4	61.6	5.0	3.6	36.3	29.4	7.48	8.1	20.5	27.8	6.0	6.0
74	BPR-639-15	173.8	174.4	3.3	4.4	2.9	4.8	71.2	81.4	214.0	187.9	78.2	78.0	51.8	56.6	4.0	4.1	33.8	37.4	9.5	7.4	27.2	20.3	5.7	5.7
75	BPR-639-17	170.0	162.8	4.3	5.6	6.5	6.0	81.0	93.8	182.4	184.7	86.4	76.4	42.0	48.0	3.9	3.9	31.3	41.9	9.5	10.9	27.9	26.2	5.3	6.6
76	BPR-667-21	158.8	167.0	4.5	4.4	6.1	4.8	70.6	84.4	192.6	200.5	70.2	79.0	40.4	53.4	4.3	3.7	41.3	30.9	11.3	9.1	26.7	29.7	5.4	6.3
77	BPR-682-24	159.4	171.8	4.7	4.4	8.9	6.6	73.6	74.2	232.8	160.5	70.6	77.8	48.2	47.6	3.6	4.7	36.3	39.4	8.9	10.4	24.1	26.6	5.6	4.1
Check	RB 50	169.7	167.2	4.7	3.8	6.3	2.3	73.7	71.4	149.4	134.6	73.8	70.4	41.3	39.7	3.8	4.6	37.8	33.5	8.0	9.6	21.0	29.7	4.3	6.3
Check	RH 819	194.2	169.2	4.6	4.4	7.7	1.7	78.5	69.2	218.4	122.2	75.5	61.4	48.4	39.4	3.4	4.1	43.7	33.2	9.6	8.7	22.0	26.6	4.1	5.1
Check	PBR 97	181.7	162.1	5.2	3.6	7.8	2.8	78.8	72.8	186.3	111.6	73.4	73.4	41.1	42.8	3.5	3.9	31.0	29.0	6.7	7.5	21.6	25.5	4.3	5.1
	General mean	177.1	162.8	4.5	3.9	6.0	3.7	75.2	72.3	171.9	140.3	74.5	71.6	42.0	41.5	4.0	4.2	40.0	33.2	9.3	8.4	23.2	25.7	4.9	5.7
	Range	110.2-209.2	129.7-185.2	2.5-6.5	2.5-7.3	0.7-15.4	0.4-15.0	53.1-90.8	55.2-102.2	66.2-276.0	49.3-265.4	43.5-187.2	53.7-90.4	27.0-54.0	30.6-61.6	3.2-5.7	3.1-5.2	23.3-75.2	11.4-56.2	3.1-18.6	1.8-16.1	12.0-33.2	13.1-42.7	3.3-6.8	4.17.0
	CD at 5%	31.6	25.6	1.5	1.8	8.4	3.4	17.2	20.8	139.8	86.8	18.9	14.2	7.0	8.7	0.7	0.5	20.4	12.8	4.4	4.9	14.0	17.7	0.7	0.9
	SEM	12.1	9.8	0.6	0.7	3.2	1.3	6.6	8.0	53.7	33.3	7.2	5.4	2.6	3.3	0.2	0.2	7.6	4.9	1.7	1.9	5.3	6.8	0.3	0.3

IR=Irrigated, RF=Rainfed

PH = Plant height, PB= Primary branches/plant, SB=Secondary branches/plant, FZL= Fruiting zone length, S/P= Siliquae/plant, MSL= Main shoot length, S/MS= Siliquae on main shoot, SL= Siliqua length, BY= Biological yield/plant, SY= Seed yield/plant, HI=Harvest index (%), 1000 SW= 1000 seed weight.

Experimentation was done in an augmented block design (Fedrer, 1956)] under normal (E_1) and water-stressed (E_2) conditions. The material was divided into seven blocks consisting of 11 progenies and three check varieties in each block, namely, PBR 97, RB 50 and RH 819. In each block, progenies and check varieties were sown in three row plots of five meter length, spaced 30 cm apart with plant-to-plant spacing of 10 cm achieved by thinning after 15-20 days of sowing. Border effect was removed by taking observations on middle plants in a row. Recommended package of practices were followed to raise a healthy crop. Water-stressed (E_2) was grown as rainfed experiment and only pre-sowing irrigation was given, while normal (E_1) environment was irrigated twice during cropping season, one at 35 days after sowing and another at 70 days after sowing. Initial moisture content of experimental area (water-stressed E_2) at sowing time was 7.93% at 0-15 cm depth, 7.75% at 15-30 cm depth and 11.06% at 30-60 cm depth. After 50 days, moisture content was reduced up to 5.53% at 0-15 depth, 7.0% at 15-30 cm depth and 9.93% at 30-60 cm depth. However, 24.3 mm rain was received in a day in January during the cropping season. Observations were recorded on 12 morphological characters *viz.,* plant height, primary branches/plant, secondary branches/plant, fruiting zone length, siliquae/plant, main shoot length, siliqua length, seeds/siliqua, biological yield, seed yield/plant, harvest index and 1000-seed weight.

The mean data were subjected to analysis of variance (Fedrer, 1956) using SPAD (Abhishek *et al.,* 2004) software. Genetic parameters and simple correlations in all possible combinations were worked out as per standard procedure (Burton, 1952; Johnson *et al.,* 1955).

Results and Discussion

Mean of different progenies in irrigated and rainfed conditions for morphological traits are presented in Table 1. The overall mean performance of progenies was comparatively higher in irrigated environment as compared to drought condition for secondary branches/ plant, siliquae/plant, main shoot length, siliquae on main shoot, and seed yield/plant. Drought appeared to have reduced the overall mean performance of these traits by 38.51%, 18.33%, 3.94%, 1.33%, 9.21%, respectively. For siliquae length and 1000 seed weight, mean performance was slightly higher in drought environment. The reduction in mean performance of progenies under drought situations for most of the traits may be ascribed to decreased translocation of assimilates and growth substances, impairing nitrogen metabolism, loss of turgidity and consequently reduced sink size (Kumawat *et al.,* 1997). The more or less similar observations were made by Singh and Choudhary (2003) and Chauhan *et al.* (2007) in *Brassica juncea* where they reported up to 60% yield reductions under rainfed environments. Analysis of variance showed that the progenies differed significantly for secondary branches/plant, siliquae/plant, main shoot length, siliquae on main shoot, siliquae length, seed yield/ plant and 1000 seed weight under rainfed conditions while progenies showed significant differences for main shoot length, siliquae on main shoot, siliquae length, 1000 seed weight, seed yield/plant under irrigated conditions. For rest of the traits there were non-significant differences in both the conditions. This indicates that material has sufficient variability for these traits and response to selection may be expected in the breeding programme for irrigated as well as rainfed conditions.

The variances of various characters were compared on the basis of coefficient of variation. It was observed that main shoot length closely followed by seed yield/ plant in irrigated environment, and secondary branches/ plant followed by seed yield/plant in rainfed conditions exhibited comparatively higher estimates of genotypic as well as phenotypic coefficient of variation (Table 2). It indicated that simple selection for these characters might be advantageous in particular condition. The estimates of heritability in the present investigation were of higher magnitude (>50%) for main shoot length, siliquae on main shoot, siliquae length, seed yield/plant and 1000 seed weight, whereas, under rainfed conditions, secondary branches/plant, siliquae on main shoot, siliquae length and 1000 seed weight recorded higher estimates of heritability. For other characters (siliquae/plant, main shoot length and seed yield/plant) moderate estimates of heritability were observed. Similar reports were made by Meena *et al.* (2008) and Singh *et al.* (2009).

The genetic advance was highest for main shoot length followed by seed yield/plant and 1000 seed weight under irrigated conditions, whereas, secondary branches/plant followed by seed yield/ plant and siliquae/ plant showed higher estimates of genetic advance under rainfed conditions (Table 2). These findings indicate that there is good scope for development of genotypes having more main shoot length and increased seed weight which would perform better under favorable conditions.

Table 2. Mean, range, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance in advanced progenies of Indian mustard

Genotype	Mean		Range		GCV		PCV		h2		GA	
	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF	IR	RF
Secondary branches/ plant	6.05	3.72	0.70-15.4	0.43-15.03	*	49.19	*	60.48	*	66.14	*	82.31
Siliquae/plant	171.90	140.39	66.2-276.0	49.38-265.4	*	14.77	*	27.96	*	27.89	*	16.07
Main shoot length (cm)	74.55	71.61	43.55-187.22	53.79-91.26	19.92	5.12	22.18	9.20	80.67	30.97	36.86	5.88
Siliquae on main shoot	42.09	41.53	27.09-54.09	30.48-61.61	9.53	9.51	11.45	12.47	68.90	58.11	16.26	14.92
Siliquae length (cm)	4.07	4.26	3.28-5.70	3.14-5.22	8.11	7.04	10.81	8.68	57.89	64.29	12.77	11.63
Seed yield/plant (g)	9.34	8.48	3.19-18.65	1.85-16.18	19.16	17.80	26.66	28.76	52.10	38.65	28.57	22.50
1000 seed weight (g)	4.93	5.73	3.31-6.8	4.11-7.06	11.16	8.02	12.58	10.12	76.92	61.76	20.07	12.95

*Mean sum of squares were non – significant,
IR=Irrigated, RF=Rainfed, GCV=Genotypic coefficient of variation, PCV=Phenotypic coefficient of variation, h2=Heritability, GA=Genetic advance expressed as % of mean

Similarly, under rainfed conditions there is enough scope for development of promising genotypes having more number of siliquae/plant. High heritability values accompanied with high genetic advance were observed for main shoot length followed by seed yield/plant under irrigated conditions. Similar reports of high heritability with high genetic advance for these characters were made by Patel *et al.* (2006). This indicates that selection will be more effective for these characters in comparison to other.

Simple correlations were estimated between seed yield and component traits in irrigated as well as rainfed conditions (Table 3). Under irrigated conditions, seed yield/plant was positively and significantly correlated with plant height (0.241), primary branches/plant (0.381), secondary branches/plant (0.493), fruiting zone length (0.295), siliquae/plant (0.562), biological yield (0.852) and harvest index (0.613), while, under rainfed conditions, seed yield/plant was significantly and positively correlated with plant height (0.445), primary branches/plant (0.443), secondary branches/ plant (0.611), fruiting zone length (0.505), siliquae/plant (0.729), main shoot length (0.410), seeds/siliqua (0.283), biological yield (0.774) and harvest index (0.482). These results were in agreement with the earlier reports of Kardam and Singh (2005), Meena *et al.* (2008) and Singh *et al.* (2011). Among other important positive and significant associations noted, the association of plant height with primary branches/plant, secondary branches/plant, fruiting zone length and biological yield/ plant was observed under both the conditions which is in accordance with the report of Meena *et al.* (2008) and Singh *et al.* (2011). Significant positive association of primary branches/plant with secondary branches (rainfed and irrigated), fruiting zone length (only rainfed), siliquae/plant (rainfed and irrigated) and biological yield/plant (rainfed and irrigated) was observed. This result of present investigation is in accordance with the report of Kardam and Singh (2005). Significant positive association of secondary branches/plant with fruiting zone length, siliquae/plant, main shoot length and biological yield/plant was observed under both the conditions. Association of fruiting zone length with siliquae/plant, main shoot length, and biological yield/ plant was found significant and positive under both the conditions. Singh *et al.* (2010) also made similar observations. Association of siliquae/plant with main shoot length (only rainfed), seeds/siliquae (only rainfed) and biological yield was observed to be positive and significant (Kardam and Singh, 2005 and Singh *et al*., 2010). Seeds/siliquae and 1000 seed weight were found to be positivity and significantly associated with siliquae/ length under both the conditions (Singh *et al.,* 2011)

On the basis of this study it can be concluded that plant height, primary and secondary branches/plant, fruiting zone length, siliquae/plant and biological yield/ plant are important traits for constructing selection index under both irrigated and rainfed situations which should be considered in selection programme.

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Table 3. Correlation coefficients between different characters in advanced progenies of Indian mustard under irrigated and rainfed conditions

Characters	Situation	PH	PB	SB	FZL	SLP	MSL	SMS	SL	SS	BY	SY	HI	1000 SW
PH	I	1												
	RF	1												
PB	I	0.156	1											
	RF	0.375	1											
SB	I	0.218*	0.527**	1										
	RF	0.292**	0.484**	1										
FZL	I	0.415**	0.138	0.328**	1									
	RF	0.624**	0.469**	0.518**	1									
SLP	I	0.362**	0.496**	0.634**	0.415**	1								
	RF	0.476**	0.563	0.764**	0.673**	1								
MSL	I	0.144	-0.038	0.438**	0.368**	0.196	1							
	RF	0.485**	0.183	0.450**	0.774**	0.556**	1							
SMS	I	0.334**	0.083	0.188	0.394**	0.459**	0.35**	1						
	RF	0.548**	0.353**	0.554**	0.675**	0.681**	0.63**	1						
SL	I	-0.233	-0.221	-0.288**	-0.078	-0.201	0.066	-0.166	1					
	RF	-0.062	-0.115	-0.165	-0.114	-0.211	-0.031	-0.176	1					
SS	I	-0.018	-0.158	0.0125	0.087	0.091	0.113	0.526**	0.525**	1				
	RF	0.052	0.161	0.33	0.031	0.291**	0.078	0.202	0.253*	1				
BY	I	0.318**	0.370**	0.531**	0.342**	0.502**	0.118	0.155	0.097	0.233*	1			
	RF	0.415**	0.433**	0.609**	0.598**	0.732**	0.519**	0.454**	-0.096	0.191	1			
SY	I	0.214	0.381**	0.493**	0.295**	0.562**	0.128	0.132	0.105	0.175	0.851**	1		
	RF	0.445**	0.443**	0.611**	0.505**	0.729**	0.410**	0.499**	-0.202	0.283**	0.774**	1		
HI	I	0.004	0.156	0.182	0.097	0.352**	0.086	0.049	0.060	0.006	0.121	0.613**	1	
	RF	0.134	0.085	0.112	-0.005	0.137	-0.039	0.154	-0.195	0.132	-0.145	0.482**	1	
1000SW	I	-0.112	-0.131	-0.376	-0.159	-0.174	0.021	-0.152	0.338**	-0.077	-0.106	0.037	0.189	1
	RF	-0.169	-0.202	-0.159	-0.053	-0.203	0.019	-0.280	0.295**	-0.127	-0.163	-0.150	-0.002	1

I=Irrigated, RF=Rainfed, PH= Plant height, PB = Primary branches/plant, SB= Secondary branches/plant, FZL=Fruiting zone length, SLP=Siliquae/plant, MSL=Main shoot length, SMS=Siliquae on main shoot, SL= Siliquae length, SS=Seeds/siliqua, BY=Biological yield, SY = Seed yield/plant, HI=Harvest index, SW=1000 seed weight

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Rice Diversity – The Genetic Resource Grid of North-East India

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Rice is the staple crop for the indigenous people of northeast India. Given the bioresource richness, being in the eastern Himalayan region, which is one of the mega-biodiversity hotspots globally; this part of India is acclaimed for rich agro-biodiversity. About 10000 indigenous rice cultivars are available in this region. These genotypes apart from their high adaptability to typical agro-climatic conditions of this region also possess important traits having premium values like medicinal properties, good cooking and nutritional qualities with pleasant aroma and resistance to different biotic and abiotic stresses. These landraces and native varieties specific to sites are the potential source for valuable molecular exploitation in rice breeding programmes. This paper addresses the utilization potential of genetic resources of rice in the North-east India.

Key Words: Genetic diversity, North-east India, Rice

Conservation and planned utilization of plant genetic resources (PGR) is essential for the survival of human beings and other living organisms *vis-à-vis* environmental sustainability (Singh, 1996). The traditional landraces and wild relatives of crop plants constituting the gene pool or genetic diversity have formed the basis of agriculture for more than 10,000 years. It continues to produce base for developing high yielding and location-specific varieties to meet the food requirement of burgeoning global population.

In the Indian sub-continent, North-eastern region (NER) has been identified as one of the 18 mega-biodiversity global hotspots areas. It comprises eight states *viz*., Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram, Nagaland, Tripura and Sikkim (21º57' to 29º28' N latitude; 89º40" to 97º25' E longitude), covering an area of 2.55×10^5 km^2 and is inhabited by 67 major ethnic groups of people (Hore and Sharma, 1995). The NER is known for its forests, water and mineral resources and agrobiodiversity. The richness of agrobiodiversity in the region is reported to be 9650 cultivars in rice, 15 races and 3 sub races in maize, 300 in taros, 230 in yams, 17 species and 52 cultivars in citrus, 16 taxa in banana, 700 taxa in orchids and 19 taxa in sugarcane (Satpathy and Sarma, 2001).

Rice is the principal food grain crop of north eastern hilly ecosystem occupying 3.51 million ha which accounts for more than 80% of the cultivated area of the region and 7.8% of the total rice area in India while its share in national rice production is only 5.9% (Ngachan *et al.*, 2014). The socio-cultural activities of the people have been dependent on the seasonality of rice cropping in the region. This paper analyses the reason for richness of rice genetic diversity in the northeast India and has collated information on the utilization pattern of rice genetic resources *per se* for possible food and environmental securities.

Reasons for Rich Genetic Diversity

NER being a secondary centre of origin of rice is endowed with rich source of indigenous cultivars. About 50% of the rice genotypes grown in a small scale by the marginal farmers are local landraces and remaining 50.42% area is occupied by the high yielding varieties released by respective state variety release committees and central variety release committee (Durai *et al.*, 2007). Being the principal food crop of the region, rice is grown in three major ecosystems *viz*., upland including *jhum* lands (shifting cultivation plots), lowlands and deep water conditions.

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The distribution of varieties depends to great extent on their specialty uses and adaptability to varied growing conditions. It has also been found that yield was not the only criterion for farmers selecting a particular variety for cultivation but also grain size, shape and aroma. Special uses and ability to grow under specific rice growing situations were also important. The genotypes having fulfilled such stringent criteria are selected by the farmers for growing in the adverse conditions of rice cultivation where no other genotype can be successfully grown.

Trait expression in these native germplasm is highly dependent upon local environment and has evolved over a long time through traditional and cultural practices. Some of the genotypes are adapted to specific rice growing situations. For instance water submergence and floods are common in places situated on the banks of river Brahmaputra during July-August causing considerable damage at the vegetative phase of the crop. Sometimes this problem is so severe that the farmers are forced to take up transplanting two or three times. Therefore, the genotypes grown in such areas should have desirable features like rapid elongation of internodes to keep the leaf canopy above the water level, elasticity to withstand the kinetic force of currents and capacity to recover rapidly after the recession of floods to perform under such situation.

These combined forces of natural and human selection, diverse climates, seasons and soil and varied cultural practices led to the tremendous diversity. Local varieties have many desirable characters like pest and disease resistance/tolerance, tolerant to low temperature, water scarcity, water inundation and adaptability to local environmental conditions such as low light intensity, various soil problems such as acidity, iron toxicity, aluminium toxicity, soils low in P, K, Zn, B and Mo. Introduction of high yielding varieties, natural calamities such as landslides, earth quake, floods and deforestation which are regular phenomenon in this part of India led to genetic erosion. With the introduction of high yielding varieties, large numbers among the genotypes are at the verge of extinction including high valued aromatic rice cultivars (Singh and Devi, 2004). However, for sustainable management of biodiversity, it is important to understand the distribution, variability for different morphological and grain characteristics, adaptability to harsh environment and specialty uses of native germplasm.

Rice Genetic Diversity

Arunachal Pradesh

Local cultivars suitable for high altitude (>1500 m asl) are predominantly grown in Tawang and West Kameng districts and some parts in West Siang and East Siang districts. Cultivars grown in East Kameng, Lohit, Tirap, east and west Siang districts are suitable for low altitude condition (<450 m asl). These *kampti* rice cultivars are soft, glutinous with typical aroma. The rice germplasm collection from the Lower Subansiri, Upper Subansiri, West Siang, East Siang and Dibang region represent mid altitude conditions (450-1500 m asl). The germplasm grown in high altitude *apatani* plateau represent wetland paddy. They are late maturing and intermediate between and *indica* and *japonica* types which have high adaptability to fluctuating local environmental conditions. *Mipya* cultivars grown in this plateau are early maturing while *pyapin* types are medium maturing and *emo* types are late maturing (Sharma, 2002). In Tawang area (~3000 m asl), rice plants exhibit *japonica* characters of globose grain, narrow and dark green leaves, drooping flag leaves, thin culm and thermo sensitivity. However, these characters become less prominent while moving towards eastern direction. This is due to fact that *japonica* cultivars are not suitable for growing in the high altitude areas of tropics (Shahi and Khush, 1986). The pubescent husk types occur in western part of the state whereas eastern parts contain many glabrous types. *Bali* is a common indigenous cultivar.

Assam

Geographically the state of Assam is classified as lower Assam and upper Assam with 23 districts. The hilly areas in upper Assam are tribal dominated and the people practice *Jhum* cultivation while in lower Assam farmers practice low-land rice cultivation. In Brahmaputra adjoining areas, deep water rice is grown. Aromatic rice varieties of Assam are known as Joha. Different variants in Joha *viz.*, *kala joha* and *amru joha* are available. Majuli island with an average area of 1245 km^2 is the largest river island in the world wherein at least 100 indigenous types of rice are grown. Important indigenous varieties of Assam are *Malshira, Manohar, Kartiksali, Bornidhan, Paroma, Bhola, Nepali Bhog, Tulsi Baon, Bogibaon, Kenkrabaon* and others. Studies on rice collected from this state have been reported extensively (Shastry *et al.*, 1971; Sharma *et al.*, 1971; Vairavan *et al.*, 1973; Rao and Srinivasan, 1978; Sharma *et al.,* 1993)

Manipur

In Manipur 91% of geographical area is in hilly tract and 9% in valley. However 90% of the population is surviving in the valley land and remaining 10% are in hilly areas (Anonymous 2000). Rice cultivated both in valley and in hill districts. The state is rich in variability of rice germplasm with distinguished qualities such as aroma, glutinous *etc*. The cultivars including *Chahou amubi, Chahou angouba, Chahou poireton, Chahou angangbi* are example of such kind. These cultivars are used for medicinal purpose and rituals in Manipur. *Chahou poireton* is usually given to expecting mothers at the last stage of their pregnancy. Lactating mothers used to take C*hahou amubi* to increase the lactation (Devi *et al*., 2008). Important rice genotypes of medicinal important grown in low lands of Manipur are *KD anganba*, *phouoibi,* C*hina tiyanbi*, *Sanaphou*, *KD amuba*, *Daramphou* and *Chinachang*. *Savanthiei*, *Changsanal*, *Chariow* and *Meriunap* are in uplands and *Moirangphou angangbi* is grown in both uplands and low lands. All these genotypes are used for preparing herbal shampoo. *Moirangphou angangbi*, *Sanaphou*, *KD amuba, KD angangba* and *Phouoibi* are used for treating muscular sprains and dog bite by local people (Devi *et al.*, 2011). *Taothabi*, a versatile deep water rice of this region is mainly grown in Loktak lake, the largest fresh water lake in Asia. These genotypes are pride of Manipuri people because of their taste, aroma and desired waxiness. Because of the progressive farmers and adoption of high yielding varieties, rice productivity in this state is higher than most of the other states in NER.

Mizoram

Mizoram have eight major districts with geographical area of 21081 km2 with 824 villages with total population of 10,97,206 (2011 Census). The people mostly practice *jhum* cultivation with long duration cultivars in hilly areas while wetland cultivation is followed in valleys and flat lands with early maturing cultivars. The early maturing and aromatic cultivar *tai* is popular among wetland farmers. Other important local rice cultivars grown are *Bibaal, Bumui, Trishaghar, Trai, Konglong, Kawlisahchuam, Vui buk bohhmui, Idaw, Rengkawi, Horpie, Panthual, Norpi, Fangthum, Rumkai, Buhban, Rizu, Rumkai, Buhban etc.*

Meghalaya

This state comprises of three groups of hills *viz*., Khasi, Garo and Jaintia with seven political districts where the topography forms with hills and plateau. In the low lying areas of hill crevices and plateaus, wet rice cultivation is practiced and *jhum* cultivation is common in hills. Local Manipuri and *Ngoba* are cultivated abundantly in wet conditions. Special rice cultivars used in preparation of ceremonial sweets like *buchar, buchath, busyaouab etc.* are *banaka bhara, lwai, lwaisaw, aghoni bora, kba pynthor, local misawar, banaprobha etc*. Predominant local varieties grown in different hills of Meghalaya are given in Table 1.

Nagaland

Rice is cultivated in plains, *Jhum* lands, hill terraces and river beds. Wide range of cultivars and landraces showing variability in grain size, shape, awn characters, glume and kernel colour are available. A tall genotype (8.5 feet) with semi woody texture, 175 tillers and 510 grains/panicle grown by Pasteur Mr. Melhite Kenye (Anonymous, 2001) was considered as wonder rice. The important varieties grown in Nagaland are *Wochetsok, Laruno, azukumnupu, Neikuotiekie, Mekrulha, Khulaghi, Thumpaktssok, kurtsumong, Chithomasu, Dzuluolha,Miakrulhakechau* and *Nyadi.* Most of these indigenous rice landraces are medium to longer in duration (130-170 days).

Sikkim

It is a hilly state within the contiguous stretch of Himalayas and covers an area of 7096 km^2 in North-east India. J.D. Hooker made the first study of the flora of the Sikkim Himalayas (Biswas, 1956). The state is a biological hot spot containing about 5000 species of flowering plants (Hajra and Verma, 1996). Agriculture is practiced only

Table 1. Local cultivars grown in different hills of Meghalaya

Hill	Cultivars
Khasi hills	*Local Manipuri, local white, Moinahai, kalajira, maloti, biruin, srigum, thangma, swait, kba dharsaw, Rynkang, local kba pnah, kba khapmaw, local bangla, kba saw, Thangmawsaw, kba lyngkot, malonti*
Garo hills	*Meni, Gurum, Nizokmil, mikudep, mirimit, sarong, Midoru, sarengma, minil doka sawar, Mitong Gjing, mima gitchak, mireti, mikotchu wakdu, mirap, misarengma*
Jaintia hills	*Manipuri, longsong, Laispati, shroi, lei khyriam, sohem tharoh, leiukho, lespan, lei hpasyieh, kopapnah, nongjugu*

in 11.7% of the total area. In that rice is cultivated only in 20,000 ha. During winter, the temperature goes down to 0°C and hence most of local rice landraces are cold tolerant. Arora (1982) classified local rice cultivars of Sikkim into direct sown and transplanted. The cultivars grown in direct sown conditions are *Buidhan, Lama, Thapachini et*c. while that grown in transplanted conditions are *Attey, Mansara, Jhapaka, Dutkalami*, local aromatic rice, *Krishna Bhog, Talasi, Poudyal* and *Brimphul*.

Tripura

Tripura is located in the southwest extreme corner of NER of India. It has a geographical area of about 10,492 km^2. Nearly 2/3 of the state is occupied by hilly topography leaving very little of the land for cultivation. At least 65 cultivars of wetland, 32 of *Jhum* types and five each of deep water and aromatic rice have been recorded from this state (Sharma and Hore, 1990). The indigenous rice cultivars having higher crude protein content *viz*., jhum binni black, *makum my mukul* and *biswa gora* could be recommended for consumption and quality enhancement. Similarly the cultivars, *Aduma, Biswas gora, Garumalathi, Katak tara*, NDR 97 and *rasi* having more than 10ppm of Iron can be used for rice improvement aiming at alleviating Fe malnutrition (Devi *et al*., 2012). The rice productivity in Tripura is the highest among the states in NER.

Wild Relatives

In addition to the commonly cultivated *O. sativa*, five wild species along with their different forms occur in NER. It is reported that *O. nivara* a closely related wild form of *O. sativa* is found in the region. *O. sativa* f. *spontanea* is another wild relative of *O. sativa* and is morphologically similar to *O. nivara*. Other species of *Oryza* found here are *O. officinalis, O. granulata, O. rufipogon* and *O. meyeriana* (Hore, 2005). These primitive wild forms are characterized by several morpho-physiological traits which gradually changed during evolution of cultivated species probably due to semi-natural selection imposed by cultural practices, diverse climate, soil and seasons (Chang, 1976). Apart from the aforesaid species of rice, four closely related taxa of *Oryza viz*., *Hygrorhiza aristata, Leersia hexandra, Porteresia coarctata* and *Zizania latifolia* are present in this region. Intermediate forms like *Tulsibaon, bogibaon* and *Kenkubaon* were also found in deep water and water logged conditions in this region (Hore, 2005).

Utilizable Rice Genetic Diversity

A detailed study of collection for Assam state showed that many of the genotypes possess desirable characters *viz*., dwarfness, tolerance to lodging, low temperature, iron toxicity, low phosphorus, and resistance to various insect pests like gall midge, stem-borer, green leaf hopper, bacterial leaf blight, tungro virus, and bacterial leaf streak. Apart from this, some of the entries showed high protein content in some *japonica* types and semi-dwarf types of *indica* rice. (Srivastava and Nanda, 1979). Seshu *et al.* (1974) evaluated short stature Assam rice collections (ARC) for yield and other attributes in order to identify alternate source of dwarfism. Among 14 dwarfs tested, ARC 5929 (mid duration), ARC 5981A (early) and ARC 12805 (mid early) were found promising for yield. Apart from yield, ARC 5929 and ARC 5981 also possess good grain type as well as resistance to major disease (bacterial leaf blight) and pests (stem borer, gall midge, green leaf hopper). *Ngoba* a collection from NER has been found to be alternate source of dwarfing gene. The genotypes P 522 and P 523 were just 60-70 cm in height (Sharma and Hore, 1989).

The local varieties of Meghalaya showed a wide variation for most of the characters. Variation in flowering duration, plant height, ear bearing tillers and 1000 grain weight were found important. *Ryllo red, rylllo red 10, kuki, mynri*, and *ryllo 9* were early maturing within 100 days. A germplasm collected from Jowai area (*Jowai early*) was found to mature in 60 days without any photoperiod sensitivity (Sarma *et al.*, 2002). Plant height is the character directly related to harvest index, growth duration, nitrogen response and lodging resistance (Chang and Lu 1980). Main stem plays an important role in the lodging resistance and may offer scope for improving taller genotypes. *Ryllo red* and *dullo 10* had stiff straw, short stature and non-lodging. *Ryllo red* 3 and *tanger* had very bold grains and had high 1000 grain weight of 32.99 and 33.63 g, respectively. Some rice cultivars including *mirikrik* had long panicles and 300-400 grains/ panicle. Significant differences were observed for plant height, leaf length, leaf width, flowering duration, ear panicle bearing tillers and 1000 grain weight (Ghosh *et al*., 1981).

The tiller number offers the advantage of buffering the plant yield when there is any damage to the plant c 1536 was an accession that had an average 11 panicles/plant (Hore, 2005). Number of effective tillers and panicle length are the useful guide in selection for higher yield.

Cultivars BD 124 and NKG 1190 recorded more than 30 cm panicle length. Test grain weight is also closely related with grain yield. The genotypes P 476, NKG 1122, NKG 1187, P522 and P523 collected from NER were identified as superior for the above economically important traits (Sharma and Hore, 1989).

Field screening of 21 traditional rice varieties for three consecutive years in Manipur showed that two local varieties *Phouren* and *Moirangphou khokngangbi* to be resistant to gall midge with no damage consistently. Six other cultivars *viz*., A*khanphou, Taotahabi, Chanphai, Kohimaphou, Kakchenphou,* and C*hakhao amubi* were almost free from gall midge attack with less than 5% silver shoots incidence (Singh 1992). Local cultivars of Mizoram *viz*., R*angtei, Kawnglawng, Bhutawi, Chhirlukpui, Mautai, Mairasa* and B*uhsete* showed differential response to *Fusarium* spp., *Alternaria tenuis* and *Cladosporium herbarum*. Seeds of the cultivars Ma*utai, Mairasa* and C*hhirlukpui* with higher germination percentage indicated the presence of potential genes for resistance against those pathogens (Vyaas, 1994). *Bali* and its derivatives like *Lite, Lipu, Gapu, Popy* etc., are important landraces of Siang districts. They serve as a typical example of adaptation through phenotypic plasticity and endurance to multiple disease and pests. These resistant cultivars may be used advantageously in breeding programmes. Other genotypes possessing many desirable yield contributing characters and tolerance to different biotic and abiotic stress prevailing different agro-ecosystems of rice cultivation are given in Table 2.

On the basis of evaluation for economically important traits local entries like *mirikrak, Khnorullo, Thimpu etc.* were involved in hybridization for evolving suitable

Table 2. Superior cultivar/landraces identified with economically important traits

Trait	Cultivars	References
Short duration (<110 days)	*Jowai, Megilai,* BDJ 2327, BDJ 2000, N 861, *Rangugallang, Charimpok*, LT 4, *Sahoksan, Pangra*	Durai *et al*. (2009)
Longer duration (> 160 days)	*Iitsuba, panthual*	Durai *et al*. (2009)
Dwarf plant stature (< 60cm)	*Panthual, Takgei, Doulimeu, Mangdhan, Chanmouri, Chinairi, Kangpui, Ngoba*	Durai *et al*. (2009)
Taller plant stature (> 160cm)	*Epyo, Chungliepyo, Dethwulu, Lal-khra, Rangugallang, Charimpok*	Durai *et al*. (2009)
Lengthy panicles (> 60cm)	*Eepyo, Mapokpasuk, Matpok,bBisbial, Chingmoirangbhai*	Durai *et al*. (2009)
Higher leaf area (150cm^2)	*Malen, Mapok, Bisbial, Meserong, Hepe, Hepenie, Kemenui*	Durai *et al*. (2009)
Higher grain weight (4g /100seeds)	*Motso, Epyo, Tsolenysk, Vikesa Ru, Ketasaru, Hepe, Kemenya Kemenui, Chinagum, Ajiu, Ajoghi, Sungmangtsuk, Trai*	Durai *et al*. (2009)
Higher number of effective tillers (>6)	*Botadhan, Sandhan, Pedhanilo, Pithidhan, Panthual*	Durai *et al*. (2009)
Higher yield (20g/plant)	*BDJ 2095, Khonorullo, Ngoba, Motso Epyo*	Durai *et al*. (2009)
Drought tolerance	*Amiong, Addy, Changpalman, Hmawrhang, Pyare*	Prasad *et al*. (1993)
Tolerance to lodging	*Manpa, Moping, Imoenkhe, Rnagagellang, Bethi*	Prasad *et al*. (1993)
Cultivars suitable for deep water condition	*Maguri, Panikekua, Herepi Bao, Ruphai, kakua, Dholabadal, Taotobi, Nagrobao, Najirsali, Pijum, Jalaj, Jalaplavan, Jaladhi.*	Prasad *et al*. (1993)
Blast resistance	*Zutsak, Ketsaru, Rukhatung, kerpu, Poppy, IC 25705, Chojul*	Prasad *et al*. (1993)
Sheath rot resistance	*Tangale, Namyi, Thebek, Lyngsi, Ryllo red*	Prasad *et al*. (1993
Cold tolerance at reproductive stage	*Khonorullo, Ryllo red 6, Nyami, abor B, Meghalaya 1, Nonglwai, ryll Red 4, Kbathangmaw, Namyi, Buhtawi, Kabasa, Thebere*	Prasad *et al*. (1993)
Cold tolerance at vegetative stage	*Khonorullo, Ryllo red -6, Nyami, Abor b, Thebere, Meghalaya 1, Nonglwai, Ryll red 4, Kbathangmaw, Lynsi, Tangla Jungarh, Ngoba, Zenith, Namyi*	Prasad *et al.* (1993)
P deficiency tolerance	*Pawnbuh, Khawji, Mirikrik, Knawnowjoma, Imoenkhe Manoharsali*	Prasad *et al.* (1993)
Iron toxicity tolerance	*Mirikarak, Pawnbuh, Kbathangmaw, BG 34-8, Nemo, Amo, Leiletbunbam, Panghkla*	Prasad *et al.* (1993)
Aroma	*Sars 7, Epyo, Tsa lha, Tonulighe, Hepe, Kemneii, Nkiapeu, Maibasa, Konpui, rankoi, kopowguni, ramarchhang, kawnlong, Changmau, sanadadhan, jhabuka rice, setijhabka, N 908, madan mowkhar and buhtial, chingphou, chakhou huikap, chambrophou, chakhao amubi,*	Durai *et al.* (2009)
Glutinous	*Nemo, IC 25682, Cekiannie, Nakvhou, Ruluonya, Nyakra, Vam, Kanenya, Kenjushye, Thevuru, Nyaranuo, Lophugu Kephunyushe*	Devi *et al.* (2008)

Table 3. Varieties released for north-eastern hill region of India utilizing the local cultivars

S. No.	Variety	Parentage	Special attributes
1	NEH *Megha* rice 1	*Khonorullo*/Pusa 33	Recommended for rainfed low land ecosystem of high altitudes (Above 1500 m asl) of Meghalaya, Mizoram and Nagaland; possess tolerance to stem borer, blast, low temperature at reproductive phase and low solar radiation
2	NEH *Megha* rice 2	*Khonorullo*/Pusa 33	Recommended for rain fed low-land ecosystem of high altitudes (Above 1500 m asl) of Meghalaya, Mizoram and Nagaland; possess tolerance to stem borer, blast, low temperature at reproductive phase and low solar radiation
3	RC Maniphou 4	*Kalinga*/palman	Recommended for early *kharif* and main *kharif* season in mid altitude lowlands of Manipur; shows moderate resistance to gall midge stem borer and blast
4	RC Maniphou 5	*Kalinga*/palman	Recommended fir early *kharif* and main *kharif* for mid altitude lowlands of Manipur; shows moderate resistance to gall midge stem borer and blast
5	Lampnah	IR 29/*Ngoba*	Recommended for mid altitude lowlands for main *kharif* season; tolerant to temporary flooding and mild iron toxicity
6	Shahsarang	*Mirikrak*/Rasi	Recommended for mid altitude lowlands for main *kharif* season; moderately resistant to stem borer, gall midge leaf and neck blast and temporary flooding and high iron toxicity
7	TRC –*Bordhan*	*Thimpu*/IR 9129-102-1/ KN 10-361-1-1-8-6-8	Recommended for cultivation in Assam and Tripura as boro rice; photo-insensitive with moderately resistance to stem borer, gall midge and blast
8	Khonorullo	A tall Local cultivar of Meghalaya	Identified for cultivation in rain fed lowland ecosystem of rice cultivation in higher altitudes (> 1500 m msl) of Meghalaya and Nagaland; long duration genotypes and matures in 170-180 days; tolerant to stem borer, blast, sheath rot, low temperature at reproductive stage and low solar radiation
9	Ngoba	Local cultivar	Identified for cultivation in rain fed shallow land areas of Meghalaya; long duration genotype and takes 150-160 days to mature; moderately resistance to stem borer and blast. It is also known for its tolerance to iron toxicity
10	Lungnilaphou	Local cultivar	Recommended for cultivation in Manipur, non-lodging and moderately resistant to gall midge, stem borer, blast and BLB, tolerant to cold at reproductive phase and shadow
11	RCPL 1-10C	*Megha* rice	Recommended for cultivation in Meghalaya, non-lodging, tolerant to acid soil, cold at both vegetative and reproductive phase, possesses high shadow tolerance
12	RC Maniphou 6	CG 988 × IR 24	Recommended for cultivation in Manipur, non-lodging and moderately resistant to gall midge, stem borer, blast and BLB, and tolerant to cold at vegetative phase
13	RC Maniphou 7	Mutant culture from *Punshi*	Recommended for cultivation in Manipur, non-lodging, slightly photo insensitive and moderately resistant to gall midge, stem borer, blast and BLB and tolerant to cold at reproductive phase.

varieties for different rice growing ecosystem. The different rice varieties developed using these local germplasm were released for cultivation in various hill state of this region (Table 3). Presently for the improvement of yield and quality local cultivars like *Ngoba, Manipuri, Chakhou, Jowai, Mantri, Naga* special were crossed with elite varieties like DR 92, IR 61919-138-1-3-2, TOX 3055-10-1-1-1-2, CT 9846-1-7-1-1-2PM and ITA 222. From these crosses RCPL 1-71 was identified as promising culture for mid-altitude conditions

Collection of germplasm of wild species of crop relatives helps to study their taxonomic and genetic relationships. Moreover, these isolated populations found in the marginal and unusual areas may have distinct traits. When the existing crop germplasm collections do not have the material with desired trait, the plant breeders can use wild material as source to develop varieties resistant to biotic and abiotic stresses. Utilization of genes from wild species for higher biomass and tolerance to various stresses can overcome the yield plateau in rice. The different wild species of rice available in North-east India and their utility is given Table 4.

Conclusions

The landraces and native varieties specific to sites are the potential source of valuable genes. Hence, there is a need to undertake systematic collection of the germplasm and they have to be evaluated both at morphological and molecular levels. The nutritional and biochemical composition in the genetic resource of special use are to be quantified. The chemical basis of specialty uses of these genetic resources needs systematic assessment and documentation. For instance, DNA fingerprinting of native germplasm shall establish their identity, which is very much essential under globalization scenario. While exploiting the PGR, the intellectual contribution of the farmers-conservers in maintaining the agrobiodiversity should be given due recognition by protecting their rights, so that their role in conserving the PGR continues.

Table 4. Wild relatives found in NER and their utilization

Species	Chromosome number (2n)	Genome type	Occurrence	Utility	References
Oryza officinalis	24	CC	Assam, Khasi Hills, Sikkim Tarai	Resistance to thrips, brown plant hopper (BPH), green leaf hopper (GLH) and white backed plant hopper (WBPH) and tolerant to acid sulphate soil	Heinrich *et al.* (1985)
O. granulata	24	GG	Khasi Hills, Sikkim	Shade tolerance and adaptable to aerobic soil	Hore and Sharma, (1993)
O. rufipogon	24	AA	Assam and Manipur	Source of cytoplasmic male sterility (CMS). Tolerant to stagnant flooding and acid sulphate soil and it can be propagated through both of sexual and asexual means. This species is resistant to bacterial leaf blight disease.	Vaughan and Stich, (1991); Chang *et al*. (1982)
O. nivara	24	AA	Assam	It is resistance to grassy stunt virus, blast resistance and drought tolerant	Hore and Sharma, (1993)
O. meyeriana	24	GG	Assam Lumding	Shade tolerance and adaptable to aerobic soil, photo- insensitive and aromatic	Hore and Sharma, (1993)
Hygrorhiza aristata	24	–	Assam, Bengal, Meghalaya and Tripura	This species is found to yield good fodder and may be utilized in breeding programme aiming at increasing bio-mass	Hore and Sharma, (1993)
Leersia hexandra	48, 60 and 90	–	Manipur, Assam and Tripura	Thrive well in varied ecological conditions from 1-2100 m MSL this may utilized for developing cold tolerant varieties for higher altitudes	Hore and Sharma, (1993)
Porteresia coarctata	48	–	–	Saline tolerant	Hore and Sharma, (1993)
Zizania latifolia	30 and 34		Manipur	It can offer unique opportunity to develop female and male flowers which can utilized in hybrid	Hore and Sharma, (1993)

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Genetic Variability and Diversity of *Sorghum* Landraces Collected from Uttar Pradesh, India

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Ninety-nine sorghum landraces collected from Uttar Pradesh were evaluated during *kharif* 2008 and 2009 for 22 agro-morphological traits using minimal descriptors developed by NBPGR. Analysis of variance showed significant differences among genotypes for 22 traits. Large variation among genotypes was found for the traits *viz.,* days to 50% flowering (66-87 days), leaf length (62.1-101.5 cm), leaf width (5.0-9.0 cm), number of leaves/ plant (9-16), plant height (215.1-383.0 cm), ear head length (10.1-34.3 cm), ear head width (3.7-9.5 cm), 100-seed weight (1.7-3.5 g), days to maturity (103-126 days), stem fresh weight/5plants (1063-3200 g) and stem dry weight/5plants (569-2038 g). Selections can be made for traits *viz*., days to flowering, leaf length, leaf orientation, days to maturity, plant height and grain luster governed by additive gene action.

Key Words: Diversity, Genetic variability, Landraces, Sorghum, Uttar Pradesh

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is a non-native species for which India is a secondary centre of diversity (Singh, 2002). The Indian Council of Agricultural Research (ICAR) promoted programmers/projects independently or in collaboration with USIAD, on germplasm collection, evaluation and utilization of sorghum during 1963-1964. The first major effort on the collection of sorghum genetic diversity was made under the auspices of Rockefeller Foundation and ICAR, and a total of 16,138 collections were assembled during 1970 (Rockefeller Foundation, 1970). Sorghum is grown during rainy and post-rainy seasons in semi-arid regions of the country on the marginal lands. Crop is well adapted to drought-prone regions with poor soil as compared to other cereal crops. In India, sorghum is mainly grown in Maharashtra, Karnataka and Andhra Pradesh during rabi (post-rainy) and in Madhya Pradesh, Rajasthan, Uttar Pradesh, Uttarakhand, Gujarat and Tamil Nadu during kharif (rainy) seasons. Sorghum is classified into five basic races *viz., bicolor*, *guinea*, *caudatum*, *kafir* and *durra*, which are further classified into ten intermediate races namely *durra-caudatum, durra-guinea, durra-kafir, durra-bicolor, caudatum- guinea, caudatum-kafir, caudatum-bicolor, guinea-kafir, guinea-bicolor,* and *kafir-bicolor* (Harlan and de Wet, 1972).

Uttar Pradesh is the home of traditional crops as well as large number of traditional/local sorghum varieties. The collection of cultivated types includes landraces from various environments where they are adapted and grown. These are all annual cultigens. Several landraces were found resistant and used to grow under severe stress condition. Collection of such genotypes from the field together with recorded data provides information for further evaluation. High temperature and low water availability during the reproductive phase of rabi sorghum are the major limitations for a healthy crop growth and thus only the adaptive and selective varieties can be grown under such environments. Loss of genetic variability leading to genetic erosion has led to greater emphasis on germplasm collection and characterization for present and future plant breeding programmes (Prasanna, 2010). The present study was undertaken to explore the genetic and environmental variability in sorghum landraces collected from different agro-ecological regions of Uttar Pradesh.

Materials and Methods

Ninety-nine sorghum landraces collected from 11 districts, 25 talukes and 54 villages of Uttar Pradesh were evaluated during kharif (rainy) season. The germplasm collection represented some basic and intermediate races of sorghum *viz*., *bicolor* (2), *durra* (44), *durra-bicolor* (5), *durra-caudatum* (42), *guinea* (2) and *guinea-caudatum* (4) (Table 1). These accessions were evaluated during kharif 2008 and 2009 seasons at Directorate of Sorghum Research, Hyderabad.

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Table 1. List of accessions collected from Uttar Pradesh with racial classification

S. No.	Accession number	Indigenous collection number	Race	Village	Taluk	District
1	ES 1	IC 333346	Durra	Kalyanpur	Kanpur	Kanpur
2	ES 3	IC 333348	Durra	Kalyanpur	Kanpur	Kanpur
3	ES 4	IC 333349	Durra	Kalyanpur	Kanpur	Kanpur
4	ES 5	IC 333350	Bicolor	Kalyanpur	Kanpur	Kanpur
5	ES 6	IC 333351	Durra	Kalyanpur	Kanpur	Kanpur
6	ES 7	IC 333352	Durra	Ruma	Kanpur	Kanpur
7	ES 8	IC 333353	Durra	Ruma	Kanpur	Kanpur
8	ES 9	IC 333354	Durra	Kalyanpur	Kanpur	Kanpur
9	ES 10	IC 333355	Durra	Gowdiya	Kanpur Nagar	Fatehpur
10	ES 11	IC 333356	Durra	Badagarh	Kanpur Nagar	Fatehpur
11	ES 12	IC 333357	Durra	Pajithpur	Kanpur Nagar	Fatehpur
12	ES 13	IC 333358	Durra	Pajithpur	Kanpur Nagar	Fatehpur
13	ES 14	IC 333359	Durra	Fatehpur	Fatehpur	Fatehpur
14	ES 15	IC 333360	Bicolor	Bilanda	Allahabad	Fatehpur
15	ES 16	IC 333361	Durra	Mayaramakapurva	Hairamva	Fatehpur
16	ES 17	IC 333362	Durra	Ganbath Sakhiya	Allahabad	Kaushambi
17	ES 18	IC 333363	Durra	Ganbath Sakhiya	Allahabad	Kaushambi
18	ES 19	IC 333364	Durra	Keshavapur	Allahabad	Kaushambi
19	ES 20	IC 333365	Durra	Keshavapur	Allahabad	Kaushambi
20	ES 21	IC 333366	Durra	Suratjung	Allahabad	Kaushambi
21	ES 22	IC 333367	Durra	Suratjung	Allahabad	Kaushambi
22	ES 23	IC 333368	Durra	Suratjung	Allahabad	Kaushambi
23	ES 24	IC 333369	Durra	Sikantharpur Vajaga	Allahabad	Allahabad
24	ES 25	IC 333370	Durra	Pannoie	Allahabad	Allahabad
25	ES 26	IC 333371	Durra	Bagadpur	Bhulpur	Allahabad
26	ES 27	IC 333372	Guinea	Bagadpur	Bhulpur	Allahabad
27	ES 28	IC 333373	Durra	Vashiki	Bhulpur	Allahabad
28	E 16	IC 333374	Durra	Bodeganj	Allahabad	Allahabad
29	E 17	IC 333375	Durra	Gowganya	Allahabad	Allahabad
30	E 18	IC 333376	Durra	Gowganya	Allahabad	Allahabad
31	E 19	IC 333377	Durra	Gowganya	Allahabad	Allahabad
32	E 20	IC 333378	Durra	Suratpur	Allahabad	Allahabad
33	E 21	IC 333379	Durra	Murka	Mau	Banda
34	E 22	IC 333380	Durra	Katya Mau	Mau	Banda
35	E 23	IC 333381	Durra	Akiri	Mau	Banda
36	E 24	IC 333382	Durra	Akiri	Mau	Banda
37	E 25	IC 333383	Durra	Devanda	Ramnagar	Chitrakut
38	E 26	IC 333384	Durra	Devanda	Ramnagar	Chitrakut
39	E 27	IC 333385	Durra	Lepura	Ramnagar	Chitrakut
40	E 28	IC 333386	Durra	Lepura	Ramnagar	Chitrakut
41	E 29	IC 333387	Durra	Rawli	Narayani	Chitrakut
42	E 30	IC 333388	Durra	Rawli	Narayani	Chitrakut
43	E 31	IC 333389	Durra	Rajputh Nagar	Choti Badokar	Chitrakut
44	E 32	IC 333390	Durra	Mahokar	Bargarh	Banda
45	E 33	IC 333391	Durra-bicolor	Mahokar	Bargarh	Banda
46	E 34	IC 333392	Durra	Pasangi	Bargarh	Banda
47	E 35	IC 333393	Durra-bicolor	Pasangi	Bargarh	Banda
48	E 36	IC 333394	Durra	Jaseipur	Tindwari	Banda
49	E 37	IC 333395	Durra	Jaseipur	Tindwari	Banda
50	E 38	IC 333396	Durra	Jawarpur	Tindwari	Banda
51	E 39	IC 333397	Durra	Indrapurva	Banda	Banda
52	E 40	IC 333398	Durra	Indrapurva	Banda	Banda

Contd.....

Table 1. Contd.....

S. No.	Accession number	Indigenous collection number	Race	Village	Taluk	District
53	E 41	IC 333399	Durra	Raipura	Kaveregi	Mahoba
54	E 42	IC 333400	Durra	Suba	Kulphakad	Mahoba
55	E 43	IC 333401	Durra	Kulphakad	Kulphakad	Mahoba
56	E 44	IC 333402	Durra	Sankara	Kulphakad	Mahoba
57	E 45	IC 333403	Durra	Panwari	Panwari	Mahoba
58	E 46	IC 333404	Durra	Ital	Gohand	Hamirpur
59	E 47	IC 333405	Durra	Beena	Gohand	Hamirpur
60	E 48	IC 333406	Durra	Chunahut	Gohand	Hamirpur
61	E 49	IC 333407	Durra	Chunahut	Gohand	Hamirpur
62	E 50	IC 333408	Durra	Rahak	Gohand	Hamirpur
63	E 51	IC 333409	Durra	Devgunpur	Panwari	Mahoba
64	E 52	IC 333410	Durra	Devgunpur	Panwari	Mahoba
65	E 53	IC 333411	Durra	Dhavapur	Mauranipur	Jhansi
66	E 54	IC 333412	Durra	Chakkara	Mauranipur	Jhansi
67	E 55	IC 333413	Durra-bicolor	Chakkara	Mauranipur	Jhansi
68	E 56	IC 333414	Durra	Chakkara	Mauranipur	Jhansi
69	E 57	IC 333415	Durra-bicolor	Bamhauri	Mauranipur	Jhansi
70	E 58	IC 333416	Durra	Bamhauri	Mauranipur	Jhansi
71	E 59	IC 333417	Durra-bicolor	Mauranipur	Mauranipur	Jhansi
72	E 60	IC 333418	Durra-bicolor	Mauranipur	Mauranipur	Jhansi
73	E 61	IC 333419	Caudatum	Mauranipur	Mauranipur	Jhansi
74	E 62	IC 333420	Caudatum	Mauranipur	Mauranipur	Jhansi
75	E 63	IC 333421	Durra	Mauranipur	Mauranipur	Jhansi
76	E 64	IC 333422	Caudatum	Mauranipur	Mauranipur	Jhansi
77	E 65	IC 333423	Caudatum	Mauranipur	Mauranipur	Jhansi
78	E 66	IC 333424	Durra	Mauranipur	Mauranipur	Jhansi
79	E 67	IC 333425	Durra	Mauranipur	Mauranipur	Jhansi
80	E 68	IC 333426	Caudatum	Pallara	Baghera	Jhansi
81	E 69	IC 333427	Caudatum	Pallara	Baghera	Jhansi
82	E 70	IC 333428	Caudatum	Pallara	Baghera	Jhansi
83	E 71	IC 333429	Durra	Orai	Orai	Jalaun
84	E 72	IC 333430	Durra	Chamari	Orai	Jalaun
85	E 73	IC 333431	Durra-bicolor	Ata	Kalpi	Jalaun
86	E 74	IC 333432	Durra-bicolor	Ata	Kalpi	Jalaun
87	E 75	IC 333433	Durra-bicolor	Ata	Kalpi	Jalaun
88	E 76	IC 333434	Durra	Ata	Kalpi	Jalaun
89	E 77	IC 333435	Durra	Ata	Kalpi	Jalaun
90	E 78	IC 333436	Durra	Bimbiraya	Kalpi	Jalaun
91	E 79	IC 333437	Durra	Itora	Kalpi	Jalaun
92	E 80	IC 333438	Durra	Chowra	Amrovdhar	Kanpur Dehat
93	E 81	IC 333439	Durra	Chowra	Amrovdhar	Kanpur Dehat
94	E 82	IC 333440	Durra	Hosemau	Bhagnipur	Kanpur Dehat
95	E 83	IC 333441	Durra	Hosemau	Bhagnipur	Kanpur Dehat
96	E 84	IC 333442	Durra	Chatteni	Bhagnipur	Kanpur Dehat
97	E 85	IC 333443	Durra	Chatteni	Bhagnipur	Kanpur Dehat
98	E 86	IC 333444	Durra	Mohamedpur	Malasa	Kanpur Dehat
99	E 87	IC 333445	Durra-bicolor	Mohamedpur	Malasa	Kanpur Dehat

The experimental field is located at 17° 19' 28.5" N latitude and 78° 24' 13.4" E longitudes at an altitude of 524 m MSL (mean above sea level). The seed material was sown in augmented block design with two replications. Each genotype was sown in three rows, 5 m long at 45 × 15 cm apart. The data were recorded in each genotype on 22 agro-morphological traits following the minimal descriptors developed by National Bureau of Plant Genetic Resources (NBPGR) (Mahajan *et al.*, 2000). Five plants in each accession were selected for data recording of

qualitative and quantitative traits. The seedling vigour was recorded in 14-day-old seedlings. The midrib colour was recorded in one-month-old seedlings. The data on days to 50% flowering (days) was recorded during the panicle emergence stage. The leaf orientation, leaf length (cm) and leaf width (cm) were measured during the physiological maturity stage. The number of leaves, plant height (cm), ear head length (cm) and ear head width (cm) were measured during the physiological maturity stage. The fresh and dry weights (g/5 plant) of stem were measured after harvesting. The 100-seed weight was recorded after threshing. The shape and compactness of ear head were recorded during the maturity stage. The glume colour, glume coverage, presence of awns, grain color, size and lustre were recorded after harvesting stage. For qualitative and quantitative traits data on average of five plants of each genotype were computed for statistical analyses.

Analysis of variance (ANOVA) was carried out assuming season effects as random and cultivar effects as fixed. The homogeneity of error variance was established (Gomez and Gomez, 1984). Co-efficient of variation (CV %), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and heritability in broad-sense (h^2) were calculated (Burton and De Vabe, 1953, Singh and Chaudhary, 1985) including expected genetic advance (Johnson *et al.*, 1955). The data were subjected to multivariate analysis (Mahalanobis, 1949) and the genotypes were further grouped into different clusters based on Ward's minimum variance method (Hair *et al.*, 1987) and principal component analysis (Rao, 1952). Genotypes were grouped on the basis of minimum generalized distance using Tocher's method (Rao, 1964). All the data analysis was performed using Indostat (2004).

Results and Discussion

Genetic Variability

Analysis of variance revealed significant differences among genotypes for all the 22 traits (Table 2). There was large variation among genotypes for the traits, days to 50% flowering, leaf length, leaf width, number of leaves/plant, plant height, ear head length, ear head width, 100-seed weight, days to maturity, stem fresh weight/5plants and stem dry weight/5plants (Table 2). Significant GxE interaction for leaf length and leaf width of the plant was observed.

Significant differences among the genotypes for all

Table 2. Genetic variability, heritability and genetic advance for different traits in sorghum germplasm

Character	Mean	CV	CD 5%	Range	Variance geno-typical	Variance pheno-typical	ECV	GCV	PCV	(%) h2 (broad sense)	Genetic advance % of mean (5%)
Days to 50% flowering (no.)	79.16	6.40	7.05	66.00-87.00	8.67	34.36	6.40	3.72	7.41	25.00	3.85
Leaf length (cm)	87.85	8.27	10.11	62.10-101.50	19.29	72.08	8.27	5.00	9.66	27.00	5.33
Leaf width (cm)	7.08	12.62	1.24	5.00-9.00	0.21	1.01	12.62	6.44	14.17	21.00	6.04
Number of leaves	13.13	10.82	1.98	9.00-16.00	0.68	2.70	10.82	6.26	12.51	25.00	6.46
Plant height (cm)	318.88	7.55	33.52	215.10-383.00	894.95	1475.09	7.55	9.38	12.04	61.00	15.05
Ear head length (cm)	19.00	14.48	3.83	10.10-34.30	17.46	25.04	14.48	21.99	26.33	70.00	37.83
Ear head width (cm)	5.85	14.71	1.20	3.70-9.50	0.65	1.39	14.72	13.77	20.15	47.00	19.37
100-seed weight (g)	2.53	14.07	0.50	1.70-3.50	0.10	0.23	14.07	12.59	18.89	45.00	17.30
Days to maturity (no.)	115.98	3.66	5.91	103.00-126.00	9.09	27.11	3.66	2.60	4.49	34.00	3.10
Stem fresh weight (g/5plants)	2093.90	30.30	883.02	1063.00-3200.00	69624.83	472249.30	30.30	12.60	32.82	15.00	9.97
Stem dry weight (g/5plants)	1165.61	38.36	622.30	569-2038	41602.61	241570.70	38.36	17.50	42.17	17.00	14.96
Vigour	2.67	0.00	–	2.00-3.00	0.22	0.22	0.00	17.77	17.77	100.00	36.60
Leaf orientation	1.17	0.00	–	1.00-2.00	0.14	0.14	0.00	32.35	32.35	100.00	66.64
Midrib colour	1.10	0.00	–	1.00-2.00	0.09	0.09	0.00	27.51	27.51	100.00	56.67
Ear head shape	3.67	0.00	–	2.00-7.00	1.53	1.53	0.00	33.74	33.74	100.00	69.51
Ear head compactness	1.86	0.00	–	1.00-3.00	0.31	0.31	0.00	29.78	29.78	100.00	61.35
Glume colour	4.00	0.00	–	2.00-10.00	6.39	6.39	0.00	63.19	63.19	100.00	130.16
Glume covering	2.09	0.00	–	1.00-4.00	0.47	0.47	0.00	32.83	32.83	100.00	67.63
Awns	0.82	0.00	–	0.00-1.00	0.15	0.15	0.00	47.38	47.38	100.00	97.60
Grain size	6.37	0.00	–	3.00-9.00	1.44	1.44	0.00	18.83	18.83	100.00	38.79
Grain colour	2.65	0.00	–	1.00-10.00	4.84	4.84	0.00	83.16	83.16	100.00	171.30
Grain luster	0.24	0.00	–	0.00-1.00	0.19	0.19	0.00	177.68	177.68	100.00	366.01

the characters indicated adequate genetic variability in the experimental material. The genetic constants for the characters revealed that the magnitude of phenotypic co-efficient of variation (PCV) was higher than the corresponding genotypic co-efficient of variation (GCV) indicating impact of environmental factors on their expression. Narrow difference between PCV and GCV suggested their relative resistance to environmental fluctuations. In the present study, the PCV and GCV were higher for days to 50% flowering, leaf length, leaf width, number of leaves, plant height, ear head length, ear head width, 100-seed weight, days to maturity, stem fresh weight, stem dry weight, vigour, leaf orientation, midrib colour, ear head shape, ear head compactness, glume colour and glume covering (Table 2). High amount of GCV and PCV suggested greater scope for selection of superior genotypes for these traits. While lower degree or equal GCV and PCV for presence of awns, grain size, grain colour, and grain luster indicated that improvement for such traits might be achieved only up to some extent and these traits cannot be influenced by the environment as they are very stable traits. Utilization of these stable traits for creating variability among the genotypes is possible. High GCV and PCV values were observed for grain luster as also reported earlier (Warkad *et al.*, 2008; Elangovan *et al.*, 2013). Equal GCV and PCV were observed in sorghum for plant height up to base of flag leaf, stigma length, plant total height and panicle length (Reddy *et al.*, 2009). High GCV and PCV values were recorded for grain luster.

The determination of the heritable portions is not based on the estimation of the GCV and PCV, alone. The estimation of heritability along with the coefficient of variability would mean the amount of advance expected. Burton (Burton, 1952) also suggested that GCV and heritability estimate would give better information about the efficiency of the selection. The heritability (%) ranged from 15% (stem fresh weight) to 100% (vigour, leaf orientation, midrib colour, ear head shape, ear head compactness, glume colour, glume covering, presence of awns, grain size, grain colour and grain luster). The utility of heritability is increased when it is used to estimate genetic advance (Johnson *et al.*, 1955). The genetic advance has an edge over heritability as a guiding factor to breeders in selection programme. High heritability coupled with high genetic advance and GCV was noticed for grain luster, grain colour, glume colour, presence of awns, ear head shape, glume covering and leaf orientation.

Genetic Diversity

Ninety-nine sorghum landraces tested for two years during the *kharif* season were grouped into 16 clusters based on D^2 values (Table 5). The distribution pattern indicated that the maximum number of genotypes were included in cluster I with 54 genotypes, followed by cluster II having 23 genotypes, cluster V and IX having four genotypes each and cluster XII having three genotypes. A total of 11 clusters have only one genotype *i.e.*, cluster III – E 83, IV – E 55, VI – E 37, VII – ES 9, VIII – E 27, X – E 87, XII – ES 22, XIII – E 24, XIV – E 43, XV – ES 5 and XVI – E 25. The cluster distance was ranging from 817.00 to 1401.19 within the clusters and 398.78 to 12709.03 between clusters (Table 6). The inter-cluster distances were higher than intra-cluster distances, which indicated wide genetic diversity among the accessions of different groups than those of same cluster. The least intra-cluster distance of 817 was found among the accessions. Cluster I showed lack of variation among the accessions.

The diversity among the present set of material was also supported by the appreciable amount of variation among cluster means for different characters (Table 3). The cluster which is diverse from other clusters was found to have different mean values for number of leaves, ear head length, 100-seed weight, days to maturity, stem fresh weight, stem dry weight, glume colour and grain colour. Cluster IV was diverse from other clusters due to different cluster mean values for days to 50% flowering, leaf length, leaf orientation, days to maturity and plant height comparable results have been reported by Reddy *et al.* (2009) and Elangovan *et al.* (2014). Genetic diversity is generally associated with geographical diversity but the former is not necessarily directly related to geographical distribution (Ganesamuthy *et al.*, 2010; Elangovan *et al.*, 2012). Principal component analysis gives supplementary information on the usefulness of the characters for the definition of the groups (Table 4). The first three principal vectors contribute to 73% of the variance. The first vector, which accounts for 46% variance, the important characters responsible for genetic divergence in the major axis of differentiation was glume covering, vigour, ear head compactness. In the second vector (17.6% of variation), the important characters responsible for genetic divergence were awns, grain size, luster and vigour. Exploitation of genetic

Table 3. Cluster mean values for different contributing characters

S. No.	Variable	PC I	PC II	PC III	PC IV	PC V	PC VI	PC VII	PC VIII	PC IX	PC X	PC XI	PC XII	PC XIII	PC XV	PC XV	PC XVI
1	Days to 50% flowering (no.)	79.75	79.03	79.25	86.50	76.69	82.00	77.25	79.50	74.44	79.25	72.75	81.17	79.25	80.25	66.00	82.00
2	Leaf length (cm)	89.20	85.18	92.60	82.60	83.29	91.25	91.33	89.70	88.69	101.48	85.58	87.45	81.53	85.85	79.18	89.83
3	Leaf width (cm)	7.18	6.97	7.33	6.55	6.81	7.68	7.68	6.50	6.89	7.55	6.20	7.26	7.20	7.35	5.95	6.18
4	Number of leaves (no.)	13.28	12.97	13.50	15.75	12.56	14.25	12.75	12.75	11.69	12.25	13.75	13.33	13.75	12.50	11.25	15.00
5	Plant height (cm)	318.01	316.74	371.63	273.80	314.09	329.60	383.00	286.5	318.50	311.63	360.13	323.46	314.13	346.63	314.75	319.38
6	Ear head length (cm)	17.85	19.29	21.63	22.13	24.64	18.83	19.03	15.93	25.51	17.85	27.83	15.19	12.63	22.78	34.28	14.45
7	Ear head width (cm)	5.93	5.96	5.75	5.68	6.20	5.88	4.50	4.73	4.79	6.40	5.80	5.84	5.80	6.00	4.15	5.63
8	100-seed weight (g)	2.58	2.52	1.80	1.83	2.14	1.95	3.13	2.90	2.18	2.90	2.08	3.01	3.03	2.13	2.33	2.95
9	Days to maturity (no.)	116.53	115.50	112.75	121.30	114.63	115.30	113.25	115.00	115.13	113.25	110.25	116.00	118.75	118.75	109.50	118.25
10	Stem fresh weight (g/5plants)	2112.89	2045.82	2187.50	2588.00	1933.40	2050.00	2525.00	2362.50	1831.25	2250.00	1575.00	2162.50	2325.00	1987.50	1762.50	2987.50
11	Stem dry weight (g/5plants)	1166.34	1143.48	1481.25	1550.00	978.13	1288.00	1750.00	1318.80	942.19	1175.00	706.25	1258.30	1662.50	1050.00	768.75	1906.30
12	Vigour	2.72	2.65	3.00	2.75	2.75	2.00	3.00	3.00	2.75	3.00	3.00	2.00	2.00	2.00	2.00	2.00
13	Leaf orientation	1.17	1.09	1.00	2.00	1.00	2.00	1.00	1.00	1.25	1.00	1.00	1.33	2.00	2.00	1.00	1.00
14	Midrib colour	1.03	1.13	1.00	1.00	1.25	1.00	2.00	1.00	2.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
15	Ear head shape	3.43	3.35	4.00	4.00	6.25	4.00	4.00	2.00	5.50	2.00	7.00	3.33	3.00	4.00	7.00	2.00
16	Ear head compactness	1.77	1.75	2.00	2.00	2.75	2.00	2.00	1.00	3.00	1.00	3.00	1.67	1.00	2.00	3.00	1.00
17	Glume colour	2.32	7.25	2.00	2.00	4.00	2.00	2.00	2.00	6.75	9.00	2.00	2.67	9.00	7.00	6.00	10.00
18	Glume covering	2.07	2.04	4.00	3.00	1.50	2.00	2.00	1.00	2.06	1.00	4.00	2.33	1.00	4.00	4.00	1.00
19	Awns	0.85	0.91	1.00	1.00	0.50	1.00	0.00	1.00	0.06	1.00	1.00	1.00	1.00	1.00	0.00	1.00
20	Grain size	6.41	6.57	5.00	3.00	6.00	3.00	9.00	9.00	5.00	9.00	5.00	7.00	7.00	5.00	5.00	9.00
21	Grain colour	2.20	2.26	1.00	1.00	1.00	1.00	3.00	1.00	7.75	3.00	1.00	9.67	2.50	1.00	1.00	10.00
22	Grain luster	0.22	0.13	0.00	0.00	0.75	0.00	1.00	0.00	0.44	0.00	0.00	0.67	1.00	0.00	0.00	0.25

Table 4. Matrix of principal components of 22 variables for 99 sorghum germplasm

S. No.	Variable	PC I	PC II	PC III	PC IV	PC V	PC VI
1	Days to 50% flowering (no.)	0.004	0.021	0.005	0.003	0.015	0.013
2	Leaf length (cm)	0.009	0.016	–0.006	–0.005	–0.014	0.023
3	Leaf width (cm)	0.005	0.014	0.001	0.001	0.002	0.002
4	Number of leaves (no.)	0.004	0.007	0.012	–0.001	0.019	0.007
5	Plant height (cm)	0.001	–0.019	0.008	–0.006	–0.057	–0.018
6	Ear head length (cm)	–0.007	–0.074	0.023	–0.064	–0.005	0.022
7	Ear head width (cm)	0.002	0.022	0.015	0.004	0.011	–0.012
8	100-seed weight (g)	–0.001	0.035	–0.028	0.020	–0.050	0.023
9	Days to maturity (days)	0.000	0.005	0.000	0.001	–0.022	0.002
10	Stem fresh weight (g/5plants)	–0.001	0.017	–0.010	0.013	0.011	–0.015
11	Stem dry weight (g/5plants)	–0.003	0.012	–0.009	0.018	–0.003	–0.006
12	Vigour	0.028	0.046	0.129	–0.064	–0.575	–0.592
13	Leaf orientation	0.005	–0.061	–0.084	0.049	0.254	–0.410
14	Midrib colour	–0.046	–0.110	–0.152	–0.087	–0.072	–0.145
15	Ear head shape	0.013	–0.455	–0.018	–0.550	–0.067	0.120
16	Ear head compactness	0.018	–0.447	–0.013	–0.435	–0.125	0.104
17	Glume colour	–0.988	–0.077	0.117	0.032	–0.002	–0.036
18	Glume covering	0.072	–0.462	0.203	0.596	–0.345	0.048
19	Awns	–0.042	0.413	0.069	–0.268	0.117	–0.146
20	Grain size	–0.064	0.411	–0.099	–0.114	–0.632	0.444
21	Grain colour	–0.098	–0.091	–0.900	0.182	–0.031	0.056
22	Grain luster	0.005	0.022	–0.269	–0.122	–0.198	–0.455
	Root	51346.61	19512.96	10034.02	8801.46	5644.06	4085.98
	% Var. Exp.	46.469	17.659	9.081	7.965	5.108	3.698
	Cum. Var. Exp.	46.469	64.128	73.209	81.174	86.282	89.980

Table 5. Grouping of genotypes into different clusters

Cluster	Genotype
I	ES 19 (IC 333364), ES 21 (IC 333366), E 63 (IC 333421), E 19 (IC 333377), E 81 (IC 333439), ES 17 (IC 333362), E 75 (IC 333433), E 82 (IC 333440), E 85 (IC 333443), E 49 (IC 333407), E 79 (IC 333437), E 76 (IC 333434), E 58 (IC 333416), ES 28 (IC 333373), E 30 (IC 333387), ES 6 (IC 333351), E 57 (IC 333416), E 22 (IC 333380), E 20 (IC 333378), E 21 (IC 333379), ES 7 (IC 333352), ES 10 (IC 333355), E 16 (IC 333374), E 71 (IC 333429), E 51 (IC 333409), E 50 (IC 333408), E 48 (IC 333406), E 18 (IC 333378), E 26 (IC 333384), ES 8 (IC 333353), E 68 (IC 333424), E 44 (IC 333402), E 40 (IC 333398), E 34 (IC 333393), E 17 (IC 333375), E 45 (IC 333403), E 77 (IC 333435), ES 25 (IC 333370), E 23 (IC 333368), ES 13 (IC 333358), E 78 (IC 333436), E 36 (IC 333395), ES 26 (IC 333371), ES 24 (IC 333369), E 56 (IC 333414), ES 20 (IC 333365), E 29 (IC 333374), E 38 (IC 333397), ES 16 (IC 333361), E 31 (IC 333390), E 73 (IC 333431), E 80 (IC 333438), E 41 (IC 333386), ES 15 (IC 333360)
II	E 69 (IC 333427), ES 1 (IC 333346), E 54 (IC 333413), E 32 (IC 333390), E 67 (IC 333425), E 66 (IC 333424), E 46 (IC 333405), E 35 (IC 333393), E 42 (IC 333400), E 52 (IC 333410), ES 14 (IC 333359), E 72 (IC 333430), E 74 (IC 333432), E 84 (IC 333442), E 60 (IC 333418), ES 11 (IC 333356), ES 27 (IC 333372), E 53 (IC 333412), E 86 (IC 333444), ES 4 (IC 333349), E 59 (IC 333418), E 33 (IC 333392), E 64 (IC 33423)
III	E 83 (IC 333441)
IV	E 55 (IC 333414)
V	ES 3 (IC 333348), ES 18 (IC 333363), E 47 (IC 333405), ES 23 (IC 333368)
VI	E 37 (IC 333395)
VII	ES 9 (IC 333357)
VIII	E 27 (IC 333385)
IX	E 61 (IC 333420), E 65 (IC 333424), E 62 (IC 333421), E 70 (IC 333429)
X	E 87 (IC 333445)
XI	ES 22 (IC 333367)
XII	E 39 (IC 333397), ES 12 (IC 333360), E 28 (IC 333386)
XIII	E 24 (IC 333382)
XIV	E 43 (IC 333402)
XV	ES 5 (IC 333353)
XVI	E 25 (IC 333383)

Table 6. Average intra- (bold) and inter-cluster distances for 99 genotypes of sorghum (Tocher method)

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	**817.00**	2846.12	1555.41	1425.34	1936.30	1330.89	1340.08	1423.21	3977.76	5064.00	2543.25	2064.90	4976.10	3511.69	4406.25	7549.68
II		**981.09**	3972.42	3859.05	2711.63	3703.11	3638.01	3587.54	2572.03	1630.20	4987.40	3809.47	1660.12	1930.63	3670.01	3290.69
III			**0.00**	721.11	2815.41	1685.06	2195.58	3741.93	4497.32	7882.89	699.64	3279.26	7730.60	2458.78	2486.08	10938.91
IV				**0.00**	2463.59	398.78	2871.36	3580.60	4240.45	7736.25	1419.78	3220.17	6649.04	2651.05	3364.38	10663.76
V					**1401.19**	2206.76	2184.27	3257.71	2863.48	5136.13	2501.00	3568.46	4563.86	3540.19	3271.46	7655.66
VI						**0.00**	3049.15	2965.68	4379.18	7087.19	2415.61	2983.56	5689.37	3299.09	4324.90	9698.86
VII							**0.00**	1691.45	3959.84	5658.79	2977.85	2210.52	5902.30	4599.82	4690.29	8018.26
VIII								**0.00**	6466.07	4070.95	5520.89	3065.99	4863.82	6071.07	8014.61	7056.13
IX									**1048.46**	4704.18	4297.89	3497.81	4150.79	2904.56	2909.14	4926.10
X										**0.00**	9659.97	5701.11	888.71	4521.88	7614.88	1299.28
XI											**0.00**	4353.52	9251.08	3170.61	1785.53	12709.03
XII												**1001.73**	5324.75	4604.14	5721.18	5676.32
XIII													**0.00**	3607.00	6837.14	1787.32
XIV														**0.00**	1283.19	6397.81
XV															**0.00**	9655.20
XVI																**0.00**

resources within and among these contrasting pools of diversity may provide a different source of germplasm with combination traits for utilization in the sorghum improvement programme.

Local cultivars or landraces are used by farmers and breeders selected for varietal improvement prgrammes. Owing to several reasons. (*i*) grain superiority, (*ii*) The improved varieties/versions do not provide anything percept visual appeal and quality and (*iii*) improved versions have as restricted adaptation as the original landraces and hence, are less suitable for wide adaptations. Sorghum germplasm collections of Uttar Pradesh represent greater genetic diversity as the crop has been grown traditionally under varied agro-climatic conditions for centuries and has adapted to the environmental conditions. These landraces with rare and useful alleles could serve as potential donors for yield enhancement and also for developing varieties to withstand biotic and abiotic stresses in the semi-arid tropical regions.

To conclude, the sorghum genotypes used for evaluation study had wide range of variation for agro-morphological characters. There is greater scope for improvement for specific characters. Highest genetic variability is likely to be created when the crosses are made between selected genotypes from different clusters than those made within a cluster. Selection for the trait *viz.*, glume colour, awns, grain colour and grain luster are governed by the non-additive gene effects and can used for developing distinct variety.

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Exploiting Genetic Divergence for Crop Improvement in Coriander (*Coriandrum sativum* L.): A Neglected and Underutilized Crop

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Coriander (*Coriandrum sativum* L.) cultivars suitable for rainfed farming situation are needed for sustainable production. Understanding the genetic divergence of the crop facilitates the manipulation of desired traits through plant breeding. One hundred and eighty three germplasm lines of coriander of diverse geographical origin were screened under rainfed conditions to determine genetic divergence following multivariate and canonical analysis. Thirteen traits including grain yield were considered for studying the divergence. Utilizing cluster analysis, the germplasm were grouped into eight clusters. The four PCA components explained 77.8% of the total variability among thirteen quantitative traits. Some 84% of the total genotypes (154/183) were grouped in two clusters (1 and 8). Remaining clusters (2, 3, 4, 5, 6 and 7) contained 16% genotypes (29/183) representing wide diversity. The genotypes of similarity were identified. Apparent diversity was noticed in 69 genotypes which diverged in seven clusters. The cluster association revealed the relationship between genetic divergence and geographical diversity. Genotypes of clusters 2, 4 and 7 can be utilized for improving yield due to its high mean performance for grain yield/plant with good amount of genetic divergence in most of the yield contributing characters. The high inter-cluster distances and the high mean performance of the clusters 2, 4 and 7 suggest that successful recombinants for high grain yield may be obtained from the crosses among the genotypes from these clusters. Similarly, members of cluster 3 can be utilized for improving the essential oil content. For breeding bolder types, genotypes from clusters 6 and 7 can be utilized. Rational strategies for effective utilization of germplasm for crop improvement are also discussed.

Key Words: *Coriandrum sativum*, Genetic diversity, Germplasm

Introduction

The species *Coriandrum sativum* L., is grown for '*grain* or *seed*' spice and green leaf. It is widely cultivated throughout the world. However, production of coriander for '*grain*' is limited to some Mediterranean, African and Asian countries. The crop is grown mainly in Bulgaria, India, Morocco, Mexico, Romania, Argentina, Iran and Pakistan (Diederichsen, 1996). It is grown mainly in two farming situations – irrigated light soils and rainfed vertisols. Most crop improvement programmes mainly aim at developing long duration varieties suitable for irrigated light soils (Bhandari and Gupta, 1993a; 1993b), sodic wastelands (Singh *et al.*, 2005) and special uses (Lopez *et al.*, 2007). Large-scale production and the development of better varieties suitable for rainfed vertisols are restricted by the lack of information about their genetic diversity, intra-specific variability and genetic relationships among this species. Due to paucity of genetic diversity, crop improvement of coriander for rainfed vertisols has become a challenge in India. In this context it is very crucial to analyze, understand and exploit the untapped genetic diversity for effective crop improvement. Multivariate (Anderberg, 1973, Smith, 1984; Cox *et al.*, 1986) and principal component (PCA) analyses (Wiley, 1981; Johnson, 1998a) help in understanding the diversity and are extremely useful

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for crop improvement programmes. Mohammadi and Prasanna (2003) opined that concerted and planned utilization of germplasm utilizing the knowledge accrued from studies on genetic diversity is needed for effective crop improvement programmes. In this context, the present study was initiated to study the genetic diversity, possible classification and ordination, and utility of the germplasm diversity in developing rational strategies for effective utilization of germplasm for improvement of coriander.

Materials and Methods

The present investigation was conducted at the field of the "All India Coordinated Research Project on Spices (AICRPS)" project, Sub-center, Horticultural Research Station, Lam, Guntur of Dr YSR Horticultural University, Tadepalligudem, Andhra Pradesh, India. The experiment was conducted during the winter seasons of 2008 and 2009. The experimental station is located at 16°18' N latitude, 80°29' N longitude and at an elevation of 31.5 m above mean sea level (MSL). The experimental soil is vertisols (black clay loam to black clay) with a pH of 7.6, Electrical Conductivity of 0.47 dS/m and Cation Exchange Capacity of 0.5 me/g. Bulk density is 1.22 g/cm and hydraulic conductivity is 1.4 cm/hour. Water holding capacity of the soil is 47%. The available Nitrogen is 282 kg/ha, Phosphorous is 40.2 kg/ha and Potassium is 717 kg/ha. The field experiment was laid out in the Augmented Block Design (ABD) with 183 entries which included four checks in ten blocks with 4 × 1.2 m plot for each entry. The design contained ten randomized blocks in each of which four standard coriander varieties and eighteen entries to be evaluated were grown. The plot was fertilized with 45 kg N/ha, 40 kg P/ha and 20 kg/ha. Data were recorded from ten plants randomly selected from the plot on plant height (cm), number of primary branches, number of secondary branches, number of umbels/plant, number of umbellets/ umbel, number of fruits/umbel, days to 50% flowering, days to maturity, yield/plant (g), bio mass (g), test weight (g) and essential oil (%).

The data set, composed of 13 variables for 183 accessions collected from important coriander growing areas of Andhra Pradesh, Maharashtra and Rajasthan and were analyzed by multivariate statistical techniques. Principal Component Analysis (PCA) was utilized for description of spatial relationships among the germplasm lines. Standard version of the computer software SPSS 10.0.1 was used for the analysis. Cluster analysis was carried out to examine whether the genotypes could be regarded as consisting of number of partially dissociated groups or clusters. Clustering of germplasm was carried out as per the degree of similarity among the germplasm lines (Peeters and Martinell, 1989; Johnson, 1998b). The coordinates of the position of each accession were determined from the value of each variable. The accessions with similar values for each variable were closer to each other and, therefore, showed a similar pattern over the variables. Cluster analysis was performed by means of incremental sum of squares (ISS) and complete, single, and average linkage strategies (Johnson, 1998b). Dendrogram was generated using the average linkage strategy using the free statistics software housed on the website www.wessa.net. (Wessa 2010).

Results

For understanding the diversity, each germplasm accession is represented by a point in a three-dimensional space, the coordinates of which provide an indication of the scores for each character (Fig. 1). Accessions with similar responses among these characters are grouped in proximity in the three-dimensional space. The first four principal components gave eigen values greater than 1, and cumulatively accounted for 77.8% of the total variance. The principal components with eigenvalue > 1.0 are considered as inherently more informative than any single original variable alone (Iezzoni and Pritts, 1991), hence these were used in this study. The perusal of correlation matrix revealed significant correlations among majority of the traits (Table 1). The matrix revealed the fitness of the dataset in PCA analysis for classification and ordination of the genotypes. The magnitude of the eigen vectors indicates the importance of the variable to one particular component axis (Tables 2 and 3). The first PCA component was positively and strongly correlated with yield per plant and plant height in decreasing order of importance; and was negatively correlated with umbellets per umbel, days to 50% flowering, fruits/ umbel and days to maturity. The second component was positively and strongly correlated with number of primary branches, biomass, number of secondary branches, umbels/plant, fruits/umbel and days to maturity in decreasing importance. The third component was positively and strongly correlated with fruits/plant and negatively correlated with test weight. The fourth component was positively and strongly correlated with

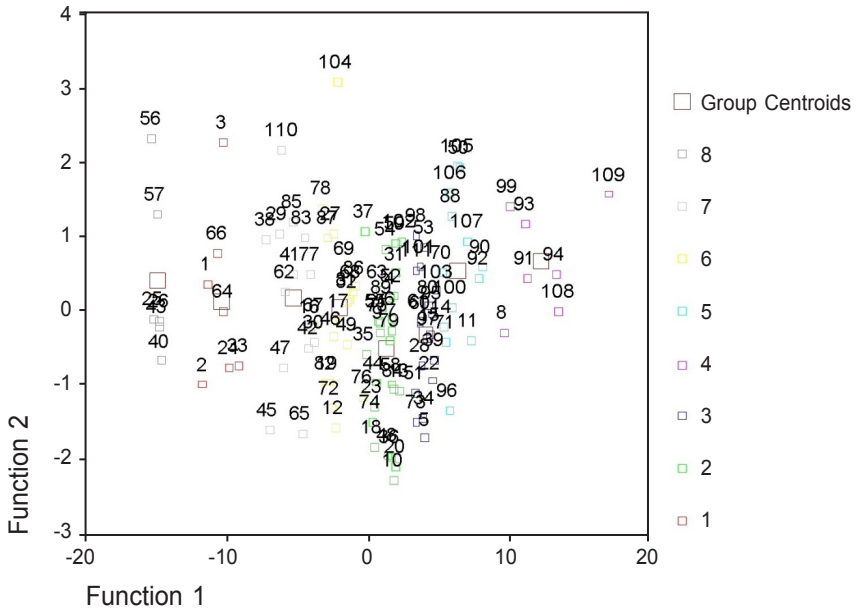

Fig. 1. Canonical discrimination of germplasm lines (accessions in ordinal numbers)

Table 1. Correlation matrix among different traits

	†PH	PBR	SBR	UPP	UPU	FPU	DF	DM	BM	YPP	OP	FPP
PBR	-0.306**											
SBR	0.103	0.625**										
UPP	0.152*	0.529**	0.871**									
UPU	-0.339**	0.313**	-0.212**	-0.284**								
FPU	-0.334**	0.465**	-0.028	-0.061	0.890**							
DF	-0.411**	0.422**	-0.102	-0.181*	0.621**	0.564**						
DM	-0.262**	0.463**	0.041	-0.037	0.608**	0.574**	0.650**					
BM	0.137	0.734**	0.863**	0.931**	0.004	0.206**	0.031	0.180*				
YPP	0.339**	0.169*	0.581**	0.652**	-0.470**	-0.284**	-0.464**	-0.373**	0.535**			
OIL	-0.017	-0.068	-0.164*	-0.112	-0.056	-0.087	0.150*	0.023	-0.124	0.021		
FPP	0.317**	-0.137	0.226**	0.268**	-0.339**	-0.278**	-0.301**	-0.328**	0.160**	0.337**	0.023	
TW	-0.087	-0.021	0.047	0.035	-0.110	-0.115	-0.100	-0.095	-0.022	0.071	-0.053	-0.322**

†PH = plant height (cm); PBR = number of primary branches; SBR = number of secondary branches; UPP = number of umbels/ plant; UPU = number of umbellets/umbel; FPU = number of fruits/umbel; DF = days to 50% flowering; DM = days to maturity; BM = biomass (g); YPP = yield/plant (g); OP = oil percentage; FPP = number of fruits/plant; and TW = test weight (g).

Table 2. Eigen values of the correlation matrix of principal components and proportion of variance

Principal Components	Eigenvalues	Variance (%)	Cumulative (%)
I	4.101	31.543	31.543
II	3.623	27.867	59.410
III	1.335	10.269	69.679
IV	1.055	8.117	77.796

essential oil percentage.

The canonical analysis revealed that yield/plant (0.801) contributed maximum divergence followed by umbellets/ umbel (-0.784), days to 50% flowering (-0.704), fruits/ umbel (-0.636), days to maturity (-0.598) and plant height (0.517) in PC I. Number of primary branches (0.908) followed by biomass (0.859), number of secondary branches (0.724), umbels per plant (0.679), fruits/

Table 3. Eigen vectors and the principal components of thirteen traits in coriander

	Principal components			
	I	II	III	IV
PH†	0.517	-0.214	0.298	-0.179
PBR	-0.045	0.908	-0.07	0.103
SBR	0.595	0.724	-0.072	0.006
UPP	0.674	0.679	-0.042	0.038
UPU	-0.784	0.395	0.14	-0.19
FPU	-0.636	0.565	0.135	-0.195
DF	-0.704	0.424	0.117	0.23
DM	-0.598	0.539	0.095	0.057
BM	0.463	0.859	0.028	-0.008
YPP	0.801	0.239	-0.032	0.107
OP	-0.074	-0.133	0.217	0.926
FPP	0.535	-0.081	0.608	-0.052
TW	0.056	-0.043	-0.869	0.096

†PH = plant height (cm); PBR = number of primary branches; SBR = number of secondary branches; UPP = number of umbels/plant; UPU = number of umbellets/umbel; FPU = number of fruits/umbel; DF = days to 50% flowering; DM = days to maturity; BM = biomass (g); YPP = yield/plant (g); OP = oil percentage; FPP = number of fruits/plant; and TW = test weight (g).

umbel (0.565) and days to maturity (0.539) contributed maximum divergence in PC II. Test weight (-0.869) and fruits/plant (0.608) contributed maximum divergence in PC III. The divergence contribution to fourth principal component was from essential oil percentage (0.926).

The PCA analysis was used to study the interrelationships in thirteen quantitative traits and to detect groupings based on similarities in trait interrelationship and to identify direct and indirect effects of characters on coriander crop improvement. The 183 coriander genotypes were grouped in eight clusters based on the genetic diversity studied (Table 4). The cluster means of the traits considered for the study of diversity are presented in Table 5. The canonical variables determined by canonical discriminant analysis were used to aggregate the accessions into groups that were similar in consequential ways by cluster analysis. The objective was to attain clusters of accessions that display small intra-cluster variation relative to the inter-cluster variation. The clusters 2, 3, 4, 5, 6 and 7 were unique containing 29 genotypes. Among the 183 genotypes, 154 accessions were grouped in 2 clusters (cluster 1 and cluster 8) representing 84.1% accessions. Apparent diversity was noticed only in 69 genotypes which diverged in 7 clusters. The cluster association revealed moderate relationship between genetic divergence and geographical diversity. Genetic drift and selection in different environments could cause greater genetic divergence. Similarly, geographical origin of the genotypes which is an embodiment of specific environment assisted by natural and human selection cause greater divergence though many similarities are found in the genotypes of similar geographical background. Further, genotypes of distant geographical origin show similarities if macro environments of the geographical origin are similar. Unless the macro environments differ, it is quite possible to see much similarity in the genotypes from different geographical regions.

The intra-cluster distances (D^2) values (Table 6) ranged from 14.4 to 279.5, the maximum was in cluster 6 followed by 1 (279.5), 5 (128.6) and 8 (60.9). The inter-cluster distance ranged from 28.2 to 289.8. The maximum inter-cluster distance was noticed between cluster '4' and '7' (289.8) followed by '1' and '7' (255.7), '3' and '7' (249.1), '2' and '7' (242.3), '6' and '7' (242.0) and '5' and '6' (221.4). Inter cluster distances between cluster 5 and clusters 1 to 6 are also considerably wide. Low inter cluster distance was found only in '2' X '4' (28.2). Such wide distances between clusters are indicative of wide diversity between these clusters and low genetic diversity was only observed between clusters '2 and '4' only. The composition of the clusters revealed that the accessions collected from nearby locations joined the similar or same cluster(s), those from geographically different locations fell in the different clusters showing that there is a relation between geographical location and diversity. Intensive selection for agronomically important characters and similarity in parentage might be the cause of narrow genetic diversity and uniformity between these clusters (Singh *et al.*, 2003). The important cluster traits

Table 4. Clusters of germplasm accessions with their cluster composition

Cluster	Number of accessions	Cluster members
1	114	LCC-121, LCC-122, LCC-123, LCC-124, LCC-125, LCC-126, LCC-128, LCC-130, LCC-131, LCC-132, LCC-133, LCC-134, LCC-135, LCC-136, LCC-137, LCC-138, LCC-139, LCC-139, LCC-140, LCC-141, LCC-142, LCC-143, LCC-144, LCC-145, LCC-146, LCC-148, LCC-149, LCC-150, LCC-151, LCC-152, LCC-153, LCC-154, LCC-155, LCC-156, LCC-157, LCC-158, LCC-159, LCC-160, LCC-161, LCC-162, LCC-163, LCC-164, LCC-165, LCC-166, LCC-167, LCC-168, LCC-169, LCC-170, LCC-171, LCC-172, LCC-173, LCC-174, LCC-175, LCC-178, LCC-179, LCC-181, LCC-182, LCC-183, LCC-184, LCC-187, LCC-188, LCC-189, LCC-190, LCC-191, LCC-192, LCC-196, LCC-197, LCC-198, LCC-199, LCC-201, LCC-203, LCC-204, LCC-205, LCC-206, LCC-207, LCC-208, LCC-211, LCC-212, LCC-213, LCC-215, LCC-216, LCC-218, LCC-219, LCC-220, LCC-222, LCC-223, LCC-224, LCC-225, LCC-226, LCC-227, LCC-228, LCC-229, LCC-230, LCC-235, LCC-236, LCC-238, LCC-240, LCC-241, LCC-242, LCC-243, LCC-244, LCC-247, LCC-248, LCC-249, LCC-250, LCC-251, LCC-252, LCC-253, LCC-254, LCC-255, Sindhu, Sadhana, Swathi, Sudha
2	12	LCC-127, LCC-147, LCC-176, LCC-185, LCC-186, LCC-193, LCC-194, LCC-195, LCC-231, LCC-233, LCC-234, LCC-246
3	4	LCC-129, LCC-200, LCC-202, LCC-221
4	1	LCC-177
5	7	LCC-180, LCC-209, LCC-210, LCC-214, LCC-237, LCC-239, LCC-245
6	4	LCC-217, LCC-256, LCC-286, LCC-297
7	1	LCC-232
8	40	LCC-257, LCC-258, LCC-259, LCC-260, LCC-261, LCC-262, LCC-263, LCC-264, LCC-265, LCC-266, LCC-267, LCC-268, LCC-269, LCC-270, LCC-271, LCC-272, LCC-273, LCC-274, LCC-275, LCC-276, LCC-277, LCC-278, LCC-279, LCC-280, LCC-281, LCC-282, LCC-283, LCC-284, LCC-285, LCC-287, LCC-288, LCC-289, LCC-290, LCC-291, LCC-292, LCC-293, LCC-294, LCC-295, LCC-296, LCC-298

Table 5. Cluster means of coriander germplasm for 13 traits

Cluster	PH†	PBR	SBR	UPP	UPU	FPU	DF	DM	BM	YPP	OIL	FPP	TW
1	69.7	5.0	12.9	18.5	5.9	31.4	52.9	91.6	45.7	4.7	0.31	319.9	15.9
2	71.1	8.2	20.4	31.0	5.2	35.8	52.1	93.3	71.8	8.0	0.31	430.6	13.9
3	64.3	5.5	11.2	12.7	5.6	22.1	55.3	91.8	36.0	5.5	0.53	160.5	18.4
4	73.4	8.3	19.1	28.6	11.0	75.9	52.0	95.2	74.0	7.2	0.18	199.8	16.2
5	65.9	5.5	13.8	18.4	5.6	29.8	51.3	90.3	45.2	4.5	0.14	206.1	22.3
6	59.6	6.5	12.5	17.5	8.3	44.3	56.3	91.7	46.2	4.7	0.33	99.8	48.8
7	66.8	8.7	21.3	36.1	4.3	30.7	53.0	95.2	78.4	7.5	0.28	149.3	30.9
8	60.8	7.3	11.9	15.1	12.0	60.3	61.1	100.2	48.0	2.4	0.31	185.6	13.5

†PH = plant height (cm); PBR = number of primary branches; SBR = number of secondary branches; UPP = number of umbels per plant; UPU = number of umbellets/umbel; FPU = number of fruits/umbel; DF = days to 50% flowering; DM = days to maturity; BM = biomass (g); YPP = yield/plant (gm); OP = oil percentage; FPP = number of fruits/plant; and TW = test weight (g).

Table 6. Intra- and inter-cluster distance (D^2) in coriander among 8 clusters formed by 183 germplasm accessions based on 13 traits

Cluster	I	II	III	IV	V	VI	VII	VIII
1	14.4	36.6	54.3	37.1	152.1	59.3	255.7	68.1
2		28.5	48.1	28.2	142.4	51.3	242.3	60.3
3			47.8	31.1	148.8	46.3	249.1	59.2
4				45.8	180.3	39.9	289.8	83.0
5					128.6	72.8	221.4	61.6
6						50.2	242.0	58.1
7							279.5	77.2
8								60.9

Table 7. Important traits of clusters of coriander germplasm

Cluster	Important traits
1	Moderate plant growth with average yield.
2	More primary and secondary branches, higher number of umbels per plant with high biomass and higher yield. Moderate essential oil content.
3	Moderate plant growth with lower number of umbels per plant with low biomass with slightly high yields with higher oil percentage. Low fruit number with slightly higher test weights. High essential oil content.
4	More primary and secondary branches, higher number of umbels per plant, higher number of umbellets per umbel with high biomass and higher yield. Low essential oil content.
5	Moderate plant growth with average yield. Low essential oil content. Slightly higher test weights.
6	Moderate plant growth, higher fruits per umbel, low number of fruits per plant with average yield. Very high test weight.
7	More primary and secondary branches, higher number of umbels/plant, low number of umbellets/umbel with high biomass and higher yield. Slightly lower essential oil content. High test weights.
8	Moderate plant growth with highest number of fruits/umbel, late maturing with low biomass and yield.

are presented in Table 7. The cluster traits revealed that the germplasm variability is scant in entries with high test weights (bold types), high number of fruits per umbel, high number of umbellets per umbel, high essential oil content, low or absence of essential oil content and high yield. Most genotypes were having low biomass (92.3 %) showing their adaptability to rainfed farming situation. The entries in the cluster 8 were having long duration, thus were unable to withstand the terminal moisture stress that prevailed in rainfed cultivation thus making them low yielders. However, the members of cluster 8 were having very high number of fruits per umbel which is a very important trait in view of crop improvement. Dendrogram clustering revealed that the genotypes grouped in eight major clusters (Fig. 2). Classification methods in conjunction with ordination techniques are very accurate in discriminating the accessions and proved useful in selecting the germplasm lines for crop improvement programmes. The cluster membership when viewed in the context of geographical origin of the accessions, certain clusters formed graciously coincided with the geographical origin. Thus, similarities in the accessions from similar geographical origin are clearly depicted in the dendrogram.

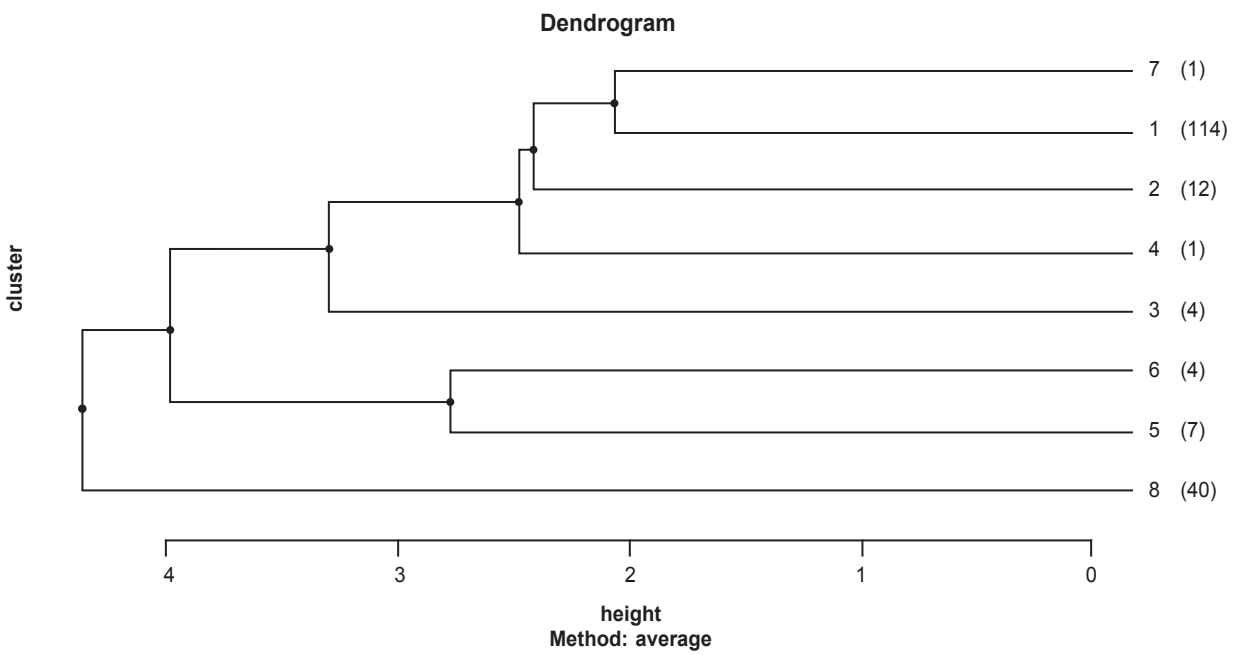

Fig. 2. Dendrogram depicting different clusters of germplasm accessions with number of accessions in parenthesis

Discussion

Crop improvement programmes using the inter-mating between diverse cluster members may generate high heterotic response and better segregants. Exploitation of such explained diversity through breeding programmes paves the way for successful crop improvement programmes. In the present study, cluster I represents the typical types grown in rainfed environments, thus having low diversity as indicated by intra-cluster distance (14.1). The members of cluster 6 are bolder types suitable for vertisols. The clusters 2, 4 and 7 are high yielders. However, members of cluster 4 and 5 are having low essential oil content. The members of cluster 3 are having high essential oil content. The members of cluster 8 are longer duration types with high number of fruits/umbel. On the basis of duration the clusters form two groups. (*i*) Medium duration (clusters 1 to 7) and (*ii*) Longer duration (cluster 8). On the basis of oil content the clusters form three major groups (*i*) Low oil content (cluster 5 and 6), (*ii*) Medium oil content (cluster 1, 2, 4, 7 and 8), (*iii*) High oil content (cluster 3). On the basis of boldness the clusters form two groups. (*i*) Medium bold types (clusters 1, 2, 3, 4, 5 and 8) *ii*) Bold types (cluster 6 and 7). On the basis of yield the clusters form three groups (*i*) Moderate yielders (clusters 1, 3, 5 and 6), (*ii*) High yielders (clusters 2, 4 and 7), (*iii*) Low yielders (cluster 8). Coriander crop improvement has several objectives such as high yield coupled with high essential oil content, bolder types, green types with higher essential oil content, green types with low essential oil content, high yielding with short duration/medium duration types and many more apart from tolerance to biotic and abiotic stresses. The present study envisages some of these objectives like high yield with high essential oil content and high yield with short duration can be met using genotypes from all the clusters using different combinations. Genotypes of clusters 2, 4 and 7 can be utilized for improving yield due to its high mean performance for grain yield/plant and most of the yield contributing characters with good amount of genetic divergence. Similarly, members of cluster 3 can be utilized for improving the essential oil content. For breeding bolder types, genotypes from cluster 6 and 7 can be utilized. The high inter-cluster distances and the high mean performance of the clusters 2, 4 and 7 suggests successful recombinants for high grain yield may be obtained from the crosses among the genotypes from these clusters.

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Variability and Correlation Studies in Garlic (*Allium sativum* L.) Germplasm Collected from Different Parts of Jammu

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Present investigations were carried out at Experimental Area-I, Division of Vegetable Science and Floriculture, SKUAST-Jammu, Chatha during *rabi* season of 2012-13. The analysis of variance revealed significant difference among the genotypes for all the traits studied except for number of leaves/plant, leaf length, dry matter content, total soluble solids and equatorial diameter indicating greater variability in the germplasm. In general, estimates of phenotypic coefficient of variance (PCV) were found higher in magnitude than corresponding genotypic coefficient of variance (GCV). PCV and GCV were high for pseudo stem diameter, plant height, average weight of cloves, average bulb weight, yield/ha and leaf length. High estimates of heritability were obtained for plant height, average weight of cloves, average bulb weight, number of leaves, equatorial diameter, leaf length and low for total soluble solids and dry matter content. High heritability coupled with high genetic advance as percent of mean was observed for plant height, average weight of cloves, average weight of bulb and yield/ha, suggesting additive gene action that can be improved through direct selection. Average bulb weight (g) showed positive and significant correlation with number of leaves/plant, leaf length (cm), average weight of cloves (g), equatorial diameter (cm), while it was negative and significantly correlated with total soluble solids (^{o}B) hence indicating genetic improvement of bulb yield in garlic by putting positive selection pressure on various characters like number of leaves/plant, leaf length, average weight of cloves and equatorial diameter of bulbs.

Key Words: *Allium sativum*, Correlation, Genetic gain, Genetic advance, Variability

Introduction

Common garlic (*Allium sativum* L.), a diploid species (2n=2x=16) is cultivated extensively throughout subtropical plains to intermediate higher reaches of Jammu, covering an area of 530 ha with a production of 7,070 MT and productivity of 13.33 MT/ha (Anonymous, 2014). Districts of Jammu region showing preponderance of garlic cultivation are Jammu, Rajouri and its adjoining areas like Nowshera, Jaba-Anjana, Dudasanwala and Mandi etc. Poonch district including Manjakot, Surankot, Mandi, Loran, Mendhar *etc*. Kathua and parts of Bani, Basoli. Udhampur (Basht, Chenani) and Doda (Baderwah).

Garlic displays considerable variability with respect to morphological features, yield, quality features as well as resistance to important insect pests and diseases. It also shows adaptation to wide range of soil types, temperatures, day length etc making its farming possible from tropics to temperate latitudes. It also showed greater climatic adaptability, some being heat tolerant and others being frost hardy (Maab and Klass, 1995). Given that the germplasm of *A. sativum* is highly variable for morpho-physiological traits (Avento *et al*.,1998; Maab and Klass, 1995), clones could be identified on the basis of canopy structure and yield related traits (Zepeda, 1997). It was, therefore, considered important to study genetic variation and estimates of the degree of heritability of traits of interest for vegetative growth, yield and quality related traits among populations of cultivated garlic under Jammu agro-climatic conditions so that potential and good performing germplasm can be identified and further utilized in *Allium* breeding programme.

Materials and Methods

A collection of garlic genotypes comprising of 14 hexaploids (*A. ampeloprasum* L.), ploidy level 2n=2x=32

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and 27 diploids (*A. sativum* L.), ploidy level 2n=2x=16, from different zones of Jammu division including four released varieties from NHRDF, Karnal, Haryana, were collected and evaluated against two checks *i.e.,* Agrifound Parvati (G-313) and Yamuna Safed (G-50) for 10 morphological, yield and quality traits (Table 1). All the genotypes were planted on October 24, 2012 in Randomized Block Design for evaluation with three replications in a plot size of 2.25 m x 2.0 m with spacing of 15 cm × 10 cm. All the recommended cultural practices were followed during the entire growth period of crop to raise a healthy crop. The Experimental Area-I is located in the subtropical zone of Jammu and Kashmir at 32°40′ North latitude and 74°58′ East longitude having an elevation of 332 m above msl. Its climate is subtropical with hot dry summer, warm humid rainy season and cold winters. The maximum temperature goes up to 47°C during summer (May to June) and minimum temperature falls below 10°C during winter (December-January). The mean annual rainfall during 2012 was 27.2 mm whereas it was 13.2 mm during 2013 (Source: *Agro meteorological Section, Division of Agronomy, SKUAST-Jammu*). The soil of the experimental area was near neutral in reaction (pH 6.3) with medium in nitrogen and phosphorus concentration but low in potassium level. All the observations were recorded as per standard procedures from five randomly selected plants of each genotype in all the three replications and their mean were worked out for statistical analysis as per Panse and Sukhatme (1967). Plant height was measured from base of the plant to the upper leaf at 80 days after sowing. Leaf length of the 4th leaf was measured from leaf axil up to its tip and leaf width was measured from the middle of the 4th leaf with the help of graduated scale whereas pseudo-stem length was measured from the soil level to inner leaf lamina notch of the plants and diameter was recorded below leaf level of the plant with the help of vernier caliper. The phenotypic and genotypic coefficient of variance were calculated according to formulae given by Burton and De-Vane (1953). Heritability (broad sense) and genetic advance was calculated as suggested by Allard (1960) and genetic gain expressed as per cent of population mean, was calculated by the method given by Johnson *et al*. (1955).

Results and Discussion

Forty one collections of garlic were assessed to know the magnitude of genetic variability and heritability of important economic characters. Considerable amount of variability was observed in all the genotypes of garlic as is evident from analysis of variance which showed significant differences among various traits like plant height, leaf length, pseudostem length, average weight of 10 cloves, equatorial diameter, average weight of bulb, yield /ha except total soluble solids, dry matter weight and number of leaves (Table 2).The results therefore clearly indicate that substantial amount of variability exists in the above mentioned traits and thus can be initialized for improvement of quantitative attributes of the crop under study. Similar results are observed by Mohanty (2001), Monpara *et al*. (2005), Gupta *et al*. (2007), Haydar *et al*. (2007), Hosamani *et al*. (2010) and Singh *et al*. (2012a).

The garlic (*A. sativum)* is being currently considered a species complex and it shows immense variability (Kamenetsky, 2007). Although belonging to a same group, the collections showed clear distinguishable features in many respects: leaf shape, colour and orientation, bulb shape and colour, days to harvest *etc*. Nine genotypes were broad leaved (leaf width >1.5cm) and spreading in orientation, 7 were narrow leaved (leaf width <1.5 cm) and erect including check Yamuna Safed (G-50), 13 were broad leaved and erect in orientation including check Agrifound Parvati (G-313), whereas 10 genotypes were broad leaved showing prostate orientation (Table 2). On the basis of clove colour, broadly two categories: white and pink white emerged among the collections. 20 genotypes showed whitish cloves where as 21 genotypes including both the checks showed pink-white cloves of the bulbs. On bulb shape basis, 30 genotypes showed ovate bulbs whereas 11 genotypes showed broadly ovate shape of the bulbs. Regarding foliage colour, four categories emerged, out of which, 6 genotypes showed green colour foliage, 11 genotypes showed dull green foliage, 14 genotypes showed light green and 10 genotypes were having bright dark green foliage. G-408 had dull dark green foliage colour. On the basis of crop duration, the genotypes were harvested in two lots *i.e.,* one at 190 days after sowing and second at 205 days after sowing, thereby showing a difference of 15 days with a mean value of (193.20 days). Eight genotypes including check Yamuna Safed (G-50) namely SJG-11-07, SJG-11-12, SJG-11-17, SJG-11-19, SJG-11-26, SJG-11-28, G-408 and Yamuna Safed (G-282) were harvested 15 days late *i.e.,*at 205 days after sowing as compared to rest of the genotypes which were harvested at 190 days after sowing. Variability with respect to the ability of formation of aerial bulbils (propagating

Table 1. List of garlic genotypes and their source of collection

S. No.	Genotype	Source	Ploidy level (2n)=16,32	S. No.	Genotype	Source	Ploidy level (2n)=16,32
1	SJG-11-01	Kanachak (Jammu, J&K)	Diploid	22	SJG-11-22	Surankote (Poonch, J&K)	Hexaploid
2	SJG-11-02	Kanachak (Jammu, J&K)	Diploid	23	SJG-11-23	Panjgran (Rajouri, J&K)	Hexaploid
3	SJG-11-03	Bhaderwah(Doda,J&K)	Diploid	24	SJG-11-24	Jaba-Anjana (Rajouri, J&K)	Diploid
4	SJG-11-04	Kathua, J&K	Diploid	25	SJG-11-25	Thanamandi (Rajouri, J&K)	Hexaploid
5	SJG-11-05	Kathua, J&K	Diploid	26	SJG-11-26	Lower Loren (Poonch, J&K)	Diploid
6	SJG-11-06	Chandak (Poonch, J&K)	Diploid	27	SJG-11-27	Surankote (Poonch, J&K)	Diploid
7	SJG-11-07	Rajouri, J&K	Hexaploid	28	SJG-11-28	Dudasanwala (Poonch, J&K)	Diploid
8	SJG-11-08	Nowshera (Rajouri, J&K)	Diploid	29	SJG-11-29	Rajouri, J&K	Diploid
9	SJG-11-09	Poonch, J&K	Hexaploid	30	SJG-11-30	Surankote (Poonch,J&K)	Hexaploid
10	SJG-11-10	Khaneter (Poonch, J&K)	Hexaploid	31	SJG-11-31	Dandidhar (Poonch,J&K)	Diploid
11	SJG-11-11	Surankote (Poonch, J&K)	Hexaploid	32	SJG-12-01	Karla Selection-1 (Udhampur, J&K)	Hexaploid
12	SJG-11-12	Surankote (Poonch, J&K)	Diploid	33	SJG-12-02	Karla Selection-2 (Udhampur, J&K)	Diploid
13	SJG-11-13	Poonch, J&K	Hexaploid	34	SJG-12-03	Marh, Jammu, J&K	Diploid
14	SJG-11-14	Poonch, J&K	Diploid	35	SJG-12-04	Marh, Jammu, J&K	Diploid
15	SJG-11-15	Manjakot (Rajouri, J&K)	Hexaploid	36	G-408	NHRDF, Karnal, Haryana	Diploid
16	SJG-11-16	Rajouri, J&K	Hexaploid	37	Yamuna Safed (G-282)	NHRDF, Karnal, Haryana	Diploid
17	SJG-11-17	Chandak (Poonch, J&K)	Diploid	38	Yamuna Safed (G-323)	NHRDF, Karnal, Haryana	Diploid
18	SJG-11-18	Mandi (Poonch, J&K)	Hexaploid	39	Yamuna Safed (G-1)	NHRDF, Karnal, Haryana	Diploid
19	SJG-11-19	Rajouri, J&K	Hexaploid	40	Yamuna Safed (G-50)*	NHRDF, Karnal, Haryana	Diploid
20	SJG-11-20	Upper Loren (Poonch, J&K)	Hexaploid	41	Agrifound Parvati(G-313)*	NHRDF, Karnal, Haryana	Diploid
21	SJG-11-21	Rajouri, J&K	Diploid				

*=check

Table 2. Mean performance of various morphological, yield and quality characters in garlic genotypes

S. No.	Genotype(s)	Average weight of 10 cloves (g)	Average weight of bulbs (g)	Bulbil formation	Bulb shape	Clove Colour	Days to harvest	Dry matter content (%)	Equatorial diameter (cm)	Foliage colour	Leaf length (cm)	Leaf type	Number of leaves/ plant	Plant height (cm)	Pseudostem length (cm)	Total soluble solids (°B)	Yield/ ha (q)
1	SJG - 11 – 01	13.26	26.23	Present	Ovate	White	190	44.6	3.63	Bright dark green	25.73	Spreading &Broad	7.60	37.50	2.40	24.50	71.73
2	SJG - 11 – 02	9.33	28.13	Present	Broadly-ovate	Pink-white	190	39.0	3.46	Bright dark green	27.20	Spreading &Broad	9.70	38.73	4.00	23.86	77.20
3	SJG - 11 – 03	15.56	27.00	Absent	Ovate	White	190	37.6	3.40	Green	37.00	Erect & Narrow	6.90	50.53	3.56	23.76	73.56
4	SJG - 11 – 04	16.16	30.30	Absent	Ovate	White	190	38.3	3.36	Green	32.50	Erect & Broad	7.60	39.30	3.30	24.26	83.86
5	SJG - 11 – 05	19.70	28.30	Absent	Ovate	Pink-white	190	39.0	4.03	Dull green	34.90	Prostate & Broad	10.00	47.03	2.70	25.40	88.00
6	SJG - 11 – 06	9.80	18.73	Absent	Broadly-ovate	White	190	28.6	2.46	Dull green	29.36	Prostate & Broad	6.80	45.36	3.33	23.93	58.20
7	SJG - 11 – 07	22.83	25.60	Absent	Ovate	White	205	39.6	3.80	Bright dark green	30.00	Prostate & Broad	8.10	46.43	4.56	24.76	79.60
8	SJG - 11 – 08	20.96	29.13	Absent	Ovate	White	190	28.0	3.70	Bright dark green	28.86	Prostate & Broad	5.80	39.33	2.93	22.80	90.63
9	SJG - 11 – 09	19.40	30.90	Absent	Ovate	White	190	38.6	3.50	Dull green	25.13	Erect & Broad	8.30	34.03	2.66	23.90	90.80
10	SJG - 11 – 10	23.50	43.40	Absent	Ovate	White	190	41.0	4.16	Light green	29.50	Erect & Broad	7.90	36.80	2.50	24.10	134.96
11	SJG - 11 – 11	15.96	21.63	Absent	Ovate	White	190	40.3	3.66	Dull green	28.26	Erect & Broad	8.40	33.16	2.13	24.80	68.23
12	SJG - 11 – 12	17.63	27.30	Absent	Ovate	White	205	36.0	3.63	Light green	25.93	Prostate & Broad	8.20	35.50	3.16	23.60	84.86
13	SJG - 11 – 13	13.13	22.83	Absent	Broadly-ovate	White	190	42.6	3.30	Bright dark green	32.73	Prostate & Broad	7.70	47.60	2.53	23.96	60.66
14	SJG - 11 – 14	16.66	16.30	Absent	Broadly-ovate	Pink-white	190	26.0	2.30	Light green	31.20	Erect & Broad	7.86	38.60	3.70	26.10	50.63
15	SJG - 11 – 15	17.50	17.16	Absent	Ovate	White	190	51.0	3.70	Light green	35.80	Erect & Broad	7.76	52.10	3.20	25.10	53.33
16	SJG - 11 – 16	7.80	8.56	Absent	Ovate	White	190	43.3	2.76	Light green	30.20	Erect & Broad	6.10	39.70	4.00	24.40	37.10
17	SJG - 11 – 17	8.00	9.30	Absent	Ovate	Pink-white	205	36.6	2.23	Bright dark green	15.40	Prostate & Broad	5.50	22.00	1.86	24.16	36.23
18	SJG - 11 – 18	9.90	17.96	Present	Ovate	Pink-white	190	27.0	2.86	Light green	31.80	Prostate & Broad	8.40	38.30	2.10	22.80	55.86
19	SJG - 11 – 19	9.33	26.83	Absent	Broadly-ovate	Pink-white	205	39.3	2.70	Bright dark green	22.83	Erect & Narrow	5.30	33.40	2.53	24.66	83.50
20	SJG - 11 – 20	30.56	38.40	Present	Ovate	White	190	34.3	4.33	Dull green	21.30	Spreading &Broad	5.50	31.50	4.50	23.53	119.53
21	SJG - 11 – 21	17.96	21.76	Absent	Ovate	Pink-white	190	23.6	2.23	Light green	19.23	Erect & Broad	4.80	27.13	3.00	26.40	57.26
22	SJG - 11 – 22	17.20	20.13	Present	Ovate	White	190	42.3	3.90	Light green	22.86	Erect & Broad	8.10	32.06	3.46	24.56	62.70
23	SJG - 11 – 23	8.26	28.73	Present	Ovate	White	190	35.3	2.73	Light green	21.56	Erect & Narrow	5.70	28.50	3.66	23.60	79.00
24	SJG - 11 – 24	12.66	28.20	Absent	Broadly-ovate	White	190	42.3	3.40	Dull green	29.66	Spreading &Broad	7.03	40.13	4.80	23.20	77.30
25	SJG - 11 – 25	9.30	25.66	Absent	Ovate	Pink-white	190	35.6	3.66	Light green	22.80	Erect & Broad	6.50	34.96	4.16	23.60	79.86
26	SJG - 11 – 26	22.76	40.86	Present	Ovate	Pink-white	205	43.0	4.40	Light green	22.66	Erect & Narrow	5.90	32.20	3.50	24.30	127.00
27	SJG - 11 – 27	7.26	32.86	Absent	Broadly-ovate	Pink-white	190	35.0	2.60	Light green	25.86	Erect & Broad	6.56	38.26	3.43	23.23	102.33

Table 2 Contd.

S. No.	Genotype(s)	Average weight of 10 cloves (g)	Average weight of bulbs (g)	Bulbil formation	Bulb shape	Clove Colour	Days to harvest	Dry matter content (%)	Equatorial diameter (cm)	Foliage colour	Leaf length (cm)	Leaf type	Number of leaves/ plant	Plant height (cm)	Pseudostem length (cm)	Total soluble solids (°B)	Yield/ ha (q)
28	SJG - 11 – 28	10.13	30.76	Absent	Ovate	Pink-white	205	39.0	2.86	Light green	21.60	Erect & Broad	8.20	25.83	2.73	23.90	95.63
29	SJG - 11 – 29	20.40	15.20	Absent	Broadly-ovate	Pink-white	190	37.3	3.56	Light green	21.66	Erect & Narrow	6.60	30.47	3.46	24.56	47.36
30	SJG - 11 – 30	18.10	34.00	Absent	Ovate	White	190	43.0	4.10	Dark green	22.03	Erect & Narrow	6.30	30.76	3.33	24.33	116.60
31	SJG - 11 – 31	14.60	20.20	Absent	Ovate	White	190	37.0	2.66	Green	25.53	Erect & Broad	7.60	33.10	3.16	23.00	73.30
32	SJG - 12 – 01	17.30	18.63	Present	Ovate	Pink-white	190	43.0	3.80	Green	25.60	Spreading &Broad	6.70	38.26	2.26	22.23	128.90
33	SJG - 12 – 02	13.53	15.20	Present	Broadly-ovate	Pink-white	190	41.6	2.83	Dull green	24.73	Erect & Narrow	5.80	36.73	3.40	24.20	49.33
34	SJG - 12 – 03	24.96	21.23	Absent	Ovate	Pink-white	190	37.0	2.66	Dull green	29.90	Spreading &Broad	7.90	40.63	2.43	27.70	100.83
35	SJG - 12 – 04	31.16	39.56	Present	Ovate	Pink-white	190	34.3	4.13	Green	32.50	Erect & Broad	9.30	41.60	2.70	29.86	88.53
36	Yamuna Safed (G-1)	21.26	38.06	Present	Broadly-ovate	Pink-white	205	37.0	4.20	Dull green	34.50	Erect & Narrow	6.53	49.76	1.76	23.73	59.16
37	Yamuna Safed (G-282)	22.90	29.10	Absent	Ovate	Pink-white	190	45.0	3.93	Bright dark green	35.66	Spreading &Broad	8.00	48.16	1.83	23.70	58.00
38	Yamuna Safed (G-323)	20.86	28.50	Absent	Ovate	Pink-white	205	44.0	3.83	Dull green	31.30	Erect & Broad	7.50	38.73	3.06	25.20	47.30
39	G – 408	21.10	25.96	Absent	Ovate	White	190	41.0	3.60	Dull dark green	25.30	Prostate & Broad	5.90	31.10	3.10	24.33	123.06
40	Yamuna Safed (G-50) (check)	6.46	19.50	Absent	Broadly-ovate	Pink-white	190	48.6	2.83	Bright dark green	28.00	Prostate & Broad	6.10	45.66	4.70	24.90	70.73
41	Agri found Parvati (G-313) (check)	30.46	15.56	Present	Ovate	Pink-white	205	44.0	2.73	Green	20.93	Erect & Broad	6.16	26.60	3.36	24.10	78.46
	Mean	16.72	25.45	–	–	–	193.20	38.5	3.35	–	27.30	–	7.13	37.50	3.14	24.36	78.56
	S.E. ±	2.48	2.59	–	–	–	–	8.5	0.40	–	3.10	–	1.07	2.59	0.61	1.41	11.76
	C.D.(5%)	6.99	7.30	–	–	–	–	23.8	1.12	–	8.74	–	N.S	7.31	1.73	N.S	33.52
	C.V.	25.73	17.66	–	–	–	–	38.32	20.63	–	19.71	–	26.07	11.99	33.87	10.03	26.25

material) is concerned, 12 genotypes including check Agrifound Parvati (G-313) and Yamuna Safed (G-50) showed the ability to produce aerial bulbils (Table 2).

An insight into the magnitude of variability present in a crop species is of utmost importance as it provides basis for effective selection. More the variability in germplasm, more is the chance for selecting desirable genotypes (Vavilov,1951). According to Fisher (1918), most of the economic traits are quantitative in nature, exhibit continuous variation under the control of both heritable and non-heritable factors and effective selection would therefore depend upon the relative heritable portion. In the present investigation, PCV was observed to be higher than the corresponding GCV for all the characters studied (Table 3). High estimates of PCV were observed for average weight of cloves (44.35%), average weight of bulbs (35.19%), yield /ha (38.81%), dry matter content (34.75%), plant height (21.62%) and leaf length (24.64%). However, the differences were narrow which implied their relative resistance to environmental variations. It also described that genetic factors were predominantly responsible for expression of these attributes and selection could be made effective on the basis of phenotypic performance. The traits which showed high phenotypic and genotypic coefficient of variation are of economic importance and there is scope for improvement of these traits through selection. The findings of Yadav *et al.* (2012), Golani *et al.* (2006) and Gashua *et al.* (2013) are similar to that of present findings.

Heritability in broad sense ranged from (4.00% to 74.80%)**.** High estimates of heritability in broad sense (Table 3) were recorded for characters like plant height (69.23%), average weight of cloves (66.3%), yield/ hectare (54.00%), leaf length (36.04%), equatorial diameter (32.20%) and average weight of bulbs (74.8%) indicating that selection for such characters be fairly easy because traits would be least influenced by environmental modifications and selections based on phenotypic performance would be reliable. Similar results were obtained by Gupta *et al.* (2007), Haydar *et al*. (2007), Singh *et al*. (2012b) and Yadav *et al.* (2012). Low heritability was obtained for characters like Stemphylium blight intensity and total soluble solids.The findings of Yadav *et al.* (2012), Agrawal *et al.* (2003), Gashua *et al.* (2013) and Degewione *et al.*(2011) are in line with the present findings.

Genetic advance is the improvement over the base population that can potentially be made from selection for a characteristic. It is the function of the heritability of the traits, the amount of phenotypic variation and the selection differential(s) that the breeder uses. The estimates of heritability and genetic advance should always be considered simultaneously as high heritability is not always associated with high genetic gain (Johnson *et al*., 1955). Burton (1952) suggested that GCV along with heritability give the best picture of the genetic advance to be expected from selection. The estimates of genetic advance as percent of mean ranged from 0.81% to 60.60 % for total soluble solids and average weight of 10 cloves, respectively (Table 3). This indicates that selection from top 5% of the base population could result in an advantage of 0.81 to 60.60% over base population mean. High genetic advance coupled with high heritability was obtained for average weight of cloves, average weight of bulb, plant height and yield/ha. Hence due to additive gene action selection for these characters is likely to be more effective (Panse *et al.,* 2013). The present study is supported by Agrawal *et al.* (2003), Trivedi *et al*. (2006), Dhotre *et al.* (2010), Singh *et al.* (2012b) and Yadav *et al.* (2012). The characters like number of leaves/plant, leaf length, pseudo stem length, dry matter content, total soluble solids and equatorial diameter had

Table 3. Estimates of various genetic parameters for various characters in garlic genotypes

Character	Mean±S.E.	Range	PCV (%)	GCV (%)	h^2 (%) Broad sense	GA (%)	GA (% of mean)
Average weight of bulb (g)	25.45 ± 2.59	8.56 – 43.40	35.19	30.44	74.80	13.80	54.23
Average weight of 10 cloves (g)	16.72 ± 2.48	6.46 – 31.16	44.35	36.12	66.30	10.13	60.60
Dry matter content (%)	3.85 ± 0.85	2.36 – 5.10	34.75	16.15	21.60	0.59	15.46
Equatorial diameter (cm)	3.35± 0.40	2.23 – 4.40	25.06	14.22	32.20	0.55	16.62
Leaf length (cm)	27.30 ± 3.10	15.4 – 37.0	24.64	14.79	36.04	4.99	18.29
Number of leaves/plant	7.13 ± 1.07	4.80 – 10.00	27.38	8.37	9.30	0.37	5.27
Pseudostem length (cm)	3.14 ± 0.61	1.76 – 4.80	37.06	15.05	16.59	0.39	12.59
Plant height (cm)	37.50 ± 2.59	22.00 – 52.10	21.62	17.99	69.23	11.56	30.83
Total soluble solids (°B)	24.36 ± 1.41	22.23 – 29.86	9.84	1.97	4.00	0.19	0.81
Yield/ha (q)	78.56 ± 11.76	36.23–134.90	38.81	28.59	54.00	34.08	43.37

low heritability coupled with high to low genetic gain and GCV depicting that these characters were governed by non-additive genes and would not be effective as it did not corroborate with the conclusion of Burton (1952) and Johnson *et al*.(1955). Similar findings were reported by Tsega *et al.* (2011) and Singh *et al.* (2010).

The phenotypic and genotypic correlation studies revealed that average weight of bulb in garlic showed significant and positive association with number of leaves/plant, leaf length and equatorial diameter at both phenotypic and genotypic levels (Table 4). These results are in conformity with the results of Agarwal and Tiwari (2009), Dhotre *et al.* (2010), Panse *et al.* (2013) and Trivedi *et al.* (2006). Negative and significant correlation with average weight of bulb was shown by total soluble solids at genotypic levels and these results are in agreement with Trivedi *et al.* (2006) and Agarwal and Tiwari (2009). Significant and positive correlation of plant height was observed with number of leaves, leaf length and equatorial diameter at both genotypic and phenotypic levels and results are supported by Figliuolo *et al.* (2001) and Panse *et al.* (2013).Significantly positive correlation of number of leaves/plant with equatorial diameter and average weight of cloves was observed at genotypic level and with leaf length at phenotypic level. The present finding was supported from the work of Panse *et al.* (2013) and Naruka and Dhaka (2004). Similarly, significant but negative correlation of number of leaves/plant was observed with pseudostem length, total soluble solids and dry matter weight at genotypic levels. The findings of Marey *et al.* (2012) and Hosamani *et al.* (2010) are in line with the present results. Leaf length showed positive and significant correlation with equatorial diameter and negative but significant correlation with total soluble solids at genotypic levels. The results are in accordance with the results reported earlier by Singh *et al.* (2006). Pseudostem length was significantly and positively correlated with total soluble solids but negatively with average weight of cloves. Average weight of cloves/bulb showed positive and significant correlation with equatorial diameter, whereas negative and significantly correlated with dry matter content and total soluble solids. Significant positive correlation was observed of equatorial diameter with total soluble solids but significant negative correlation with dry matter content. On the other hand, dry matter showed positive significant correlation with total soluble solids. The findings are in line with Morsey *et al.* (2011), Singh *et al.* (2006) and Singh *et al*.(2012a).

The present investigations indicated that there is a good scope for garlic improvement through selection of suitable genotypes for desirable traits in this region of Jammu and Kashmir state. Also, as the present study was conducted on single location using limited number of local accessions, the results need further confirmation across locations with more cultivars/genotypes including exotic accessions.

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Table 4. Estimates of genotypic (G) and phenotypic (P) correlation coefficients among various characters in garlic genotypes

Character		Average weight of 10 cloves (g)	Dry matter content (%)	Equatorial diameter (cm)	Leaf length (cm)	Number of leaves/ plant	Plant height (cm)	Pseudostem length(cm)	Total soluble solids (°B)
Average weight	(G)	–							
of 10 cloves (g)	(P)	–							
Dry matter	(G)	-0.178*	–						
content (%)	(P)	-0.030	–						
Equatorial	(G)	0.748**	–0.528**	–					
diameter (cm)	(P)	0.389**	0.073	–					
Leaf length (cm)	(G)	0.173	–0.048	0.480**	–				
	(P)	0.093	0.035	0.127	–				
Number of	(G)	0.405**	–0.276**	0.690**	0.150	–			
leaves/ plant	(P)	0.016	–0.038	0.170	0.337**	–			
Plant height (cm)	(G)	0.045	–0.172	0.356**	0.222*	0.859**	–		
	(P)	0.018	0.002	0.181*	0.618**	0.202*	–		
Pseudostem	(G)	–0.252**	–0.146	–0.171	–0.190*	–0.599**	0.046	–	
length (cm)	(P)	–0.045	0.000	0.031	–0.091	–0.085	0.002	–	
Total soluble	(G)	–0.282**	–0.334**	0.187*	–0.299**	–0.269**	–0.060	0.842**	–
solids (°B)	(P)	0.221*	0.005	0.010	0.079	0.073	0.048	0.016	–
Average weight	(G)	0.478**	0.103	0.898**	0.211*	0.256**	0.114	–0.026	–0.220*
of bulb (g)	(P)	–0.278**	0.074	0.409**	0.054	0.128	0.049	–0.041	–0.004

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

providing financial assistance for the survey of garlic germplasm in Jammu region.

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Recent Developments for Access to Plant Genetic Resources in India and their Implications

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Being party to the Convention on Biological Diversity (CBD), Parliament of India enacted the Biological Diversity Act (BDA), 2002 and the National Biodiversity Authority (NBA) was established in 2003. The implementation of the BDA, 2002 was initiated after the Biological Diversity Rules (BDR), 2004 were notified and the application forms for access to biological resources and for seeking intellectual property rights were put in place through these notifications/regulations. Access to biological resources in India is now regulated as per the provisions laid out in BDA, 2002 and BDR, 2004. However, there were many issues which were not addressed in the first set of rules notified through BDR 2004. Such issues have been highlighted here. The implications of these notifications especially for access to biological resources for researchers within and from outside India are discussed here. Relevant and important clauses from the notification/regulations are reproduced for ready reference.

Key Words: Access, Biological resources, Biological Diversity Act, ITPGRFA, Material Transfer Agreement, National Biodiversity Authority, Standard Material Transfer Agreement, Value added products

Introduction

Genetic resources were freely accessible as they were regarded as common heritage of humankind before the Convention on Biological Diversity (CBD) came into existence. Sovereign rights over these resources were highlighted in the context of managing and accessing genetic resources by different countries. Thus, access to genetic resources post-CBD is a highly deliberated issue amongst the researchers/breeders/community dealing with their utilization and conservation. However, exchange of plant genetic resources (PGR) is essential for all crop improvement programmes. Crop improvement eventually plays a significant role in sustainable agriculture, food and nutritional security, and helps to mitigate adverse effects of climate change on agricultural production. Apprehensions related to access to biological resources raise several questions such as ownership and accessibility (Evenson, 1999; Hamilton *et al.,* 2005) such as who owns the biological resources conserved at national level or at International Research Centers. Can these resources be shared or priced? How to ensure their utilization by others and share equitable benefits? These issues are being put forth in various national level meetings to the policy makers at different levels, including those beyond the scientific communities. This paper is an attempt to raise awareness on these issues and to define and bring clarity on access to biological resources in the light of recent developments and notifications.

After the enactment of BDA, 2002 and dealing with exchange of PGR in the country at NBPGR, it was noted that the flow of Plant Genetic Resources for Food and Agriculture (PGRFA) was much restricted after the CBD came into force when compared to before its implementation by different countries. However, collections from International Research Centres were not affected by CBD (Tyagi *et al*., 2006). On the other hand countries that were party to International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) including India were obliged to provide facilitated access to PGRFA to all member countries for the crops listed in Annex 1 of ITPGRFA. The BDA, 2002, therefore, needs to be implemented in synergy with ITPGRFA obligations. Specific provisions in the BDA, 2002 were needed to be included/revised/amended for accessing PGRFA which includes PGRFA beyond their origin/sovereignty [*e.g. In trust* material – held by Consultative Group on International Agricultural Research (CGIAR) Centers collected before 1993 and referred to as CG institute hereafter].

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For such policy deliberations, Indian Council of Agricultural Research (ICAR) had established a high level National Advisory Board on Management of Genetic Resources (NABMGR) to discuss and advise the concerned departments for harmonization of access and benefit sharing issues. During its tenure of three years, five meetings were held. Important recommendations were made to streamline the process of access of germplasm. It was one of the recommendations of the Board that the implementation of the ITPGRFA in the national system needed to be adopted urgently and the proposal put forth by India for designation of material for the Multilateral System (MLS) of the ITPGRFA. In response, the guidelines for 'Implementation of ITPGRFA were developed and Central Government, in consultation with National Biodiversity Authority (NBA) notified exemption for access to Annex I crops of the ITPGRFA, and declared that Department of Agriculture and Co-operation (DAC), Ministry of Agriculture (MoA) as the nodal department. DAC may from time to time notify the crops listed in Annex 1 of the Treaty to the NBA for exemption. This exemption came after a series detailed discussions in the Board meetings and its sub-committees.

Further, as per the definition provided for 'Biological resources' under BDA, 2002, biological resources include plants, animals and microorganisms or parts thereof, their genetic material and by products (excluding value added products) with actual or potential use or value, but does not include human genetic material. Therefore, PGRFA were included under the definition of biological resources. BDA, 2002, hence, does not differentiate between biological resources and PGRFA, which are of utmost importance for food and nutritional security, and sustainable agriculture. Most of the cultivated crops are part of PGRFA but not all of them are of Indian origin. The term research is also defined under the Act as study or systematic investigation of any biological resource or technological application that uses biological systems, living organisms or derivatives thereof to make or modify products or processes for any use.

The value added products defined under the Act are products which may contain portions or extracts of plants and animals in unrecognizable and physically inseparable form. This definition does not specifically mention vegetable oils, proteins, starch, *etc*. which are used directly as food products. Another definition in the Act on commercial utilization says, the end uses of biological resources such as drugs, industrial enzymes, food flavours, fragrances, cosmetics, emulsions, oleoresins, colours, extracts, and genes used for improving crops and livestock through genetic interventions, but does not include conventional breeding or traditional practices in use in any agriculture, horticulture, poultry, dairy farming, animal husbandry or bee keeping. The definitions and use of term conventional breeding or traditional practices is being interpreted differently by different stakeholders. Do conventional practices include hybrid seed production, or use of artificial insemination in animals to produce desirable progeny was highly debated.

Regulations on Access to Biological Diversity

Chapter II of the BDA, 2002 defined the Regulations for access to biological diversity and the Section 3 mentions that certain persons cannot obtain any biological resource occurring in India for research or commercial utilization, without the approval of the NBA (www.nbaindia.org). These persons include those who are not citizens of India, or are non-resident Indians, or companies not registered or incorporated in India. These also include Indian companies registered in India with foreigners managing the company or provide fund to these.

Section 5 of the Act provides for exemptions from Section 3 and Section 4 for access to Indian genetic resources by nationals of other countries, covered under the collaborative research projects/Memoranda of Understanding (MoU)/Work Plans. Such collaborative research projects must conform to the policy guidelines issued by the Ministry of Environment, Forests and Climate Change (MoEF &CC), S.O 1911 (E). However, if any researcher/institutions was intending to send any biological material for deposition in international repositories for the purpose of patents or for new species recognition or taxonomic review were not able to do so under Section 5. A cost of paying requisite fees was also involved in transfer of material. For all other requests not covered under any collaborative research projects the non-Indian applicant as described above, was required to obtain prior approval of NBA.

The above provisions were subjected to individual interpretations with regard to access under BDA, 2002. After detailed deliberations in various meetings/fora, notifications/regulations were put in place by NBA and MoEF & CC to bring more clarity on access of biological resources by different types of users of biological

resources for example, the term 'occurring in India' is ambiguous as all the PGRFA occurring in the country are not 'Indian'. Thus, these questions are being raised on the interpretation of the definitions from time to time.

Recent Notifications

The notification issued recently has further stressed some of the provisions, as indicated below:

G.S.R 827 dated November 21, 2014 on access to genetic resources and the fair and equitable sharing of benefits arising from their utilization (see Annexure 1) (http://nbaindia.org/uploaded/pdf/Gazette_Notification_of_ABS_Guidlines.pdf).

***(A) Regulation 13*:** Conducting of non-commercial research or research for emergency purposes outside India by Indian researchers/government institutions–

(1) Any government institution which intends to send biological resources to carry out certain urgent studies to avert emergencies like epidemics, *etc.*, shall apply to NBA.

(2) The NBA shall, on being satisfied with the application accord its approval within a period of 45 days from the date of receipt of the application. The applicant shall be required to deposit voucher specimens in the designated national repositories before carrying/ sending the biological resources outside India and a copy of proof of such deposits shall be endorsed to NBA.

Implications

This provision implies that any Indian researcher going abroad for any approved basic research activity could carry biological resource with the approval of NBA which shall be granted within 45 days, as opposed to six months as prescribed for other cases of access and sending material outside India.

Secondly, any government institution could send material in the interest of the nation in the same manner for testing/screening or taxonomic studies to a foreign institution in cases of emergent threats to biological resources and complete taxonomic studies, without the need to formulate any collaborative research project. Such approval shall also be granted by NBA within 45 days. Fees for access shall not be required in such cases.

(***B) Regulation 17***: Certain activities or persons are exempted from approval of NBA or State Biodiversity Board (SBB), namely:

(a) Indian citizens or entities accessing biological resources and/ or associated knowledge, occurring in or obtained from India, for the purposes of research or bio-survey and bio-utilization for research in India;

(b) Collaborative research projects, involving the transfer or exchange of biological resources or related information, if such collaborative research projects have been approved by the concerned Ministry/ Department of the State or Central Government and conform to the policy guidelines issued by the Central Government for such collaborative research projects

(c) Local people and communities of the area, including growers and cultivators of biological resources, *vaids* and *hakims*, practising indigenous medicine, except for obtaining intellectual property rights;

(d) Accessing biological resources for conventional breeding or traditional practices in use in any agriculture, horticulture, poultry, dairy farming, animal husbandry or bee keeping, in India;

(e) Publication of research papers or dissemination of knowledge, in any seminar or workshop, if such publication is in conformity with the guidelines issued by the Central Government from time to time;

(f) Accessing value added products, which are products containing portions or extracts of plants and animals in unrecognizable and physically inseparable form and

(g) Biological resources, normally traded as commodities notified by the Central Government under section 40 of the Act.

Implications

This implies that all Indians could access biological resources for research use within India. Secondly, local communities and traditional medical practitioners could use biological resources occurring in India without the need for prior intimation to the SBB except when seeking a patent.

Also, any Indian or non-Indian entity could access biological resource for traditional plant breeding and for other traditional practices of plant and animal improvement if the research was being carried out within India. Therefore, any seed company or private research organization doing conventional (traditional) plant breeding in India could access plant varieties and germplasm from public or private resources. Such

access shall however be based on the mutual agreements/ terms and conditions as laid down by the provider(s)/ Institution(s).

Scope of International Treaty of Plant Genetic Resources for Food and Agriculture

This Treaty relates to PGRFA and defines PGRFA as any genetic material of plant origin of actual or potential value for food and agriculture (http://www.planttreaty.org/). Genetic material is defined as any material of plant origin, including reproductive and vegetative propagating material, containing functional units of heredity. Thus, the scope of BDA, 2002 being all biological resources, it does not differentiate PGRFA from other resources but these are of utmost importance for food and nutritional security and sustainable agriculture.

Regulations of Access to PGRFA

The provisions for facilitated access to PGRFA are laid down in Article 12 of the Treaty. The access to be provided solely for the purpose of utilization and conservation for research, breeding and training for food and agriculture, provided these are not for chemical, pharmaceutical and/ or other non-food/feed industrial uses. Access is provided with all available passport data. However, Intellectual Property (IP) or other rights which limit the facilitated access cannot be claimed. There is a provision for the material which is under development and access to such material is at the discretion of the developer.

Article 12.4 describes the provisions of providing access to PGRFA pursuant to a standard material transfer agreement (SMTA), adopted by the Governing Body, which embodies the benefit-sharing provisions set forth in Article 13.2d.

Article 10 defines the establishment of a multilateral system (MLS), which is efficient, effective, and transparent, both to facilitate access to PGRFA, and to share the benefits arising from the utilization of these resources in a fair and equitable way. Treaty also recognizes the sovereign rights of States over their own PGRFA and access should be consistent with national legislation.

The PGRFA covered under the MLS established under the Treaty is covered under Article 11. The PGRFA covered under the MLS and referred to as Annex I crops is listed according to criteria of food security and interdependence (see list at Annexure I). The MLS as identified in Article 11 includes all PGRFA which are in the public domain, *ex situ* collections of the CG institutes, and in other international institutions, and encourages contracting parties to put their collections in the multilateral system.

Article 15 states that PGRFA listed in Annex I of this Treaty and held by the CG institutes and those collected before its entry into force and held by the CG institutes shall be made available in accordance with the provisions of the Material Transfer Agreement (MTA) pursuant to agreements between the CG institutes and the Food and Agriculture Organization (FAO).

A total of 4, 87,793 accessions (as on February 2015) are included in the MLS by 33 contracting parties (countries) *viz*. Armenia, Austria, Belgium, Brazil, Canada, Cyprus, Czech Republic, Egypt, Estonia, France, Germany, Italy, Jordan, Kenya, Lebanon, Madagascar, Malawi, Morocco, Namibia, The Netherlands, Poland, Portugal, Romania, Rwanda, Senegal, Spain, Sudan, Sweden, Switzerland, Tanzania, UK, Uruguay and Zambia.

India being signatory to ITPGRFA has an obligation as a Contracting Party and needs to provide facilitated access to the Contracting Parties of Treaty for the crops listed in Annex 1. Notification for exemption of Annex 1 crops is issued by Government of India through DAC, MoA on February 16, 2014 including the approved Guidelines for the implementation of the ITPGRFA (Office Memorandum No. 13-5/2013 SD-V). MoEF & CC has also issued a notification for exemption of Annex crops of the Treaty. (http://nbaindia.org/uploaded/pdf/Gazette_Notificaiton_on_exemption_of_crops_listed_in the_Annex-I_of_the_ITPGRFA.pdf) (Annexure 2) Thus, as per the notification issued the access under the MLS is exempted from Section 3 and 4 of the BDA, 2002 (18 of 2003) and is on par with Section 5 under which the collaborative research projects are exempted from Section 3 and 4.

Implications

As per the guidelines developed which are notified by DAC, MoA, Government of India (GOI), the supply of PGRFA of Annex 1 Crops and held in 'trust' by the CG institutes shall also be made available in accordance with the provisions of SMTA with the concurrence of the DAC, MoA, the National Focal Point (Fig. 1).

The exemption thus ensures facilitated access to PGRFA as per the provisions of the Treaty and use of SMTA for

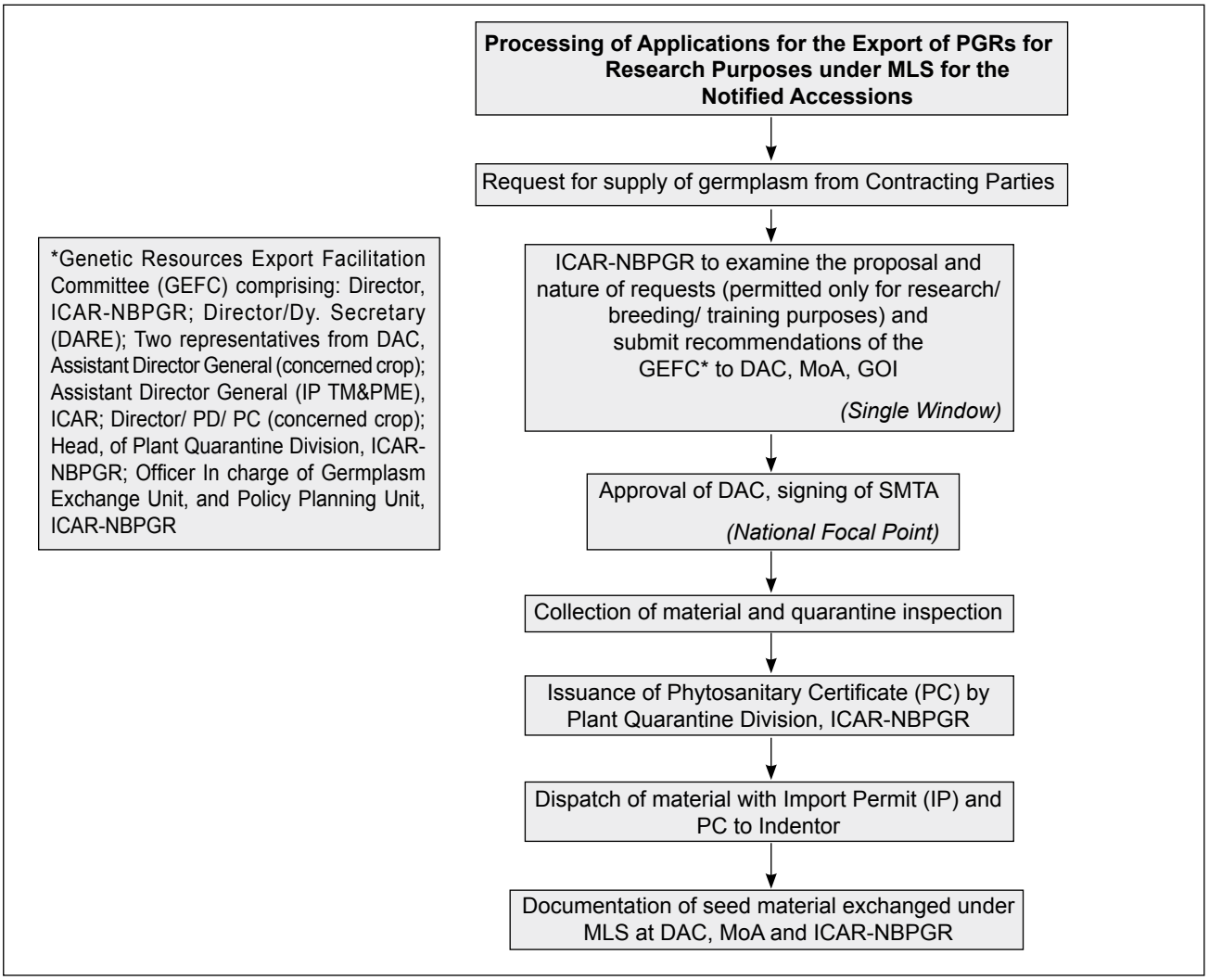

Fig. 1

such transfer of PGRFA. The following are the major categories of accessing PGRFA:

- Access to crops listed in Annex 1 of the Treaty only
- Access to and from contracting parties only
- Access to and from CG Centers
- Access for the purpose of utilization and conservation for research, breeding and training for food and agriculture only
- Access to PGRFA held by CG Centers including those collected before 1993 referred to as "in trust" or "FAO designated material"
- Access with the terms and conditions of the SMTA
- Use of SMTA required for material accessed through SMTA to any third or subsequent user
- No Intellectual Property Rights (IPR) is to be granted on the material "in the form received"
- Transfer of any material accessed from MLS and received under SMTA to any third party after signing the SMTA

For example, as an obligation, ICRISAT a CG Institute based in India has the mandate to undertake export of germplasm of their mandate crops and can be categorized under these sub-heads for exporting germplasm to its collaborators as described in Fig. 2.

However, if IPR (patents) is sought on derivatives of the PGRFA accessed from India, permission from NBA would be mandatory, as the above mentioned notification

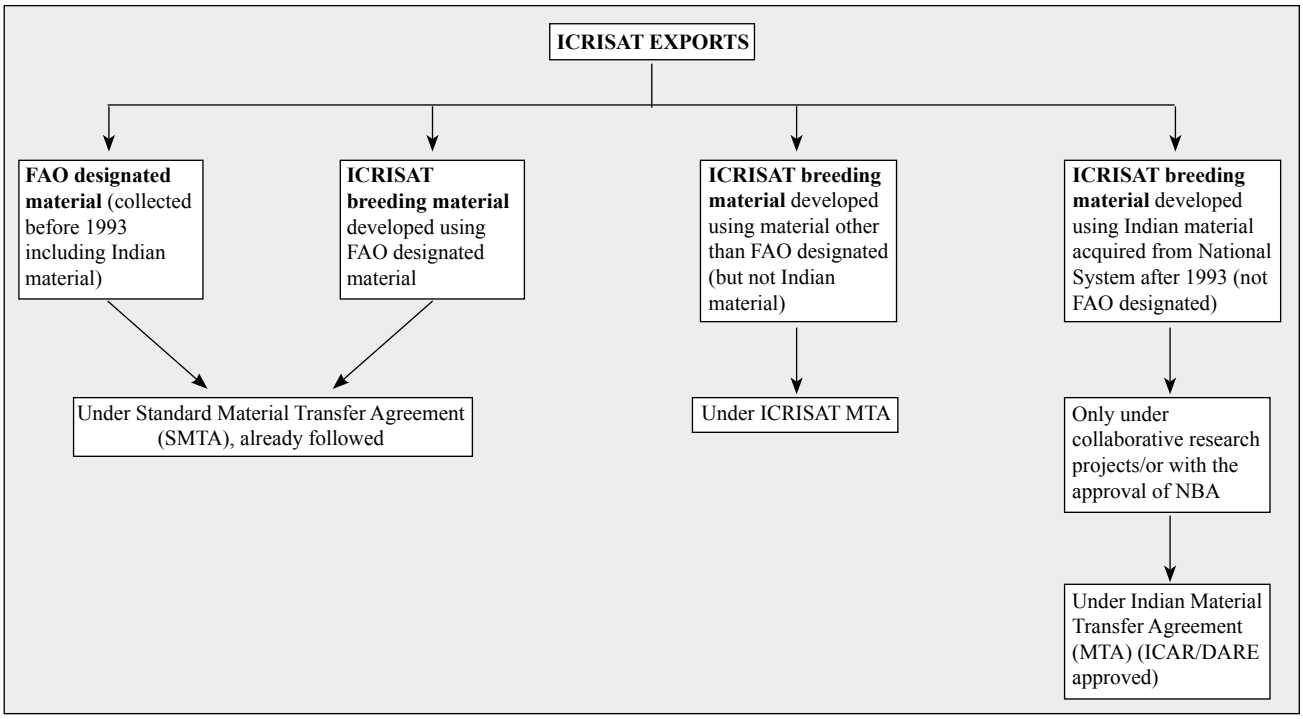

Fig. 2. Categories on material ICRISAT shares with its collaborators

provides exemption for access to PGRFA, only for Section 3 and 4 of the BDA, 2002 and not Section 6.

It may also be noted that India has also ratified the Nagoya Protocol (NP) on Access and Benefit Sharing (ABS) and is one of the countries already having domestic measures in place on ABS (http://www.cbd.int/abs/). The NP recalls and recognises the MLS of ABS established under the ITPGRFA in the context of poverty alleviation and climate change and acknowledges the fundamental role of Treaty and FAO Commission on Genetic Resources for Food and Agriculture in harmony with the CBD. The protocol provides a strong basis for greater legal certainty and transparency for both providers and users of genetic resources. However, some issues in the NP were not covered by BDA, 2002 such as user country measures. These also need to be put in place now.

Conclusions

After notification of the BDR, 2004, the application forms for access to biological resources and for seeking IPRs were put in place. It was felt that some issues were not addressed in the first set of rules notified through BDR, 2004. Researcher/institutions in India intending to send any biological material abroad were not able to do so under Section 5. Also, a cost of paying requisite fees was involved in transfer of material. Now, with the notification as discussed above any Indian researcher/ government institution which intends to carry/send the biological resources outside India to undertake basic research other than collaborative research referred as per section 5 of the Act, shall apply to the NBA. Further, Indian or non-Indian entities could access biological resources for traditional plant breeding and for other traditional practices of plant and animal improvement if the research is being carried out within India. Also, PGRFA, which are of utmost importance for food and nutritional security and sustainable agriculture may be exchanged as per the provisions of the Treaty and guidelines notified by Government of India, including those held in 'trust' by IARCs could be made available in accordance with the provisions of SMTA with the concurrence of the DAC, MoA, GOI the National Focal Point. This paper is an attempt to generate awareness on above issues.

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http://www.nbaindia.org/ home page National Biodiversity Authority (accessed on March 1, 2015) http://nbaindia.org/uploaded/pdf/Gazette_Notification_of_ABS_Guidlines.pdf) Notification for Guidelines on Access to Biological Resources and Associated Knowledge and Benefits Sharing Regulations, 2014 (accessed on March 1, 2015).

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http://www.planttreaty.org/home page ITPGRFA (accessed on March 1, 2015).

Office Memorandum No. 13-5/2013-SD-V, Department of Agriculture and Cooperation, Ministry of Agriculture, Government of India. Notification to facilitate exchange of Plant Genetic Resources under Multilateral System of International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA).

Annexure I

CROPS OF THE TREATY (ANNEX I)

Food crops (35)

Crop	Genus	Observations
Breadfruit	*Artocarpus*	Breadfruit only.
Asparagus	*Asparagus*	
Oat	*Avena*	
Beet	*Beta*	
Brassica complex	*Brassica* et al.	Genera included are: *Brassica, Armoracia, Barbarea, Camelina, Crambe, Diplotaxis, Eruca, Isatis, Lepidium, Raphanobrassica, Raphanus, Rorippa*, and *Sinapis*. This comprises oilseed and vegetable crops such as cabbage, rapeseed, mustard, cress, rocket, radish, and turnip. The species *Lepidium meyenii* (maca) is excluded.
Pigeonpea	*Cajanus*	
Chickpea	*Cicer*	
Citrus	*Citrus*	Genera *Poncirus* and *Fortunella* are included as root stock.
Coconut	*Cocos*	
Major aroids	*Colocasia, Xanthosoma*	Major aroids include taro, cocoyam, dasheen and tannia.
Carrot	*Daucus*	
Yams	*Dioscorea*	
Finger Millet	*Eleusine*	
Strawberry	*Fragaria*	
Sunflower	*Helianthus*	
Barley	*Hordeum*	
Sweet Potato	*Ipomoea*	
Grass pea	*Lathyrus*	
Lentil	*Lens*	
Apple	*Malus*	
Cassava	*Manihot*	*Manihot esculenta* only.
Banana/Plantain	*Musa*	Except *Musa textilis*.

Contd.

Contd.

Crop	Genus	Observations
Rice	*Oryza*	
Pearl Millet	*Pennisetum*	
Beans	*Phaseolus*	Except *Phaseolus polyanthus*.
Pea	*Pisum*	
Rye	*Secale*	
Potato	*Solanum*	Section *tuberosa* included, except *Solanum phureja*.
Eggplant	*Solanum*	Section *melongena* included.
Sorghum	*Sorghum*	
Triticale	*Triticosecale*	
Wheat	*Triticum* et al.	Including *Agropyron, Elymus,* and *Secale*.
Faba Bean/Vetch	*Vicia*	
Cowpea *et al*.	*Vigna*	
Maize	*Zea*	Excluding *Zea perennis, Z. diploperennis*, and *Z. luxurians*.

Forages (29)

Genera	Species
Legume Forages	
Astragalus	*chinensis, cicer, arenarius*
Canavalia	*ensiformis*
Coronilla	*varia*
Hedysarum	*coronarium*
Lathyrus	*cicera, ciliolatus, hirsutus, ochrus, odoratus, sativus*
Lespedeza	*cuneata, striata, stipulacea*
Lotus	*corniculatus, subbiflorus, uliginosus*
Lupinus	*albus, angustifolius, luteus*
Medicago	*arborea, falcata, sativa, scutellata, rigidula, truncatula*
Melilotus	*albus, officinalis*
Onobrychis	*viciifolia*
Ornithopus	*sativus*
Prosopis	*affinis, alba, chilensis, nigra, pallida*
Pueraria	*phaseoloides*
Trifolium	*alexandrinum, alpestre, ambiguum, angustifolium, arvense, agrocicerum, hybridum, incarnatum, pratense, repens, resupinatum, rueppellianum, semipilosum, subterraneum, vesiculosum*
Grass Forages	
Andropogon	*gayanus*
Agropyron	*cristatum, desertorum*
Agrostis	*stolonifera, tenuis*
Alopecurus	*pratensis*
Arrhenatherum	*elatius*
Dactylis	*glomerata*
Festuca	*arundinacea, gigantea, heterophylla, ovina, pratensis, rubra*
Lolium	*hybridum, multiflorum, perenne, rigidum, temulentum*
Phalaris	*aquatica, arundinacea*
Phleum	*pratense*
Poa	*alpina, annua, pratensis*
Tripsacum	*laxum*
Other Forages	
Atriplex	*halimus, nummularia*
Salsola	*vermiculata*

Annexure II

MINISTRY OF ENVIRONMENT, FORESTS AND CLIMATE CHANGE
(National Biodiversity Authority)
NOTIFICATION
New Delhi, the 21st November, 2014

G.S.R 827.—In exercise of the powers conferred by section 64 read with sub-section (1) of section 18 and sub-section (4) of section 21 of the Biological Diversity Act, 2002 (18 of 2003), hereinafter referred to as the Act, and in pursuance of the Nagoya Protocol on access to genetic resources and the fair and equitable sharing of benefits arising from their utilization to the Convention on Biological Diversity dated the 29th October, 2010, the National Biodiversity Authority hereby makes the following regulations, namely-

13. Conducting of non-commercial research or research for emergency purposes outside India by Indian researchers/ Government institutions.-

(1) Any Indian researcher/ Government institution who intends to carry/ send the biological resources outside India to undertake basic research other than collaborative research referred to in section 5 of the Act shall apply to the NBA in Form 'B' annexed to these regulations.

(2) Any Government Institution which intend to send biological resources to carry out certain urgent studies to avert emergencies like epidemics, etc., shall apply in Form 'B' annexed to these regulations.

(3) The NBA shall, on being satisfied with the application under sub-regulation (1) or sub-regulation (2), accord its approval within a period of 45 days from the date of receipt of the application.

(4) On receipt of approval of the NBA under sub-regulation (3), the applicant shall deposit voucher specimens in the designated national repositories before carrying sending the biological resources outside India and a copy of proof of such deposits shall be endorsed to NBA.

17. Certain activities or persons exempted from approval of NBA or SBB –

The following activities or persons shall not require approval of the NBA or SBB, namely:--

(a) Indian citizens or entities accessing biological resources and/ or associated knowledge, occurring in or obtained from India, for the purposes of research or bio-survey and bio-utilization for research in India;

(b) collaborative research projects, involving the transfer or exchange of biological resources or related information, if such collaborative research projects have been approved by the concerned Ministry or Department of the State or Central Government and conform to the policy guidelines issued by the Central Government for such collaborative research projects;

(c) local people and communities of the area, including growers and cultivators of biological resources, and vaids and hakims, practising indigenous medicine, except for obtaining intellectual property rights;

(d) accessing biological resources for conventional breeding or traditional practices in use in any agriculture, horticulture, poultry, dairy farming, animal husbandry or bee keeping, in India;

(e) publication of research papers or dissemination of knowledge, in any seminar or workshop, if such publication is in conformity with the guidelines issued by the Central Government from time to time;

(f) accessing value added products, which are products containing portions or extracts of plants and animals in unrecognizable and physically inseparable form; and

(g) biological resources, normally traded as commodities notified by the Central Government under section 40 of the Act.

Annexure III

MINISTRY OF ENVIRONMENT, FORESTS AND CLIMATE CHANGE
NOTIFICATION
New Delhi, the 17th December, 2014

S.O. 3232(E).—Whereas, India is a party to the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) having signed and ratified the said treaty on 10th June, 2002;

and Whereas, the objectives of the ITPGRFA are conservation and sustainable use of plant genetic resources for food and agriculture and fair and equitable sharing of the benefits arising out of their use, in harmony with the Convention on Biological Diversity, for sustainable agriculture and food security;

and Whereas, article 12 of the ITPGRFA provides for facilitated access to plant genetic resources for food and agriculture under the Multilateral System by the contracting parties; and Whereas, the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits arising from their Utilization to the Convention on Biological Diversity dated the 29th October, 2010 is the instrument for implementation of access for benefit sharing provisions of the Convention on Biological Diversity;

and Whereas, article 4 of the said Nagoya Protocjol provides that the protocol does not apply for the party or parties to the specialized instrument in respect of the specific genetic resource covered by and for the purpose of the specialized instrument;

and Whereas, Section 40 of the Biological Diversity Act, 2002 (18 of 2003) empowers the Central Government to exempt certain biological resources from the provisions of the said Act.

Now, therefore, in exercise of the powers conferred by section 40 of the Biological Diversity Act, 2002 (hereinafter referred to as the said Act), and in fulfilment of the obligations of the Government of India to the ITPGRFA for providing facilitated access to the plant genetic resources for food and agriculture, the Central Government, in consultation with the National Biodiversity Authority, hereby declares that the Department of Agriculture and Cooperation may, from time to time specify such crops as it considers necessary from amongst the crops listed in the Annex I of the ITPGRFA, being food crops and forages covered under the Multilateral System thereof, and accordingly exempts them from Section 3 and 4 of the said Act, for the purpose of utilization and conservation for research, breeding and training for food and agriculture: Provided that such purposes shall not include chemical, pharmaceutical and/or other non-food or feed industrial uses. 2. The Department of Agriculture and Cooperation shall keep the National Biodiversity Authority informed of all crops as may be specified by it from time to time, for providing access to plant genetic resources for food and agriculture under the ITPGRFA for the purposes aforesaid.

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SHORT COMMUNICATION

Fingerprinting Based on Microsatellite Markers for the Identification of Rice Varieties in Chhattisgarh

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Molecular markers are useful tools for determining cultivar identity. The purpose of this study to establish fingerprints of four rice varieties in Chhattisgarh. Microsatellite combines several features of an ultimate molecular marker and they are being used increasingly in various plant genetic studies and applications. The varieties were evaluated utilizing 115 microsatellite markers distributed over the whole rice genome. A total of 160 alleles were detected using 24 microsatellite primer-pairs, and the number of alleles/marker ranged from 2 to 4 with an average of 2.95 alleles/locus. The result suggested that a relatively rapid and small number of microsatellite markers could be used for the identification of rice varieties.

Key Words: DNA Fingerprinting, Markers Rice, Microsatellite, Variety identification

Rice, *Oryza sativa* (2n = 24) belonging to the family *Graminae* and subfamily *Oryzoidea* is the staple food for one-third of the world's population and occupies almost one-fifth of the total land area covered under cereals. It is grown under diverse cultural conditions and over wide geographical range. Most of the world's rice is cultivated and consumed in Asia, which constitutes more than half of the global population. High-quality seeds and elite cultivars play a crucial role in its production. However, since new cultivars normally arise from hybridizations between members of an elite group of genetically similar parents, the amount of genetic variability among newly developed cultivars is likely to become even smaller (Rahman *et al*., 2009), which makes it more difficult to distinguish one cultivar from other by visual observation, but keeping track of many commercial inbreeds, hybrid varieties and landraces makes the task dauntingly inefficient. Fingerprinting with molecular markers allows precise, objective and rapid cultivar identification, which has been proved to be an efficient tool for crop germplasm characterization, collection and management. Simple sequence repeat (SSR) markers have been widely used for genetic analysis and cultivar identification because of their abundance, co-dominance inheritance, high polymorphism, reproducibility, and ease of assay by polymerase chain reaction (PCR) (Kuleung *et al*., 2004; Xie *et al*., 2011). Therefore, it has been applied widely in the identification, registration of plant variety, and in monitoring of the seed purity and the authenticity with high accuracy, high reliability and low cost. The usefulness of DNA fingerprinting for cultivar identification in rice was first demonstrated by Dallas (1988). Establishing the identity of crop varieties has assumed greater importance for protecting plant breeders and farmers rights in the post-CBD scenario particularly in the developing countries. This investigation is conducted to fingerprint the four main commercial rice cultivar under cultivation now in Chhattisgarh region based on SSR markers.

The nucleus seed of four released rice varieties from Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, namely, Karmamasuri, Danteshwari, Samleshwari and Mahamaya were taken for the present study for developing DNA fingerprinting.

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DNA of five plants from nucleus seed of four varieties was used for molecular studies. DNA was isolated by mini prep method (Doyel and Doyel 1990) quantified using nanodrop (*NANODROP 2000c,* Thermo Fisher Scientific, Wilmington, USA) and diluted appropriately to working solution of 20 ng/µl.

For the development of DNA based fingerprinting of each of four varieties, 115 rice microsatellite primer pairs (http://www.gramene.org/) were used in the analysis. PCR reactions were performed in a volume of 20 µl. Amplification protocol consisted of an initial denaturation at 95°C for 5 min, followed by 34 cycles of 94°C for 1 m, annealing for 1 m at 55°C, 72°C for 1 min and a final extension step of 72°C for 7 min. was carried out with the established program in thermal cycler (AB applied Biosystem/Verti 96 well thermal cycler). After PCR amplification the amplicons were electrophoresed in five percent polyacrylamide gels for 1 hours at 120 volts. The gel was then stained with ethidium bromide (Sambrook *et al.,* 1989) and visualised in a gel documentation system (make Bio-RAD/gel dox^{TM} XR+, Bio-Rad Laboratories, Inc., USA)

The size (in nucleotides) of the most intensely amplified band for each microsatellite marker was determined based on its migration relative to the molecular weight (mw) size markers, 50bp DNA ladder (GENEI Pvt. Ltd. Bangalore, India) and the polymorphism information content (PIC) was calculated according to formula

$$PIC = 1-\Sigma P_i^2$$

Where P_i is the allele frequency for the i-th allele (Nei, 1973).

$$\text{Per cent polymorphism} = \frac{\text{Number of polymorphic bands}}{\text{Total number of bands}} \times 100$$

Molecular marker data were recorded from gels upon band size classification and expressed in binary code. Cluster analysis was conducted on similarity estimates, by using Unweighted pair group method on arithmetic averages (UPGMA). The comparison of similarity matrices of different markers was made by MAXCOMP module of NTSYSpc.

A total of 115 microsatellite primer-pairs distributed across the genome throughout the 12 chromosomes were used for fingerprinting of four rice varieties, out of which only 24 SSR primers were found to be polymorphic. A total of 71 alleles were obtained using these 24 polymorphic SSR primers with an average of 2.95 alleles per primer. The number of alleles amplified for each primer ranged from two to four. The PIC for

Table 1. Size and frequency of alleles at twenty four microsatellite loci in four rice varieties released in Chhattisgarh

Locus	Number of alleles	Allele size (bp)	Allele frequency	Gene diversity (PIC = 1-ΣX_i^2)	Location on chromosome	Primer sequence (5' to 3')
RM 55	3	240	0.25	0.625	3	TCCCGGTTATTTTAAGGCG
		245	0.25			CCGTCGCCGTAGTAGAGAAG
		300	0.50			
RM 169	4	170	0.25	0.75	5	TCCCGTTGCCGTTCATCCCTCC
		175	0.25			TGGCTGGCTCCGTGGGTAGCTG
		195	0.25			
		305	0.25			
RM 164	4	253	0.25	0.75	5	GCAGCCCTAATGCTACAATTCTTC
		260	0.25			TCTTGCCCGTCACTGCAGATATCC
		275	0.25			
		290	0.25			
RM 204	3	105	0.50	0.625	6	GTGACTGACTTGGTCATAGGG
		110	0.25			GCTAGCCATGCTCTCGTACC
		120	0.25			
RM 211	2	150	0.75	0.375	2	CCGATCTCATCAACCAACTG
		152	0.25			CTTCACGAGGATCTCAAAGG
RM 85	3	100	0.25	0.625	3	GCACAAGGTGAGCAGTCC
		115	0.25			CCAAAGATGAAACCTGGATTG
		125	0.50			
RM 418	3	310	0.50	0.625	7	GAGCACATATGCCACGTACG
		320	0.25			TCGCGTATCGTCATGCATAG
		340	0.25			

Locus	Number of alleles	Allele size (bp)	Allele frequency	Gene diversity (PIC = 1-ΣX_i^2)	Location on chromosome	Primer sequence (5' to 3')
RM 13	4	135	0.25	0.75	5	GGTGGCATTCGATTCCAG
		140	0.25			TCCAACATGGCAAGAGAGAG
		145	0.25			
		160	0.25			
RM 1	2	80	80	0.375	1	GCGAAAACACAATGCAAAAA
		120	120			GCGTTGGTTGGACCTGAC
RM 206	3	130	0.25	0.625	11	CCCATGCGTTTAACTATTCT
		155	0.50			CGTTCCATCGATCCGTATGG
		160	0.25			
RM 72	4	170	0.25	0.75	8	GCATCGGTCCTAACTAAGGG
		185	0.25			CCGGCGATAAAACAATGAG
		195	0.25			
			0.25			
RM 332	3	170	0.25	0.625	11	GCGAAGGCGAAGGTGAAG
		185	0.25			CATGAGTGATCTCACTCACCC
		195	0.50			
RM 19	4	230	0.25	0.75	12	CAAAAACAGAGCAGATGAC
		245	0.25			CTCAAGATGGACGCCAAGA
		250	0.25			
		253	0.25			
RM 247	2	145	0.50	0.375	12	CATATGGTTTTGACAAAGCG
		150	0.50			TAGTGCCGATCGATGTAACG
RM 21	3	140	0.25	0.625	11	ACAGTATTCCGTAGGCACGG
		155	0.25			GCTCCATGAGGGTGGTAGAG
		175	0.50			
RM 202	3	120	0.5	0.625	11	CCAGCAAGCATGTCAATGTA
		125	0.25			CAGATTGGAGATGAAGTCCTCC
		130	0.25			
RM 254	2	115	0.25	0.375		
		125	0.75			
RM 474	3	230	0.50	0.625	10	TATGAGCTGGTGAGCAATGG
		250	0.25			AAGATGTACGGGTGGCATTC
		255	0.25			
RM 432	4	175	0.25	0.75	7	TTC TGT CTC ACG CTG GAT TG
		180	0.25			AGC TGC GTA CGT GAT GAA TG
		190	0.25			
		350	0.25			
RM 484	3	148	0.25	0.625	10	TGCTGCCCTCTCTCTCTCTC
		155	0.25			TCTCCCTCCTCACCATTGTC
		160	0.50			
RM 152	2	140	0.25	0.375	8	CCGTAGACCTTCTTGAAGTAG
		155	0.75			GAAACCACCACACCTCACC G
RM 144	3	225	0.25	0.625	11	GCTAGAGGAGATCAGATGGTAGTGCATG
		245	0.5			TGCCCTGGCGCAAATTTGATCC
		255	0.25			
RM 303	3	200	0.5	0.625	4	GCATGGCCAAATATTAAAGG
		205	0.25			GGTTGGAAATAGAAGTTCGGT
		210	0.25			
RM 108	4	70	0.25	0.75	9	CGTGCACCACCACCACCACCAC
		75	0.25			TCTCTTGCGCGCACACTGGCAC
		80	0.25			
		90	0.25			

these primers ranged from 0.37 to 0.75 (Table 1). Of the twenty four microsatellite markers seven microsatellite markers *viz.,* RM169, RM164, RM13, RM19, RM 108, RM 72 and RM 432 differentiated all the four varieties at least with a single marker allele difference.

Allele sizing technologies are well established and can be readily used to size microsatellite alleles from any organism (Song *et al.,* 1999). SSR genotypic data from a number of loci have the potential to provide unique allelic profiles or DNA fingerprints for precisely establishing genotypic identity. Comparisons between SSR band positions against each marker in this study are shown in Table 2. The band patterns corresponding to individual variety help to recognize the variety in question. When one primer would not distinguish individual variety from others, another primer should be considered

Table 2. Analysis of band positions due to microsatellite primers for four rice varieties

Varieties	Band Positions Due to Primers (bp)																			
	RM 55			RM 169				RM 164				RM 204			RM 211	
	A	B	C	A	B	C	D	A	B	C	D	A	B	C	A	B
KARMAMASURI		245				195				275				120		152
DANTESHWARI	240			170				253				105			150	
SAMLESHWARI			300		175				260			105			150	
MAHAMAYA			300				305				290		110		150	

Varieties	Band Positions Due to Primers (bp)																					
	RM 85			RM 418			RM 13				RM 1		RM 206			RM 72				RM 332		
	A	B	C	A	B	C	A	B	C	D	A	B	A	B	C	A	B	C	D	A	B	C
KM	100					340			145		80		130			98				170		
DN		115		310			135					120			160				160			195
SM			125	310				140				120		155			145				185	
MH	100				320					160		120		155				150				195

Varieties	Band Positions Due to Primers (bp)																					
	RM 21			RM 202			RM 19				RM 247		RM 474			RM432				RM 484		
	A	B	C	A	B	C	A	B	C	D	A	B	A	B	C	A	B	C	D	A	B	C
KM		155				135				253	145		230						350		155	
DN	140			120				245				150		250		175				148		
SM			175	120			230				145				255		180					160
MH			175		125				250			150	230					190				160

Varieties	Band Positions Due to Primers (bp)																		
	RM 144			RM 303			RM 254		RM 152		RM108			
	A	B	C	A	B	C	A	B	A	B	A	B	C	D
KM	225				205			125		155	70			
DN		245		200			115		140					90
SM		245				210		125		155			80	
MH			255	200				125		155		75		

and sometimes, combination of more than one primer should be taken into account. Thus, additional primer or set of primers might be needed to test or identify all the expected varieties. In the present study four rice varieties were discriminated successfully and it shows 100 per cent polymorphism by the seven SSR markers namely, RM169, RM164, RM13, RM19, RM 108, RM72 and RM 432, respectively. Twenty-four primers on an average produced 96 bands across the four varieties and out of which, 71 were polymorphic accounted for high level of per cent polymorphism (73.95%). Microsatellite DNA markers based on simple sequence repeats (SSRs) as amplified by PCR have been used successfully as tools for varietal identification (Yang *et al*., 1994; Rongwen *et al*., 1995). DNA based molecular markers have proven to be a powerful tool in identification of genetic variation and in the elucidation of genetic relationships within and among species, characterized by abundance and untouched by environmental influence (Powell *et al*., 1996). Several workers have also demonstrated the usefulness of SSR markers in determining the relationship between closely related genotypes (Ravi *et al*., 2003; Ganeshram *et al*., 2007).

Cluster I consisted of variety namely Karmamahsuri having 40.5 percent whereas, Cluster II consisted of Danteshwari, Samleshwari and Mahamaya having 50.7 percent similarity among them. Cluster II again partitioned into two sub-clusters in which one sub-cluster had Danteshwari and Samleshwari with 58 percent similarity, whereas another sub cluster had Mahamaya with 50.7 percent similarity with Danteshwari and Samleshwari. Thus, microsatellite markers provided more definitive separation of clusters, indicating a higher level of efficiency for determining the relationship between closely related genotypes.

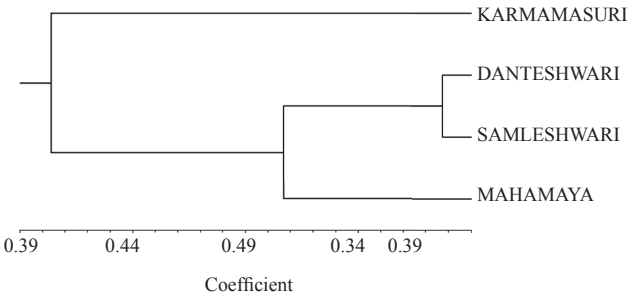

Fig. 1. Dendrogram of rice varieties based on microsatellite markers

In this study, an elementary DNA fingerprinting database of the four main commercial rice cultivars under cultivation in Chhattisgarh region was built using 24 SSR primer-pairs, which could be expanded as the number of additional cultivars and molecular markers (systems) increase. Dendrogram of SSR markers divided the four cultivars into two major clusters. It suggests that SSR markers were efficient to generate locus specific allelic information which can serve as molecular IDs for four rice varieties namely, Karmamasuri, Danteshwari, Samleshwari and Mahamaya.

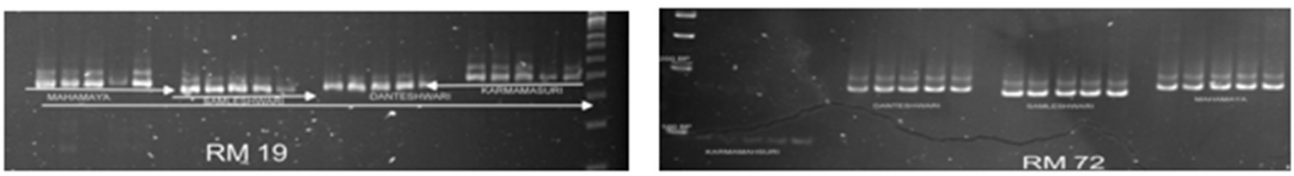

Fig. 2. DNA profile of four rice varieties obtained through microsatellite markers

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SHORT COMMUNICATION

"*Tikdi*" – A Fruit Fly Resistant Land Race of Ber (*Ziziphus mauritiana* Lamarck)

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"*Tikdi*"– a land race of ber collected from Rajasthan has shown strong resistance to fruit fly infestation, high tolerance to drought and resistance to frost and owing to these traits it is used as a root stock for other commercial varieties of ber. Its fruits are preferred by affluent people and sold at higher prices as fruits are free from larva of fruit fly and their excreta and dehydrated fruits can be stored for more than six months. The upright growth habit of tree of Tikdi enables it suitable for agro-forestry. Full grown up tree of Tikdi produce higher leaf fodder to feed livestock.

Key Words: Ber, Fruit fly, Genetic resources

The Indian *ber* (*Ziziphus mauritiana* L) and Chinese *ber* (*Ziziphus jujube* Mill) are two domesticated species, which are cultivated to vast areas of old world (Liu, 2006) and adapted to hot arid conditions. The *Ziziphus mauritiana* (L.) is cultivated on a wide range of soils from gravelly, shallow soils to deep aridisols and to some extent on entisols (Pareek, 1983). *Ber* trees can withstand high temperature and can be grown in regions reaching temperature of even upto 42°C. Although, ber tree can tolerate temperature as high as 50°C but, fruit set is adversely affected at temperature above 35°C.

Ber is considered to be multi-use tree and commonly used for live fencing and to control soil erosion. Due to the high dry weight protein content, leaves are an important feed source of protein for animals (Arndt and Kayser, 2001). Leaves of ber can be used to feed silkworms and lac insects; flower are a source of nector for honeybees.

The use of the fruits is the major focus of interest. The pulp of fruit is most important in relation to its nutritional value. The content of pulp in fruit is cultivar specific and ranges from 81 to 92% (Pareek, 1983). Ber is richer than apple in protein, phosphorus, calcium, carotene and vitamin C and oranges in phosphorus, iron, vitamin C and carbohydrates and exceeds them in calorific value. Ripe fruits provide 20.9 Kcalories per 100 g of pulp (Singh *et al.*, 1973). The amino acids, asparagine, aspartic acid, glycine, glutamic acid, serine and threonine are found in the pulp. Ber has been reported as an immune stimulant, anti-biotic, anti-nephritic, anti-ulcer, anti-diabetic, anti-inflammatory and anti-oxidant (Ali *et al*., 2006).

The productivity and quality of ber fruits are adversely affected by a number of insect pests like fruit fly, stone weevil, fruit borer, bark eating caterpillars and hairy caterpillars. The fruit fly (*Carpomyia vesuviana*), considered the most serious pest of ber has been observed to damage up to 80% of the crop under severe damage (Cherian and Sunderam, 1941). Although, these insects can be controlled by applying insecticides on the crop (Gyi *et al*., 2003), inbuilt genetic resistance offers better option to control the incidence of the insects. The infestation starts with the fruit setting. The adult female lays eggs singly by inserting its ovipositor in the young developing fruit. After 2 to 5 days the larvae hatch, start feeding on the pulp and make galleries in it. Generally, only one larva is found in one fruit. The excreta of the larva accumulates in the galleries, results in rotting of the fruit. Infested fruits become deformed and their growth becomes stunted. A large number of such fruits drop off. The larval stage lasts 9 to 12 days. Full grown (6 mm length) larva finds its way out by making a hole in the fruit skin and drops to the ground. The larva bores down into the soil upto the depth of 2 to 12 cm where

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it pupates and occasionally pupation takes place within infested fruits (Bagdavadze *et al*., 1977). The pupal period lasts about 2 weeks after which the adult fly (5 to 8 mm long and 3 mm broad) emerges. Pairing and oviposition occur during day light and at night, fly usually rests in the canopy and it completes two generations per year (Berdyeva, 1978).

At Jodhpur Regional Station of National Bureau of Plant Genetic Resources, the 57 live trees of wild, land races and cultivated varieties are maintained in the field genebank. A wide range of variation for vegetative, leaf, floral fruit and quality traits has been observed (un-published data). Traits specific pooled values of three replications over two years of some of the selected cultivars of ber has been recorded for fruit and seed characters (Table 1).

Data were recorded on infestation of fruit fly on the selected cultivars at the interval of 10 days in three trees during 2012-13 and 2013-14. In all cases, 10 randomly selected fruits were examined carefully for occurrence of hole in the fruits then all fruits were peeled, with knife, to confirm the stone and fruit fly damage and percentage of infested fruits was calculated. The TSS of these fruits was also recorded (Table 2 & 3).

From Table 2 & 3 it is evident that a large genetic variation is present among cultivars for fruit fly resistance and TSS concentration. "*Tikdi*" the land race of ber that had been collected and planted by Shri DP Chopra, Economic Botanist, at NBBPGR, Regional Station, Jodhpur, on 28.06.1968 had shown absolute resistance to fruit fly. It also appears from the table that concentration of TSS in the ber fruits is not having any impact on

Table 1. Pooled value of three trees for two years on selected cultivars for fruit and stone traits

Cultivar	Fruit Shape	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (gm)	Stone weight (gm)	Stone length (cm.)	Stone diameter (cm)	Pulp weight (gm)
Pemily	Oblong	3.38	2.54	12.24	0.89	2.16	0.92	11.35
Illaychi	Round	1.68	1.68	2.83	0.25	1.18	0.62	2.58
Tikdi	Long	1.94	1.40	1.90	0.32	1.72	0.92	1.47
Seb (hard)	Oblong	3.10	2.94	17.53	1.36	1.98	1.10	16.17
Seb (soft)	Round	2.60	2.36	7.77	0.73	1.70	0.98	7.04
Mundia	Long	3.30	2.36	9.71	0.78	2.26	0.88	8.93
Gola	Round	2.60	2.42	8.15	0.87	1.78	1.04	7.28
Gola (Kakwan)	Round	2.52	2.52	9.94	0.83	1.68	1.02	9.11
Aliganj	Round	2.68	2.10	6.69	0.83	1.74	0.98	5.86
Gola (Delhi)	Oblong	2.42	2.32	7.82	0.92	1.72	1.04	6.90
Umran	long	3.52	2.84	15.62	0.98	2.20	0.92	14.64

Table 2. Infestation (%) by fruit fly and TSS of fruits of selected cultivars during 2013-14

Cultivars	Dec. 30, 2014		Jan.10, 2014		Jan. 20, 2014		Jan 30, 2014		Feb.10, 2014	
	Inf. (%)	TSS	Inf. (%)	TSS	Inf. (%)	TSS	Inf. (%)	TSS	Inf. (%)	TSS
Gola	80	13.6	60	15.4	50	15.8	60	22.0	50	24.4
Gola (Delhi)	40	13.2	40	13.8	50	14.2	20	24.2	30	23.8
Gola (Kakwan)	90	17.0	80	19.0	60	19.6	40	21.0	60	23.2
Seb (soft)	60	15.0	60	15.0	40	17.0	10	17.4	20	19.8
Seb (Hard)	20	17.4	40	21.0	30	20.8	20	24.0	20	25.0
Pevandi	30	18.2	30	18.8	40	19.0	30	19.4	40	21.6
Umran	40	14.4	10	17.2	20	17.8	30	20.2	20	21.4
Aliganj	90	18.0	70	19.0	60	19.4	60	19.8	50	20.8
Pemily	50	14.0	20	14.0	30	15.4	60	18.4	40	20.2
Chhuhara	40	13.0	20	14.2	30	16.4	40	16.4	40	19.2
Tikdi	0	14.2	0	14.6	0	15.8	0	19.6	0	22.4
Mundia	50	13.8	30	14.0	40	14.2	20	14.6	30	16.8

Table 3. Infestation (%) by fruit fly and TSS of fruits of selected cultivars during 2012-13

Cultivars	Dec. 27, 2012		Jan.05, 2013		Jan. 16, 2013		Jan 28, 2013		Feb.06, 2013	
	Inf.(%)	TSS	Inf.(%)	TSS	Inf.(%)	TSS	Inf.(%)	TSS	Inf.(%)	TSS
Gola	60	14.5	70	16.6	50	16.0	60	22.6	60	25.3
Gola (Delhi)	50	13.9	60	14.3	60	15.4	30	24.5	30	23.5
Gola(Kakwan)	70	17.7	80	18.2	70	19.0	50	20.8	50	23.8
Seb (soft)	70	14.8	50	14.5	50	18.7	30	18.4	30	20.7
Seb(Hard)	40	16.2	50	22.0	30	22.1	40	24.7	20	24.8
Pevandi	50	18.6	30	19.3	30	19.6	40	18.3	30	22.1
Umran	60	15.1	30	17.8	30	18.7	20	20.0	10	21.9
Aliganj	100	16.9	80	18.5	50	19.0	50	18.8	60	22.0
Pemily	30	14.5	10	14.4	30	17.5	60	19.6	30	20.0
Chhuhara	40	12.5	40	15.8	30	17.6	40	17.6	50	18.9
Tikdi	0	15.1	0	14.9	0	16.8	0	18.9	0	23.0
Mundia	30	14.6	40	13.7	50	15.4	30	15.4	40	17.3

resistance or susceptibility for fruit fly. On the basis of experience and ITK information on selected cultivars for drought and frost tolerance, shelf life, taste etc. has been compiled (Table 4).

The fruits of *Tikdi* rarely contain insect larva and their excreta. Its shelf life is more than six months and can be dried and store even for longer time. Because of its better quality, fruits of *Tikdi* are sold at higher price than others. The grown plants of *Tikdi* are highly tolerant to drought and resistant to frost. Owing to these qualities it is used as a root stock for other commercial varieties of *ber*. Trees are vigorous with upright growth habit and have higher leaf fodder production potential

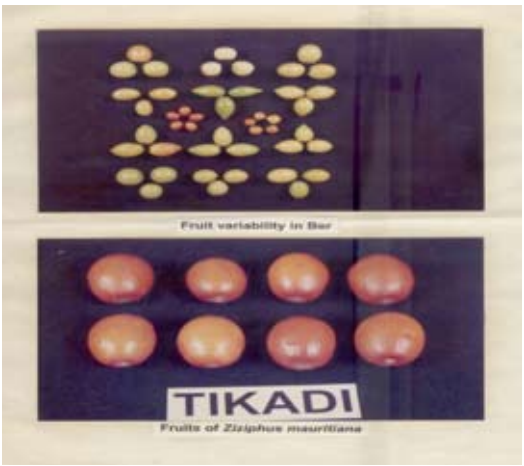

Fig. 1. Fruits of *Tikdi* land race of ber

Table 4. Useful traits of Tikdi on the basis of experience and ITK

Cultivars	Drought tolerance	Tolerance to frost	Used as root stock	Shelf life of fruit	Taste	Market Price of 2013-14 Rs./Kg
Gola	Moderate	Susceptible	No	3-5 days	Sweet	30-40
Gola (Delhi)	Moderate	Susceptible	No	3-5 days	Sweet	30-40
Gola (Kakwan)	Moderate	Susceptible	No	3-5 days	Sweet	30-50
Seb (soft)	Moderate	Susceptible	No	3-5 days	Sweet	40-50
Seb(Hard)	Moderate	Susceptible	No	5-7 days	Sweet	40-50
Pevandi	Moderate	Susceptible	No	3-5 days	Sweet	25-40
Umran	Moderate	Susceptible	No	5-10 days	Sweet	40-60
Aliganj	Moderate	Susceptible	No	3-5 days	Sweet	40-60
Pemily	Moderate	Susceptible	No	3-5 days	Sweet	20-40
Chhuhara	Moderate	Susceptible	No	3-5 days	Sweet	20-30
Tikdi	High	Resistant	Yes	6 months or more (dehydrated)	Sweet	60-80
Mundia	Moderate	Susceptible	No	3-5 days	Sweet	20-30

to feed livestock and camels. The upright growth habit of tree enables it for agro-forestry.

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SHORT COMMUNICATION

Screening of *Coffea arabica* Germplasm for Caffeine Level

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A total of 76 collections of coffee bean (*Coffea arabica*) are being maintained in the germplasm bank at Coffee Research Sub Station in North Kodagu, Karnataka, India. Following evaluation of caffeine level in 34 collections, a wide variability ranging from 1.18% (*Misan Taferikala*) to 2.07% (*Sumatra*) with an overall mean value of 1.84%, was observed.

Key Words: Caffeine, *Coffea arabica*, Germplasm bank

Coffee is a popular beverage consumed worldwide. Although more than 80 coffee species have been identified worldwide, only two species *viz*., *Coffea arabica* (arabica coffee) and *C. canephora* (robusta coffee) are economically important. India grows both arabica and robusta coffee almost in equal proportions mainly in the southern states of Karnataka, Kerala and Tamil Nadu covering 4 lakh ha. The annual production is around 3.1 lakh MT with 4.5% share in global production. Regarding processing methods, 75% of arabica coffee is processed by wet method and 80 to 85% of the robusta produce is processed by dry method. In wet method, only ripe fruits are harvested and pulped by passing through a pulping machine to remove the fruit skin. Later, the pulped bean along with mucilage is kept overnight for natural fermentation and then the beans are washed with water. The washed beans are soaked in water for four to six h and then sun dried for 6 or 7 days by spreading them evenly on drying yards. In certain cases, the pulped beans with the mucilage are immediately passed through aqua washers to remove mucilage by friction and thus skipping the natural fermentation step. The coffee thus prepared is called parchment coffee. In dry method, the ripened or un-ripened mature green fruits are sun dried for 12 to 15 days on drying yards. Coffee obtained by this method is called cherry coffee which is inferior in quality to parchment and fetches less price (Anonymous, 2000).

Arabica and robusta coffee have different chemical composition including the caffeine level. The stimulating effect of coffee, one of the most popular beverages of the world, is due to caffeine (1, 3, 7- trimethylxanthine). It is an alkaloid synthesized from purines and is found in coffee seeds. Caffeine-containing beverages are popular due to their effect on decreasing fatigue and increasing mental acuity following their intake in moderation. However, several medical conditions including hypertension and arrhythmias call for medical professionals to recommend caffeine-less (or) caffeine-free diets. In an effort to abstain from caffeine, many people substitute decaffeinated coffee in place of caffeinated coffee. Over the years, there has been an increasing demand for decaffeinated coffee and currently, it accounts for 10% of total coffee consumption (Silvarolla *et al*., 2004; Mazzafera *et al*., 2009).

There are problems associated with the artificial decaffeination methods and hence development of varieties with low caffeine is the best option. However, breeding for low caffeine requires variability for caffeine either in cultivated or in wild species. With an increasing interest of consumers for low caffeine coffee, there is a need to extensively evaluate the coffee germplasm available in the germplasm bank, established at Coffee Germplasm Research Sub Station (CRSS), North Kodagu, Karnataka for caffeine level as most of the collections

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are yet to be characterized for biochemical constituents. It was, therefore planned to screen all the 76 arabica collections in two phases. In the first phase, only 34 collections representing different origins were tested for caffeine levels. The most promising collection from this screening exercise can be exploited as a potential genetic stock in a commercial breeding programme for producing low caffeine level coffee beans.

Thirty four *C. arabica* collections having a designated accession number (Table 1) were analysed for caffeine level. These collections are part of exotic germplasm introduced from different parts of the world including the wild Ethiopian land races collected during an FAO-sponsored expedition to Ethiopia in 1964 (Narasimmaswamy, 1965). These collections were originally introduced in Central Coffee Research Institute (CCRI), Chikmagalur, Karnataka and from these, a sub collection was established at Coffee Research Sub Station (CRSS), North Kodagu in 1967. In CRSS, these collections were established in contiguous plot and each collection was planted in two continuous rows with 15 to 20 plants in each row. These arabica collections were maintained following the agronomic practices adopted at the estate level. The coffee samples for caffeine estimation were prepared during the harvest season of 2011-12.

Mature coffee fruits were handpicked from all the plants in each collection. From this, 12 kg of fruits were pulped, naturally fermented overnight, washed and dried under sun till it reached the desired moisture level of 10%. The raw coffee samples thus obtained were hulled to obtain the coffee beans. The coffee beans were cleaned to remove the defective beans and a representative sample

Table 1. Caffeine content of various progenies from *Coffea arabica* germplasm bank

S. No.	Source of material	Accession No.	Name of progeny	Caffeine content range	% dry basis Mean ± SD
1	Congo	S. 1502	Bourbon Mayagese	1.63 – 1.70	1.66 ± 0.05
2	Congo	S. 1504	Mysore	1.77 – 1.95	1.86 ± 0.13
3	Congo	S. 1695	Antigua	1.94 – 1.97	1.95 ± 0.02
4	Congo	S. 1698	Local Bronze de Mulungu	1.89 – 1.91	1.90 ± 0.01
5	Ethiopia	S. 1576	S. 26 Enneria	1.17 – 1.53	1.35 ± 0.25
6	France	S. 1659	Kouti	1.64 – 1.84	1.74 ± 0.14
7	France	S. 1661	Nkourgan	1.86 – 1.99	1.92 ± 0.09
8	France	S. 1662	Foumban	2.03 – 2.08	2.00 ± 0.04
9	France	S. 1663	Reunion	1.83 – 1.88	1.85 ± 0.04
10	France	S. 1667	Mazeron	1.81 – 1.82	1.81 ± 0.01
11	FAO, Ethiopia	S. 1497	S.12 Kaffa	1.58 – 1.86	1.73 ± 0.21
12	FAO, Ethiopia	S. 1768	Murta	1.82 – 2.00	1.91 ± 0.13
13	FAO, Ethiopia	S. 1783	Babaca Kaffa	1.29 – 1.48	1.38 ± 0.13
14	FAO, Ethiopia	S. 1784	Misan Taferikala	1.14 – 1.22	1.18 ± 0.06
15	FAO, Ethiopia	S. 1785	Ainamba Kaffa	1.93 – 2.00	1.96 ± 0.05
16	Guinea	S. 1656	Salvador	1.88 – 1.96	1.92 ± 0.06
17	Guatemala	S. 1467	Sumatra	2.06 – 2.09	2.07 ± 0.02
18	Guatemala	S. 1468	Surinam	1.94 – 2.03	1.98 ± 0.06
19	Guatemala	S. 1469	San Ramon	1.70 – 2.02	1.86 ± 0.23
20	Kenya	S. 1587	Rume Sudan	1.73 – 1.99	1.86 ± 0.18
21	Kenya	S. 1591	Dilla (Melville)	1.97 – 2.00	1.98 ± 0.02
22	Kenya	S. 1593	Gimma Galla Sidamo	1.77 – 2.06	1.91 ± 0.21
23	Maryland, USA	S. 1490	Bourbon Amarelho	1.87 – 1.91	1.89 ± 0.03
24	Maryland, USA	S. 1492	Caturra Amarelho	1.83 – 2.07	1.95 ± 0.17
25	Portugal	S. 2126	S6 Cioccie (113/1)	1.80 – 1.82	1.81 ± 0.01
26	Portugal	S. 2127	S6 Cioccie (113/2)	1.95 – 1.96	1.95 ± 0.01
27	Portugal	S. 2129	S4 Agaro (110/2)	1.97 – 1.98	1.97 ± 0.01
28	Portugal	S. 1582	S. 16 Wollamo	1.46 – 1.67	1.56 ± 0.15
29	Portugal	S. 1699	Mbrizi de Mulungu	2.01 – 2.02	2.01 ± 0.01
30	Portugal	S. 1726	Cundina Marca	1.94 – 2.03	1.98 ± 0.06
31	Tanzania	S. 1483	KP 423 Kents	2.04 – 2.08	2.06 ± 0.03
32	Tanzania	S. 1741	Burbok Sudan	1.75 – 1.80	1.77 ± 0.04
33	Tanzania	S. 1743	Geisha	1.79 – 1.88	1.83 ± 0.06
34	USDA, USA	S. 1494	Munda Nova	1.85 – 1.93	1.89 ± 0.06

of 100 g was drawn for both moisture and caffeine estimation. The moisture content in coffee beans was estimated by oven dry method adopting the procedure set out in the ISO 6673 (2003). The caffeine level in coffee beans was determined by high performance liquid chromatography following extraction detailed in ISO 20481 (2008). The caffeine level in coffee bean was expressed as percentage by mass (g/100g) on dry matter basis (% db). All the results were expressed as mean ± SD of three replications.

In the present study, 34 collections from the arabica germplasm bank were tested for caffeine level. The analytical data revealed that there were significant differences in the caffeine level among these collections ranging from 1.18% (*Misan Taferikala*) to 2.07% (*Sumatra*) with a mean caffeine content of 1.84% (Table 1).

Similar to the present study, Silvarolla *et al*. (2000) also analyzed 99 arabica collections conserved in the germplasm bank, at the experimental center of Instituto Agronômico de Campinas in Brazil, for caffeine level. The results indicated that the caffeine level ranged between 0.46 and 2.82% (mean 1.18%) in 68 collections from Kaffa region, and it was between 0.42 and 2.90% (mean 1.10%) in 22 collections from Illubabor region. The caffeine content in five collections from Gojjam region was in the range of 0.98-1.99 (mean 1.10%). Further, the arabica collection obtained from Giesha, Eritrea, Harar and Shoa regions had a mean caffeine content of 0.93, 0.95, 1.18 and 1.42%, respectively. Regarding caffeine content of arabica collections of different origins it is clear from the present study that collections from Ethiopia exhibited the lowest mean caffeine content of 1.59% and those from Guatemala recorded the highest mean caffeine content of 1.97% (Table 2).

In the present study, the mean caffeine value (1.84%) of the arabica collections was much higher than that the (1.2%) reported in *C. arabica* varieties by Mazzafera and Carvalho (1992) and Silvarolla *et al*. (2000). This is probably due to limited number of progenies examined in the present study. Nevertheless, Silvarolla *et al*. (2000) reported caffeine value as high as 2.9% in certain arabica coffees collected from Illubabor region of Ethiopia. Some cultivars like *C. arabica* cv. *Laurina* and species like *C. salvatrix* have low caffeine content of 0.6% and 0.71%, respectively. Recently, an Ethiopian *C. arabica* cultivar has been reported to have close to zero caffeine content (Silvarolla *et al*., 2004). This plant was obtained from the Tropical Agricultural Research and Higher Education Center (CATIE), Turrialba, Costa Rica, coffee collection and deposited at CATIE after the FAO 1964-1965 coffee mission to Ethiopia.

With respect to 34 collections analyzed in the present study, there is no correlation based on geographical origin of the collections. However, they can be classified into two groups based on caffeine levels *i.e*. collections with less than 2% caffeine level and collections with more than 2% caffeine level. Based on the results of the present study coupled with similar observations reported by others, it can be inferred that there exists a greater scope for identifying the variability for low caffeine coffees in natural population that can be exploited for commercial cultivation directly or it can be used in breeding programmes.

The available options for obtaining decaffeinated arabica coffee beans include (a) industrial extraction, (b) selection and breeding and (c) genetic modification. As of now, major portion of decaffeinated coffee beans is obtained by industrial decaffeination. Nevertheless,

Table 2. Mean caffeine content of *Coffea arabica* progenies of different origin

S. No.	Origin	Number of progenies	Caffeine content range	% dry basis Mean ± SD
1	Congo	4	1.66 – 1.90	1.85 ± 0.13
2	Ethiopia	6	1.18 – 1.96	1.59 ± 0.32
3	France	5	1.74 – 2.00	1.88 ± 0.13
4	Guinea	1	1.88 – 1.96	1.92 ± 0.06
5	Guatemala	3	1.86 – 2.07	1.97 ± 0.14
6	Kenya	3	1.86 – 1.98	1.92 ± 0.14
7	Maryland, USA	2	1.85 – 1.95	1.93 ± 0.10
8	Portugal	6	1.56 – 2.01	1.81 ± 0.17
9	Tanzania	3	1.77 – 2.06	1.89 ± 0.14
10	USDA, USA	1	1.85 – 1.93	1.89 ± 0.06

the size of the market for each type of decaffeination process in future will depend on the price and also health concerns related to the way the decaffeinated coffee beans are obtained. Hence, identifying a low caffeine coffee cultivar from the *C. arabica* genebank through screening for variability will be advantageous over the other options considering the apprehension over the artificial decaffeination methods and also the cost-effectiveness. In this direction, it is contemplated to continue the screening process for the remaining collections available in the *C. arabica* germplasm bank in search of low caffeine coffees.

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SHORT COMMUNICATION

HUBR-16: A High Yielding Early Maturity Rice Line Coupled with Extra Long Kernel and High Kernel Elongation

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In the present study, the development of new basmati line HUBR-16 has been reported from single plant selections from an F_2 population of the cross between TBD-2 and Pusa Sugandh-2. HUBR-16 has attained uniformity in morphological and grain cooking characters. The genotype HUBR-16 recorded superiority over Taraori Basmati and Pusa 1121 with respect to earliness, and yield potential at par with Pusa 1121. Along with earliness and high yield, HUBR-16 is as good as Pusa 1121 for major grain quality traits *viz.,* kernel length, kernel breadth and kernel length after cooking. This line may be utilized as a parent in breeding programmes for accumulation of favorable genes for kernel elongation after cooking.

Key Words: Early maturity, Grain quality, High yield, HUBR-16, Selection

The demand for superior quality basmati rice, irrespective of its price, dictates the most important feature governing basmati breeding. Since the last decade, kernel elongation after cooking and cooked rice quality have dictated the national and international markets and channelized research on this important aspect of Basmati rice breeding. Type-3 and Basmati 370 were the most popular basmati varieties exported from India in the seventies. Later on, Taraori Basmati, a collection from Karnal, India was released for commercial cultivation in 1996. Taraori Basmati had longer grains and replaced Basmati 370, fetching a premium price both in national and international markets. The research became focused on developing semi dwarf, high yielding, rice varieties possessing the typical basmati quality with higher kernel length after cooking, during the eighties. In 1989, Pusa Basmati 1 was released and it soon became popular among farmers because it had a semi-dwarf plant type coupled with the traditional basmati features of grain elongation, fragrance and cooking quality. Pusa Basmati 1 had 1.0 to 1.5 t/ha yield advantage over the traditional basmati varieties (Siddiq, 1990). Further, increased rice kernel length and linear elongation after cooking became an important objective of basmati breeding. In 2003, Pusa 1121 (Pusa Sugandh 4) was developed through selective inter mating of two advanced breeding sister lines of Pusa basmati 1 and released for cultivation in 2005. This variety is known for its extra ordinary kernel length which can be as much as 8.2 mm for single grain, the longest ever known released cultivar in the world. It also has very high kernel elongation ratio ranging from 2 to 2.5. When cooked the kernel length is more than 18 mm with minimum breadth wise expansion. This variety became popular among farmers as Pusa 1121 is photo-insensitive, requires less water, matures early and yields 48-50 q/ha compared to 23-25 q/ha for traditional tall basmati. These unparallel features of Pusa 1121 have led to revolution in domestic cultivation and demand in foreign markets. Presently, this variety is being grown over 70% of basmati growing area of India and fetches a farmer more than ₹3,000/- per quintal of paddy.

We report here the development of HUBR-16 an extra long grain genotype and its yield, maturity, grain and cooking quality characters. During *kharif* 2007 a large number of single plant selections were made from an F_2 population of a cross (TBD-2/Pusa Sugandh 2). TBD-2 is a mutant derived from Taraori Basmati and possesses dwarf plant habit along with grain quality characters of Taraori Basmati parent. The second parent, Pusa Sugandh 2 released in 2001, is a high yielding, long grain rice variety possessing basmati grain quality characteristics. Three F_3 families possessing high yield and desirable grain and cooking quality and earliness were found promising. One of these selections showed high

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kernel length, high kernel length after cooking (KLAC) apart from improved yield. In subsequent generations it showed variation in brown rice grain dimensions, kernel dimensions, alkali spreading value and bursting during cooking but remained stable for KLAC. From F_3 to F_7 generations, selection for yield *per se* and grain quality characteristics was carried out in this particular family in each generation. Of the nine selections in F_8, HUBR-16 has attained uniformity in morphological and grain cooking characters coupled with high yield and early maturity.

The agronomic features and quality characteristics of HUBR-16 are compared with Taraori Basmati (quality check), Pusa Basmati 1(yield check) and Pusa 1121 (extra long grain check). The experiment was conducted with three replications in randomized block design for three years (2011-13) and the data were recorded on yield and quality traits. The mean values over three years are presented for genotype HUBR-16 and the three basmati checks (Tables 1 and 2). HUBR-16 is about 10 and 20 days early in maturity than Taraori Basmati and Pusa 1121, respectively. HUBR-16 gave about 10 and 20 q/ha higher yield than Pusa 1121 and Taraori Basmati, respectively. It can be concluded that the genotype HUBR-16 is superior to Taraori Basmati and Pusa 1121 with respect to earliness, with yield at par with Pusa 1121. The Fig. 1 depicts the grain, brown rice, polished rice and cooked rice of HUBR-16 in comparison to the basmati check varieties.

Taraori Basmati, Pusa Basmati-1 and Pusa 1121 have an average milled kernel length of 7.86, 7.53 and 8.51 mm with KLAC of 13.65, 14.72 and 18.50 mm, respectively (Table 2). HUBR-16 recorded 8.62 mm kernel length, 17.86 mm KLAC along with intermediate alkali digestion value. Along with earliness and high yield potential, HUBR-16 is as good as Pusa 1121 for major grain quality traits *viz.*, kernel length, kernel breadth and KLAC. The thresh ability of HUBR-16 is very easy as husk is loosely bound to the kernel and about 2 mm space is empty in the shell of the grain which is 12.33 mm. The data on the grain characteristics of parents TBD-2 and Pusa Sugandh-2 is presented in Table 2.

Linear elongation of kernel on cooking is one of the major characters of fine rice (Sood and Siddiq, 1979). Khush *et al*. (1979) considered lengthwise expansion without increase in girth a highly desirable trait in high quality rice. Singh *et al*. (2002) stressed on the accumulation of genes for kernel elongation in the sister

Table 1. Agronomic features and quality characters of HUBR-16 rice line in comparison to basmati check varieties

Variety/Check	Pedigree	Plant height (cm)	Duration (days)	Average yield (q/ha)	Alkali digestion	Amylose content (%)	Aroma
Taraori Basmati	Pure line sel. from local basmati	146 (Tall)	132	32.79	5.0	23.51	SS
Pusa Basmati-1	Pusa167/ Karnal local	100 (Semi dwarf)	138	42.50	7.0	24.80	SS
Pusa 1121	Pusa 614-1-2/ Pusa 614-2-4-3	118 (Semi tall)	141	44.61	7.0	22.79	MS
HUBR-16	Taraori Basmati Dwarf - 2/ Pusa Sugandh-2	114 (Semi tall)	121	53.40	5.0	24.35	MS
X	–	119.5	133	43.32	6.0	23.86	–
SE (±)	–	8.34	3.81	3.84	2.0	0.38	–
CD 5% (±)	–	19.60	8.96	9.02	4.7	0.90	–

Table 2. Grain characters of HUBR-16 rice line in comparison to basmati check varieties and parental lines

Variety/Line	Grain length (mm)	Grain breadth (mm)	L/B	Brown length (mm)	Brown breadth (mm)	L/B	Kernel length (mm)	Kernel breadth (mm)	L/B	KLAC (mm)	ER
Taraori Basmati	10.9	1.84	5.86	8.49	1.68	4.96	7.86	1.70	4.62	13.65	1.74
Pusa Basmati 1	10.19	1.87	5.34	8.40	1.59	5.16	7.53	1.58	4.76	14.72	1.95
Pusa 1121	11.94	2.10	5.60	9.5	1.81	5.15	8.51	1.65	5.16	18.5	2.17
HUBR-16	12.33	1.93	6.38	9.32	1.70	5.48	8.62	1.73	4.98	17.86	2.07
TBD-2 (Parent*)	10.76	1.96	5.48	7.95	1.78	4.46	7.06	1.68	4.18	13.13	1.86
Pusa Sugandh-2 (Parent*)	12.23	2.18	5.61	8.51	1.92	4.43	7.64	1.83	4.17	15.56	2.03
X	11.39	1.98	5.71	8.70	1.75	4.94	7.87	1.70	4.65	15.57	1.97
SE (±)	0.42	0.05	0.19	0.24	0.03	0.09	0.23	0.03	0.10	1.02	0.08
CD 5% (±)	0.99	0.12	0.45	0.57	0.09	0.22	0.53	0.07	0.24	2.40	0.19

B= breadth, ER= Elongation ratio, KLAC= Kernel length after cooking, L= length

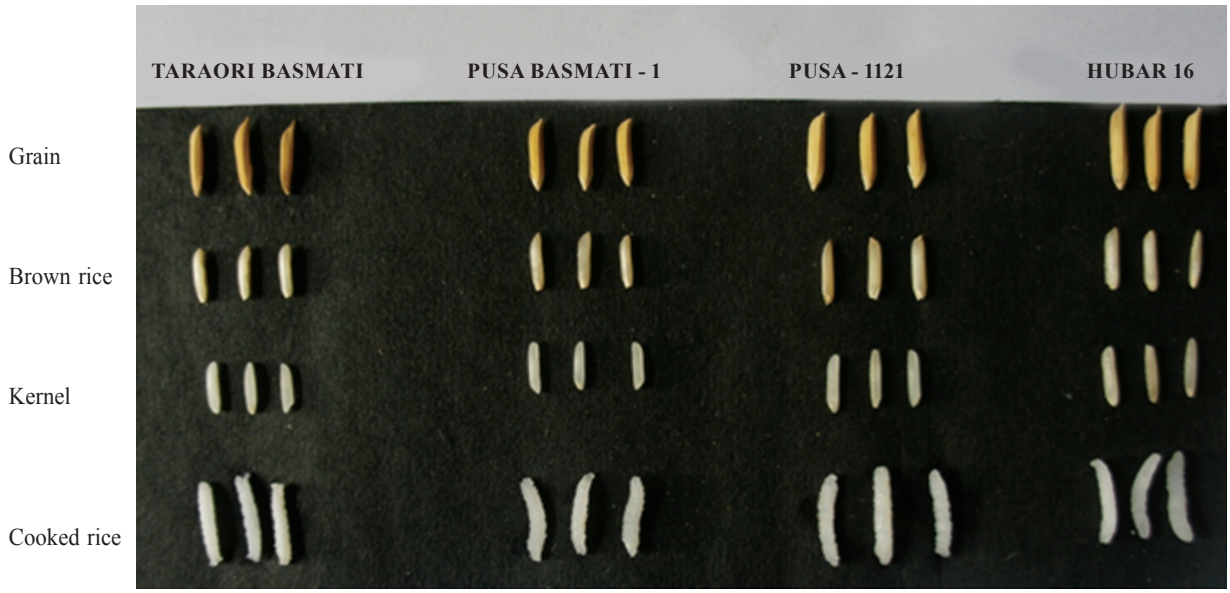

Fig. 1. Grain, brown rice, kernel and cooked rice of HUBR-16 in comparison to basmati check varieties

lines with which Pusa 1121 was developed. In the case of HUBR-16, KLAC is 17.86 mm. The involvement of many independent loci in the genetic control of kernel elongation after cooking has been suggested by Sood *et al*. (1983). This line can be used as a parent for further accumulation of favourable genes for kernel elongation after cooking.

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SHORT COMMUNICATION

Genetic Divergence of Tossa Jute (*Corchorus olitorius* L.) for Fibre Yield and its Related Component Characters Under Moisture Stress Condition

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The present investigation studied genetic divergence of 60 genotypes of tossa jute (*Corchorus olitorius* L.) which included sixteen standard varieties to identify the most diverged genotypes under moisture stress condition. On the basis of Mahalanobis D^2 analysis, genotypes were grouped into five clusters. Maximum inter-cluster distance was observed between cluster IV and V while cluster III showed the maximum intra-cluster distance. Cluster V exhibited highest means for days to 50% flowering, plant height, number of node, internode length, base diameter, mid diameter, top diameter, bark thickness and fibre weight. The highest contribution (12.63%) was exerted by plant height of total divergence. The results of the present study suggested that hybridization between genotypes in cluster V and IV could provide a wide spectrum of variation in the segregating generation which could provide opportunity for isolation of drought tolerant with high fibre yielding lines.

Key Words: D^2 analysis, Divergence, Moisture stress, Tossa jute

Jute, adorably called as "Golden Fibre" is obtained from bark of the two cultivated species of the genus *Corchorus,* viz., *C. capsularis* L. and *C. olitorius* L. of the family, Malvaceae (formerly, it was placed in Tiliaceae family) having chromosome number 2n=14. According to Kundu (1951), primary centre of origin of *C. olitorius* is Africa and its secondary centre of origin may be India or the Indo-Burma region, while the origin of *C. capsularis* is Indo-Burma region. Commercially, tossa jute covers 90 percent of the area and *C. capsularis* covers 10% of the total jute in India (Karmakar *et al.,* 2008). In West Bengal, jute is sown within first fortnight of April often accompanied by unpredictable and very low rainfall which exposes jute crop to moisture stress condition. Therefore, timely sowing and seedling establishment of jute mostly depends on availability of assured irrigation. Moreover, total precipitation during the jute growing season is decreasing day-by-day due to changed climatic conditions. Owing to erratic nature of rainfall over space, time and quantity, the crop is often subjected to phasic spell of moisture stress during early growth stage. There is limited scope for further improvement of cultivated varieties of jute against moistures stress in the absence of requisite variability and genetic diversity due to its narrow genetic base. Therefore, the present investigation was carried out to identify the most diverged genotypes under moisture stress condition from the existing germplasm so that it would help in planning hybridization programme to develop moisture-stress tolerant hybrids.

The experimental material consisted of 60 genotypes of *C. olitorius* of which sixteen were standard varieties collected from BCKV, All India Network Project on Jute and Allied Fibres, Kalyani, in collaboration with ICAR-CRIJAF, Barrackpore, Kolkata. The experiment was laid out in randomized block design with three replications. In each replication each genotype was grown in a plot of five rows of three meter length maintaining 30 cm space between the rows. The size of each plot was 3 m x 1.5 m and plot-to-plot distance was 0.5 m. Sowing was done under fully moisture stress condition on 5th April 2012 and 29th March 2013. The moisture stress condition was maintained when the plants showed symptoms of permanent wilting point (*viz.* failed to recover from wilting next morning), the plots were watered to half the field capacity. Recommended doses of major nutrient (40 kg N, 20 kg P_2O_5 and 20 kg K_2O) and FYM at 3 tons/ha were applied. Except days to 50% flowering, which was studied on plot basis, observations on other ten quantitative characters, namely, plant height (cm/plant), node number/plant, internode length (cm/plant),

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base diameter (cm/plant), mid diameter (cm/plant), top diameter (cm/plant), bark thickness (mm/plant), green weight (g/plant), stick weight (g/plant) and fibre weight (g/plant) were recorded from ten plants randomly selected from each genotype from each replication. From pooled data, genetic divergence was estimated by multivariate analysis using Mahalanobis D^2 statistic described by Rao (1952) and the genotypes were grouped into different clusters by employing Ward method.

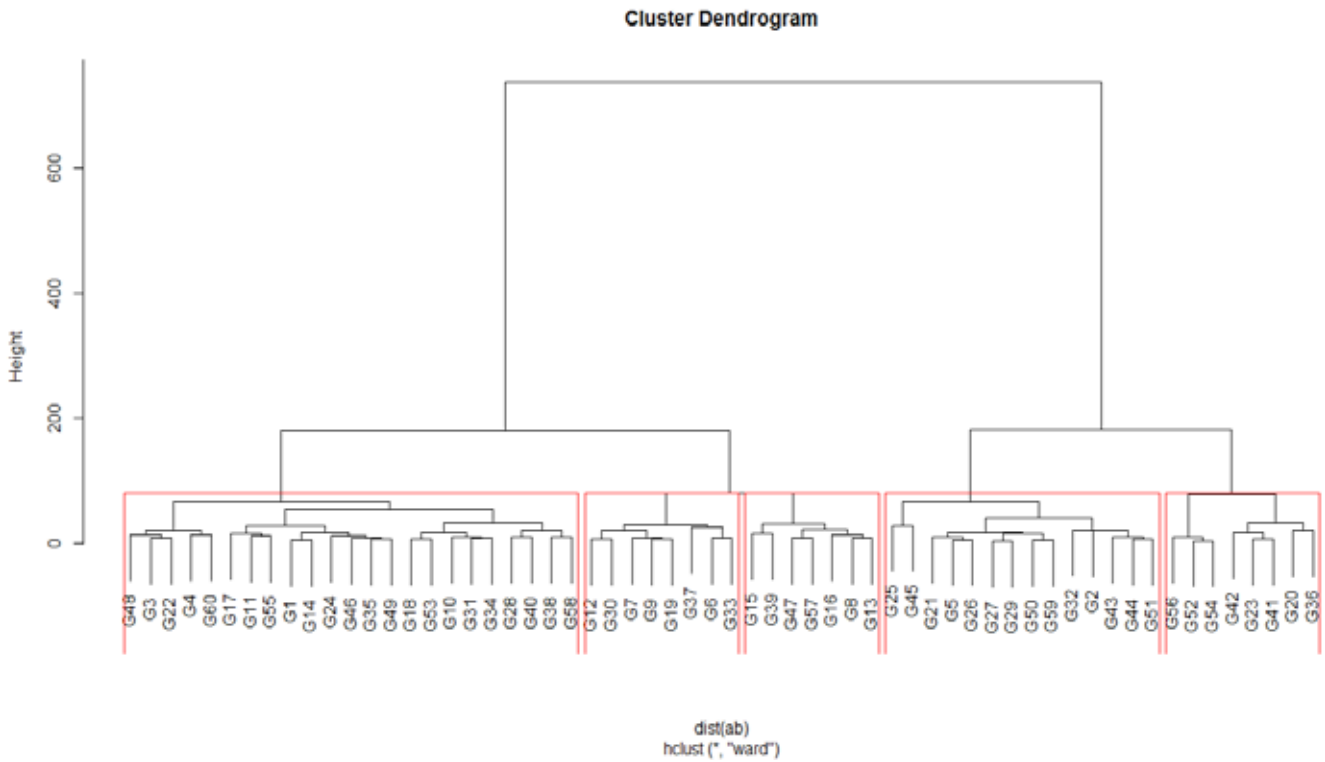
On the basis of Mahalanobis D^2 analysis, 60 genotypes were grouped into five clusters. (Table 1). Cluster I comprised of maximum number i.e. 23 genotypes (JRO 3690,S 19, TJ 40, JRO 878, JRO 7835,CO 58, OIN 259,OIN 409,OIJ 266,OIN 427,OIN 975,OIJ 213,OIN 986, OIJ 054,OIN 981, OIN 082,OEX 014,OIJ 264, OIN 915,OIN 666,OIN 926, OIN 581 and OIN 378). Cluster II was comprising of 14 genotypes (JRO 204, JR0 128, OEX 039, OIJ 104, OIN 714, OIN 309, OIN 515, OIN 959, OIN 623, OIJ 937,OIN 533,OIJ 168, OEX 019, OIJ 257), Cluster III and V with 8 genotypes each and cluster IV with 7 genotypes. Earlier Roy *et al.* (2011) grouped 52 genotypes into twenty clusters, Das and Kumar (2012) grouped fourteen varieties of white jute into three clusters, Das *et al.* (2012) grouped twenty eight genotypes of *C. olitorius* jute into five clusters, Majumdar *et al.* (2012) studied 27 genotypes of tossa jute and grouped them in 11 clusters. The genotypes belonging to the same cluster indicated that they were more closely related than those present in separate clusters. In respect of the characters studied, grouping of the genotypes into more number of clusters indicated presence of greater divergence among these genotypes. Cluster analysis of the 60 genotypes based on these characters had also been illustrated by the dendrogram (Fig.1). The results of grouping of the genotypes in different clusters obtained through D^2 statistic were also confirmed with the help of dendrogram where it clearly showed five clusters and the number of genotypes belonging to each cluster. The results obtained through classification of germplasm using D^2 statistic would provide a set of groups from which desirable parents may be selected for further breeding programme with respect to yield in particular.

Considering the averages of inter-cluster distance (Table 2), it was noticed that the values varied from 4.118-7.167. Maximum inter-cluster distance was observed between clusters IV and V followed by between clusters II and V, clusters I and V, and clusters III and V. Cluster III showed the maximum intra-cluster distance followed by cluster V and II. Wide genetic distance was evident among the genotypes of different group than those within the same cluster. The higher inter-cluster distance between cluster IV with cluster V followed by between cluster II and cluster I indicated that the genotypes belonging to cluster V was widely distanced genetically from those of cluster IV, II and I. Minimum inter-cluster distance was observed between clusters II and IV followed by clusters I and IV and clusters II and III which indicated that genotypes of clusters II and IV, clusters I and IV and clusters II and III were more or less closely related. It could be predicted that the genotypes belonging to different clusters separated by high estimated statistical distance could be used in hybridization programme to develop moisture stress tolerant line in jute which can successfully overcome water stress at early phase of growth.

Variations in mean values of different characters were observed in different clusters (Table 3). Among 11 characters studied cluster V exhibited highest means for days to 50% flowering, plant height, number of node, internode length, base diameter, mid diameter, top diameter, bark thickness and fibre weight, while the lowest values for these characters were recorded for cluster IV except for internode length which was observed in cluster I. Lowest value for top diameter,

Table 1. Grouping of sixty genotypes of *C. olitorius* in different clusters under moisture stress condition from pooled data of 2012 and 2013

S.No.	Cluster no.	Total no. of genotypes	Name of genotypes
1	I	23	JRO 3690, S 19, TJ 40, JRO 878, JRO 7835,CO 58, OIN 259, OIN 409, OIJ 266, OIN 427, OIN 975, OIJ 213, OIN 986, OIJ 054, OIN 981, OIN 082, OEX 014, OIJ 264, OIN 915, OIN 666, OIN 926, OIN 581, OIN 378
2	II	14	JRO 204, JRO 128, OEX 039, OIJ 104, OIN 714, OIN 309, OIN 515, OIN 959, OIN 623, OIJ 937, OIN 533, OIJ 168, OEX 019,OIJ 257
3	III	8	JRO 66, JRO2407,IRA, JRO 632, OIJ 218, OIJ 214, OIN 990, OEX 05
4	IV	7	JRO 524, JRO 8432, Bidhan Rupali, KOM 62, OIN 976, OIN 937, OIN 970
5	V	8	OIJ 263, OIJ 284, OIN 124, OIJ 216, OIN 196, OIN 791, OIJ 177, OEX 29



G1=JRO3690; G2=JRO204; G3=S19; G4='TJ40; G5=JRO128; G6=JRO66; G7=JRO2407; G8=JRO524; G9=IRA; G10= JRO878; G11=JRO7835; G12=JRO632;G13=JRO8432; G14=CO58; G15=BIDHAN RUPALI, G16=KOM62; G17-OIN259; G18=OIN409; G19=OIJ218; G20=OIJ263; G21=OEX039; G22=OIJ266; G23=OIJ284; G24=OIN427; G25=OIJ104, G26=OIJ714; G27=OIN309; G28=OIN975; G29=OIN515; G30=OIJ214; G31=OIJ213; G32=OIN959; G33=OIN990; G34=OIN986; G35=OIJ054; G36=OIN124; G37=OEX05; G38=OIN981; G39=OIN976; G40=OIN082; G41=OIJ216; G42=OIN196; G43=OIN623; G44=OIJ937; G45=OIN533; G46=OEX014; G47=OIN937; G48=OIJ264; G49=OIN915; G50=OIJ168; G51=OEX019; G52=OIN791; G53=OIN66; G54=OIJ177; G55=OIN926; G56=OEX29; G57=OIN970; G58=OIN581; G59=OIJ257; G60=OIN378.

Fig 1. Cluster analysis of sixty *C. olitorius* genotypes represented by dendrogram

Table 2. Intra and inter-cluster distances of *C. olitorius* under moisture stress condition from pooled data of 2012 and 2013

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	2.511	4.400	4.217	4.140	6.179
Cluster II		3.530	4.169	4.118	6.293
Cluster III			4.078	4.614	6.107
Cluster IV				3.504	7.167
Cluster V					3.697

Table 3. Cluster mean of *C. olitorius* under moisture stress condition from pooled data of 2012 and 2013

Cluster	Days to 50% flowering	Plant height (cm)	No. of node	Internode length (cm)	Base diameter (cm)	Mid diameter (cm)	Top diameter (cm)	Bark thickness (mm)	Green weight (g)	Dry stick weight (g)	Fibre weight (g)
Cluster I	102.102	257.419	74.942	4.163	1.147	0.893	0.629	0.782	140.582	23.787	6.464
Cluster II	102.509	260.796	74.905	4.210	1.136	0.919	0.637	0.741	179.267	29.350	6.503
Cluster III	102.027	272.148	76.229	4.439	1.174	0.843	0.580	0.815	123.655	21.550	6.969
Cluster IV	99.936	254.260	73.167	4.358	1.102	0.805	0.584	0.760	115.681	24.643	6.028
Cluster V	105.292	290.875	79.292	4.778	1.305	0.929	0.653	0.872	172.940	28.375	8.344

dry stick weight was recorded in cluster III, for bark thickness in cluster II and for green weight and days to 50% flowering in cluster IV. Cluster V appeared to be most important since it showed highest mean value for a number of important desirable characters including fibre yield and from this cluster improved genotypes could be directly selected or could be considered parents to complement the deficit of other parents present in distant group. Interestingly, most of the minimum and maximum mean values were distributed in relatively distant clusters. Therefore, hybridization between genotypes falling in different clusters may provide ample scope for development of desirable lines. The results of the present study suggested that hybridization between genotypes in cluster V could provide a wide spectrum of variation in the segregating generation which might provide an opportunity for isolation of elite lines. Cluster V was found with genotypes showing highest mean for as many as nine characters and most of them were related to yield. On the contrary, cluster IV comprised of the genotypes which resulted into lowest mean for as many as seven characters among eleven characters studied. Further, in case of cluster I, II and III some characters produced higher mean while for others were very low mean. Highest contribution towards total genetic divergence (12.63%) was exerted by plant height followed by bark thickness (12.42%), green weight (12.12%), dry stick weight (10.12%), top diameter (9.24%%), internode length (8.48%), mid diameter (8.02%), node number (7.84%), fibre weight (7.68%), base diameter (5.81%) and days to 50% flowering (5.59%) (Table 4).

Thus, on the basis of cluster mean and also on the basis of mean performance and *per se* performance of individual genotypes, it could be suggested that selection of the genotypes from clusters V and IV could be proposed for earliness and high fibre yield and clusters V and II containing genotypes for base diameter, mid diameter and green weight may be fruitful to develop desirable lines. Noticeably, genotypes OIJ 263, OIJ 284, OIN 124, OIJ 216, OIN 196, OIN 791, OIJ 177, OEX 29 belonging to the cluster V and JRO 524, JRO 8432, Bidhan Rupali, KOM 62, OIN 976, OIN 937, OIN 970 from cluster IV may be used as parents for hybridization programme to evolve a line with drought tolerance and high fibre yielding.

Table 4. Contribution of individual characters towards total genotypic divergence in sixty genotypes of *C. olitorius* under moisture stress condition from pooled data of 2012 and 2013

S. No.	Characters	Per cent contribution towards divergence D2 statistics
1	Days to 50% flowering	5.591%
2	Plant height(cm)	12.635%
3	Node No.	7.878%
4	Internode length(cm)	8.482%
5	Base diameter (cm)	5.809%
6	Mid diameter(cm)	8.024%
7	Top diameter (cm)	9.238%
8	Bark thickness (mm)	12.422%
9	Green weight (g)	12.124%
10	Dry stick weight(g)	10.123%
11	Fibre weight (g)	7.674%

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

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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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CONTENTS

Interplay of National and International Laws on Access to Biological Resources and Benefit Sharing 165
Rai S Rana

Identification of Gaps in Pigeonpea Germplasm from East and Southern Africa Conserved at the ICRISAT Genebank 180
HD Upadhyaya, KN Reddy, M Irshad Ahmed, CLL Gowda, M Thimma Reddy and Senthil Ramachandran

Diversity Analysis among Chickpea Genetic Stock as Revealed Through STMS Marker Analysis 189
Nandakini Lahiri, Tapan Kumar, C Bharadwaj, Ashutosh Sarker, Aqeel Hasan Rizvi, SK Chauhan, AK Verma and Guru Prasad

Patterns of Genetic Variation, Correlations under Irrigated and Rainfed Conditions in Indian Mustard [*Brassica juncea* (L.) Czern. & Coss.] 198
VV Singh, ML Meena, BR Singh and Dhiraj Singh

Rice Diversity – The Genetic Resource Grid of North-East India 205
A Anna Durai, JMS Tomar, Premila Devi, A Arunachalam and H Mehta

Genetic Variability and Diversity of *Sorghum* Landraces Collected from Uttar Pradesh, India 213
M Elangovan and P Kiran Babu

Exploiting Genetic Divergence for Crop Improvement in Coriander (*Coriandrum sativum* L.): A Neglected and Underutilized Crop 222
Giridhar Kalidasu, S Suryakumari, C Sarada, A Rajani, N Hariprasada Rao, SR Pandravada and L Naram Naidu

Variability and Correlation Studies in Garlic (*Allium sativum* L.) Germplasm Collected from Different Parts of Jammu 229
Shilpi Khar, Satesh Kumar, RK Samnotra, Manoj Kumar, Sandeep Chopra, Manish Kumar and Sachin Gupta

Recent Developments for Access to Plant Genetic Resources in India and their Implications 237
Pratibha Brahmi and Vandana Tyagi

SHORT COMMUNICATIONS

Fingerprinting Based on Microsatellite Markers for the Identification of Rice Varieties in Chhattisgarh 247
Jitendra Kumar Tiwari, NK Rastogi, PK Chandrakar and SB Verulkar

"Tikdi" – A Fruit Fly Resistant Land Race of Ber (*Ziziphus mauritiana* Lamarck) 252
Om Vir, Sharmila Roy, RK Tyagi, AK Singh and PR Meghwal

Screening of *Coffea arabica* Germplasm for Caffeine Level 256
TN Gopinandhan, NS Prakash, BR Shivalingu and DR Shanmukappa

HUBR-16: A High Yielding Early Maturity Rice Line Coupled with Extra Long Kernel and High Kernel Elongation 260
HK Jaiswal, Showkat A Waza and T Sravan

Genetic Divergence of Tossa Jute (*Corchorus olitorius* L.) for Fibre Yield and its Related Component Characters Under Moisture Stress Condition 263
Ashutosh Sawarkar, Sonika Yumnam, SG Patil and S Mukherjee

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