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Regulating Access to Genetic Resources and Promoting Benefit Sharing in India

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The Convention on Biological Diversity (CBD) recognizes sovereign rights of States over their bioresources and also on determining terms of accessing to them, subject to their national legislation. India is among the 193 Contracting Parties to CBD and enacted the Biological Diversity Act, 2002 to claim sovereign rights over its bioresources, and associated traditional knowledge (TK), and to meet its national obligations on conservation of biodiversity, sustainable use of its components and fair and equitable sharing of benefits arising from their utilization. This legislation, and the Biological Diversity Rules, 2004 framed under it, provide a three-tier legal framework for regulating access to bioresources (and associated TK) while ensuring fair and equitable sharing of resulting benefits. For a national legislation on access and benefit sharing (ABS) to be effective, its recognition at the international level is essential so as to provide enabling legislation in user countries and also to support an effective monitoring mechanism for proper realization of the equity benefits. Adoption of the Nagoya Protocol to CBD on ABS on 29 October, 2010 during the COP-10 meeting, held in Japan, is the first step in this direction. This paper presents salient features of this landmark national legislation, discusses its implications to biodiversity-related international treaties bearing on this subject and also overviews the progress made in implementing its provisions while making some suggestions as the way forward.

Key Words: Implementing CBD in India, ABS in India under CBD, Indian Legislation on ABS, Legal Access to Bioresources with Benefit Sharing in India, India's National Biodiversity Authority, 3-Tier System for Operating ABS Regime in India

Introduction

Sovereign rights of States over their biological resources, reaffirmed in the preamble of the Convention on Biological Diversity (CBD), 1992 and articulated clearly in its Articles 8 (*In-Situ* Conservation) and 15 (Access to Genetic Resources) brought the twin issues of access and benefit sharing (ABS) to the centre stage, linking them inseparably to the conservation of biodiversity and sustainable use of its components. Regulating access to bio-resources is considered the most common mechanism for sharing of benefits, arising from their authorized use, but it is expected that the benefit sharing terms, subject to which approval for access is granted, should be encouraging greater use of these bio-resources rather than posing barriers to their availability to users.

With the emergence of highly restrictive intellectual property rights (IPR) systems, it became imperative to enact national legislation to claim sovereign rights of ownership over bio-resources to ensure realization of fair and equitable sharing of benefits arising from their utilization. When the national access regulations are not properly balanced with provisions of the laws protecting monopolistic patent rights or exclusive breeders' rights,

it is likely to have adverse effects on the utilization and management of genetic resources in developing countries (Tvd and Young, 2007). For a national legislation on ABS to be effective and develop proper monitoring mechanism for realization of equity benefits, however, its recognition at the bilateral/ multilateral or international level is essential (Andersen *et al.*, 2010).

The key ethical principles of obtaining prior informed consent (PIC) and equity in benefit sharing, along with the rights of farmers and local communities, brought in focus by the CBD, are also now widely recognized (Engels *et al.*, 2010). This development calls for a re-look at our current approach and strategy for conservation, sustainable use and management of bio-resources, adding a new dimension of sustaining livelihoods for local farming communities and forest dwellers, the primary benefit claimers, who even now continue to conserve and use their bio-resources, and also add value to them, under *in-situ* on-farm conditions where they have developed their distinctive traits and where they are still evolving for better adaptation in response to increasing selection pressures exerted by demands of their varying natural growth environments and also farmers' preferences.

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Background Information on Agricultural Biodiversity

It is interesting to study human cultures and their preferred plant sources for food, feed, fiber, healthcare, shelter, rituals or aesthetics. Although about 250,000 species of plants (divided into 460 families) have so far been documented worldwide, products from only around 300 species (belonging to 20 families); just a tiny fraction of what's available in nature, are being more commonly used. Again, nearly 3,000 species of plants are used and cultivated by humans under managed conditions but a remarkably small number of these species contribute greatly to the global harvest of food crops. Ranked in order of their annual production, the world's most important 15 food crops are: sugar cane, wheat, rice, maize, potato, sugar beets, barley, sweet potato, cassava, soybean, grape, tomato, bananas, legumes (beans and peas), and oranges.

i. Centres of Origin and Diversity of Crop Plants

Another remarkable fact is that different crop plants were selected and domesticated from their wild relatives by humans in different parts of the globe at different times. Scientific studies have been made to broadly identify these 'Primary Centres of Origin and Diversity of Crop Plants'. Vavilov, the renowned Russian botanist and explorer, recognized the following eight such primary centres (Vavilov, 1926):

- I. The Chinese Centre – in which he recognized 138 distinct species of which probably the earlier and most important were cereals, buckwheat and legumes.
- II. The Indian Centre (including the entire subcontinent) – based originally on rice, millets and legumes, with a total of 117 species.
- IIa. The Indo-Malayan Centre (including Indonesia, Philippines, etc.) – with root crops (*Dioscorea* spp., *Tacca*, etc.) preponderant, also with fruit crops, sugarcane, spices, etc., some 55 species.
- III. The Inner Asiatic Centre (Tadjikistan, Uzbekistan, etc.) – with wheats, rye and many herbaceous legumes, as well as seed-sown root crops and fruits, some 42 species.
- IV. Asia Minor (including Transcaucasia, Iran and Turkmenistan) – with more wheats, rye, oats, seed and forage legumes, fruits, etc., some 83 species.
- V. The Mediterranean Centre – of more limited

importance than the others to the east, but including wheats, barleys, forage plants, vegetables and fruits -especially also spices and ethereal oil plants, some 84 species.

- VI. The Abyssinian (now Ethiopian) Centre – of lesser importance, mostly a refuge of crops from other regions, especially wheats and barleys, local grains, spices, etc., some 38 species.
- VII. The South Mexican and Central American Centre – important for maize, *Phaseolus* and Cucurbitaceous species, with spices, fruits and fibre plants, some 49 species.
- VIII. South America Andes region (Bolivia, Peru, Ecuador) – important for potatoes, other root crops, grain crops of the Andes, vegetables, spices and fruits, as well as drugs (cocaine, quinine, tobacco, etc.), some 45 species.
- VIIIa. The Chilean Centre – only four species – outside the main area of crop domestication, and one of these (*Solarium tuberosum*) derived from the Andean centre in any case. This could hardly be compared with the eight main centers.
- VIIIb. Brazilian-Paraguayan Center – again outside the main centers with only 13 species, though *Manihot* (cassava) and *Arachis* (peanut) are of considerable importance; others such as pineapple, *Hevea* rubber, *Theobroma cacao* were probably domesticated much later.

Notwithstanding the unending human migrations and trade exchanges over the past nearly ten millennia, these Vavilovian Primary Centres can still be broadly defined because putative ancestral species and wild relatives continue to evolve there where they developed their recognizable distinctive traits (Auer, 2009). Zeven and de Wet (1982) further elaborated this concept enlarging them into 12 regions. These areas are rich in genes for valuable traits like resistance to diseases and pests, adaptations to specific stress environments and also tastes and qualities preferred by the local communities. And, these are essentially the target genes most commonly sought after for their identification, characterization, cloning and manipulation by the researchers using modern tools and techniques of biotechnology (Rana, 2004).

ii. Pre-CBD Movement of Genetic Resources

Seed samples of these landraces and farmers' varieties were taken away freely from these areas, mostly the

developing countries, through systematic explorations and collections by scientists of developed countries in general, and researchers of International Agricultural Research Centres in particular, and stored subsequently in their gene banks. These operations were undertaken mostly during the 1930-1980 period without signing any agreements and benefit sharing/ technology transfer arrangements. This was done by technology-rich countries and international organisations under the pretext that all global biological resources were shared heritage of mankind and needed to be safeguarded by storing them under ex-situ conditions, both for their protection from unforeseen calamities and also for promoting their greater use in crop improvement programmes (Rana and Arora, 1990). The International Undertaking (IU) on Plant Genetic Resources (PGR), voluntary in nature and facilitated by the FAO, supported this movement.

Following the recognition of sovereign rights of States over their biological resources by the CBD in 1992, biodiversity-rich developing countries pressed for repatriation of their seeds to their national programmes and demanded adoption of appropriate procedures to ensure authorized access to their bio-resources, subject to fair and equitable sharing of benefits arising from their use. Unauthorized taking away of genetic resources and their use without sharing benefits with the country of their origin was considered 'biopiracy'. These discussions led to referring of two issues by the CBD to the FAO for further deliberation and finding acceptable solutions to them. These included matters related to the fate of genetic resources collected (and taken away) prior to CBD and the realization of Farmers' Rights as developers, conservers and primary users of agricultural bio-resources (MSSRF, 1996). The FAO revised the text of the IU on PGR and adopted it in November 2001 as the legally binding International Treaty on Genetic Resources for Food and Agriculture (ITPGRFA). Farmers' Rights were recognized under this Treaty but their realization was left to the national governments in their jurisdiction. The issue of collecting genetic resources from countries of their origin, prior to CBD, still hangs on but the designated accessions stored in CGIAR's International Gene Banks have been brought under the operative jurisdiction of the FAO.

iii. Management and Governance Systems for Access and Benefit Sharing

Management and governance of genetic resources need to be looked from three dimensions, namely, perspective

of developers and users, governance at the state and national levels, and national obligations under international treaties/agreements.

The first dimension of developers and primary users comprises local farming communities, public sector research institutions, private sector seed companies and multinational corporations. They represent the main stakeholders and key beneficiaries. The second dimension involves policy makers, legislators, managers and administrators. 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 management systems of genetic resources globally and also at the national level, more so in the developing countries (Andersen, 2008). 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/protection laws that grant monopolistic/exclusive rights to IPR holders/breeders to the exclusion of the rights of farmers and other primary beneficiaries. These three are legally binding treaties and India is a contracting party to all of them. Considering that agro-biodiversity is 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.

CBD

Article 15 of CBD on 'Access to Genetic Resources' recognises sovereign rights of States over their natural resources and also affirms that the authority to determine access to genetic resources rests with the national governments, subject to national legislation. Access, where granted, shall be on mutually agreed terms (MAT) and subject to prior informed consent (PIC) of the Contracting Party providing such resources.

CBD also points to the importance of cultural diversity and traditional knowledge (TK). Article 8(j) of CBD on Traditional Knowledge, Innovations and Practices, calls on Parties to "respect, preserve and maintain knowledge, innovations and practices of indigenous and local communities embodying traditional lifestyles relevant for the conservation and sustainable use of biological diversity and promote their wider application with the approval and involvement of the holders of such knowledge, innovations and practices and encourage the equitable sharing of the benefits arising

from the utilization of such knowledge innovations and practices”.

It needs to be appreciated that the three main objectives of the CBD (stated under Article 1), conservation of biodiversity: both in-situ (Article 8) and ex-situ (Article 9), sustainable use of its components (Article 10), fairly and equitably sharing the benefits arising from such use (Article 15), access to and transfer of technology (Article 16) and Handling of biotechnology and distribution of its benefits (Article 19) are inseparable in implementing the CBD and form the foundation of biodiversity-rich developing countries' expectations to gain substantially from their genetic resources (and associated TK) by providing them to users, based on PIC and MAT, and gaining from access to modern biotechnology tools/techniques and products.

It is not only that genetic resources form a necessary and continuous input into all crop improvement and animal breeding efforts, including the on-going programmes of the public and private sectors, they also sustain livelihood activities of farming communities. Developing more insect-resistant and herbicide-tolerant crop varieties, employing new tools and techniques of modern biotechnology, also requires bio-prospecting to locate target genes, cloning their DNA and injecting them into locally adapted high yielding varieties hoping that the projected expression and stability of the added genetic information from exotic sources will dramatically increase the yield and, hence, marketability of their proprietary crop varieties/livestock breeds (Gepts, 2006).

ITPGRFA

The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) was intended to bring conformity in provisions of the International Undertaking, facilitated by the FAO, and the CBD, under the UNEP. After lengthy negotiations, delegates from 116 countries adopted the text of this treaty in November 2001, with the American and Japanese delegates abstaining. This treaty, serviced by the FAO in the interest of global food security, mandates conservation and sustainable use of plant genetic resources for food and agriculture, seeks to promote fair and equitable sharing of benefits arising out of the use of these resources and also establishes a multilateral system to facilitate access to 64 crops listed in Annexes I and II of the Treaty so as to share benefits derived from such facilitated access under the terms of a Standard Material Transfer Agreement (SMTA), based on mutually agreed terms. Thus, ITPGRFA

is in harmony with the CBD and upholds the objectives of conservation, sustainable use and equitable benefit sharing with respect to agricultural bio-resources. Union Ministry of Agriculture is the nodal implementing ministry in India.

There is, however, still a lack of consensus regarding “fair and equitable” benefit sharing. It is also somewhat hazy how the benefits will be shared under this Treaty when the products are IPR protected and not freely available to farmers and researchers.

Unlike the CBD, which provides for bilateral negotiations to establish the terms of access and benefit sharing for each specific exchange of materials, all germplasm exchanges under the multilateral system will be subject to the standard MTA. Monetary benefits will be paid to a fund established by the Governing Body (FAO, 2009). This fund, as the Global Crop Diversity Trust Fund, will be used primarily to support farmers who conserve and sustainably use plant genetic resources for food and agriculture, especially such farmers in developing countries or in countries with economies in transition. The financing of germplasm conservation has been addressed only in general terms, making this aspect of the treaty potentially difficult to implement. The overall impact of the treaty also seems to be limited because of the omission of soybeans, peanuts, and some other important food crops from the list of 35 crops covered in its Annex I.

WTO-TRIPS

Another international agreement, namely, the Trade Related Intellectual Property Rights (TRIPS), under the World Trade Organisation (WTO), 1995, also impacts the access and benefit sharing processes as it requires under its Article 27.3b that plant varieties must be given some form of protection to intellectual property rights, either through patents or an effective *sui generis* national system. This article is now due for revision based on the experience gained so far from implementing its provisions. Doha Round of negotiations is, however, underway though the progress made so far is much below the developing countries' expectations.

National Legislation for Implementing the International Treaties

Under CBD, the 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 in response

to this requirement (NBA, 2004) 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, development and sustainable use of bio-resources.

Access and Benefit Sharing under India's Biological Diversity Act, 2002

Following an extensive and intensive consultation process involving all major stakeholders, the Central Government enacted the Biological Diversity Act, 2002 with the following salient features:

- to regulate access to biological resources of the country with the purpose of securing equitable share in benefits arising out of the use of biological resources; and associated traditional knowledge (TK) relating to biological resources;
- to conserve and sustainable use of all biological diversity components;
- to respect and protect traditional knowledge of local communities related to biodiversity;
- to secure sharing of benefits with local people as developers and conservers of biological resources and holders of knowledge and information associated with their use;
- to promote conservation and development of areas of importance from the standpoint of biological diversity by declaring them as biological diversity heritage sites;
- to provide support to on-going programmes on protection and rehabilitation of rare, endangered and threatened species;
- to ensure increasing involvement of institutions and state governments in the broad scheme of implementing the Biological Diversity Act, through constitution of appropriate committees.

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.

In exercise of the powers conferred by Sub-Section (1) (4) of Section 8 of the Biological Diversity Act, 2002 (No.18 of 2003), the Central Government established a body called the National Biodiversity Authority (NBA), on 1st October, 2003. The main functions of this Authority are:

1. To lay down procedures and guidelines to govern the activities provided under Section 3, 4 and 6. (Permission to foreigners/non-resident Indians and foreign companies).
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:
 - Certain persons not to undertake Biodiversity related activities without approval of National Biodiversity Authority (Section 3) (Access to biological resources or Associated knowledge).
 - Results of research not to be transferred to certain persons without approval of National Biodiversity Authority (Section 4) (Transfer of Research Results).
 - 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 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.
7. 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.

To sum up, this Act seeks to regulate access to

India's biological resources, and associated TK, with a view to securing equitable sharing of benefits arising from their use. Its primary objectives include promoting in-situ conservation of bio-resources and their sustainable use and linking them to the goals of food security, healthcare, livelihoods and eco-friendly development concerns through suitable applications of the National Gene Fund. It also addresses supportive mechanisms like documenting and protecting biodiversity-related TK, conservation and development of designated areas as biological diversity heritage sites and also the protection of threatened species and their habitats.

Recognising that the Indian citizens owe allegiance to the Indian Constitution and can be called upon in person to ensure compliance to this Act's provisions, a practical 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 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.

All the entities in this category are also required to seek prior approval of the NBA for transferring research results abroad (Section 4), for applying for IPR (Section 6) and also for third party transfer of the granted approval (Section 20), by submitting applications in specified formats and after payment of prescribed fee for each of the above mentioned purposes. As explained earlier, the provisions of this law are differentiating but not discriminatory.

Access of Indian citizens to bio-resources for research is unrestricted and free. However, the 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.

Restrictions Imposed on Granting Access

Certain restrictions have been imposed under Rule 16

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on NBA's 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:

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

Exemptions Provided under the BD Act

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

- 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 policy guidelines issued by the Ministry of Environment and Forests (MoEF) vide its notification dated 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.
- Provisions of Section 7 (prior intimation to SBB for commercial use) shall not apply to the local people and communities including village healers/*vaid*s, farmers and other traditional growers and also to Indian users of these bio-resources for research.
- Normally traded commodities, 190 bio-resources as notified by the MoEF vide its notification dated 26 October, 2009, subject to the clarification issued on 16 February, 2010, would be exempt from purview of this Act provided they are traded as commodities.

Link to the Patents Act

Section 6 (1) of the BD Act links to the requirement under Section 10 (4) of the Patents (Amendment) Act, 2002 that requires disclosure of the source and geographical origin of the biological material, used in developing an invention/innovation. A sample of the bioresource is also required to be deposited in the designated national depository institution.

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)).

Realizing Fair and Equitable Benefit Sharing under the Biological Diversity Act

The NBA is required to develop and notify guidelines for imposing terms for fair and equitable benefit sharing and efforts in this context are going on. A National Consultation was also organized on 23 April 2010 at Chennai to obtain further inputs from different experts and stakeholders for this purpose. Until these guidelines are finalized and notified, some working guidelines have been developed and followed while making recommendations regarding benefit sharing on a case-by-case basis.

Options for sharing non-monetary benefits, adopted from the non-binding Bonn Guidelines, are provided under Section 21 as listed below:

- Transfer of technology
- Location of production, R&D units in areas inhabited by 'benefit claimers'
- Associating Indian scientists and benefit claimers with the R&D activities
- Setting up of venture capital
- Payment of monetary [and royalty] benefits
- Product development
- Institutional capacity building
- Education and awareness raising activities

For sharing benefits in monetary form, consideration is given to potential commercial value of the innovation/product/process/technology, expected volume of potential business and the capacity to pay of the applicant. Applying terms for benefit sharing on a case by case basis notwithstanding, a generalized and indicative scheme for sharing monetary benefits, arising from use of biosources and associated TK, is given in Table 1 for guidance purpose only.

Approval for accessing bioresource, bio-survey & bio-utilization, transfer of research results, seeking IPR and third party transfer of already accessed bioresource is given by NBA by signing a written agreement with the applicant as required under Rule 14 (5).

The amount realized by the NBA through fees, royalties and other sources goes to the National Biodiversity Fund that is used for the following purposes:

Table 1.

Category Commercial use	Benefits from direct commercial use	Benefits from commercial use after licensing to a licensee (third party)
The Applicant commercialises the process/product	The applicant shall pay royalty @ up to 3% of the highest ex-factory sale price of the product sold or used for captive consumption (in such cases, the price would be determined on the basis of the price which the product would get if sold in the market).	The applicant pays a mutually agreed upfront amount until the product/innovation enters into commercial production.
The Applicant licenses the process/product to a licensee	The Applicant shall pay up to 5% of the license fee received from the Licensee as one-time benefit sharing at this stage. The Applicant shall also provide a copy of the contract, entered into, to the Authority.	Upon commercialization, the applicant shall further pay, in addition to the payment made earlier, up to 4% royalty on the amount received by him as his royalty-charges from the licensee on an annual basis.
The Applicant collects the bioresource from its natural populations, with prior approval of the concerned SBB/BMC/State Wildlife Board, and exports it under DGFT permit.	The Applicant shall pay 5% of the total FOB value of the bioresource under export to the Authority.	

- Channeling benefits to the ‘benefit claimers’.
- Helping the conservers and developers of biological resources/ local communities in support of their on-location efforts towards conservation and sustainable use.
- Promoting conservation of bio-resources and development of areas from where these are accessed.
- Supporting conservation efforts for the designated ‘Biodiversity Heritage Sites’.
- Capacity building.

Implementing Access and Benefit Sharing under the Biological Diversity Act

Biodiversity is a multi-disciplinary subject, involving diverse activities. Its major stakeholders include the Central Government, State Governments, institutions of local self-government, local communities, farming communities, research institutions, industry and civil society organizations. Notwithstanding the fact that the Contracting Party to the CBD is the national government and the Union Ministry of Environment & Forests is the nodal ministry, biodiversity is essentially a state subject. Even at the Central Government level, several union ministries have overlapping authority in managing different components and concerns of biodiversity. Thus, implementing the Biological Diversity Act requires effective coordination among all the concerned authorities and also other major stakeholders.

The Act provides for its implementation through a 3-tier system comprising the National Biodiversity Authority (NBA), the State Biodiversity Boards (SBBs) and the Biodiversity Management Committees (BMCs) at the local communities level. Functions of this system at all the three levels have been well defined. There is a provision for setting up of a Committee on Agriculture and also some expert committees as needed. The NBA has been established and it is operating from Chennai. SBBs have also been constituted in 24 States though they often lack the guidance of technical experts at the top. The task of setting up of BMCs remains a challenge although some states have gone ahead notably in this

direction and 31,542 BMCs have already been constituted. Over 400 People’s Biodiversity Registers are under preparation. However, infrastructure still remains poor and there is lack of adequate capacity at the lower two levels, particularly at the level of local communities. There is an urgent need for generating awareness at all levels about the Act’s main provisions and objectives and also about the benefits that are likely to accrue following its effective implementation.

The NBA has also constituted the following expert committees to assist in its functioning:

- Expert Committee on Access and Benefit Sharing for processing all the Applications.
- Expert Committee for framing the guidelines for determining contributions to and utilization of National Biodiversity Fund.
- Expert Committee on preparing guidelines on ameliorative measures for biodiversity rich areas that are threatened by overuse, abuse or neglect.
- Expert Committee on Agro-biodiversity
- Expert Committee for implementing the Project for establishing “Indian Biodiversity Information System (IBIS)”.
- Expert Committee for the preparation of Training Module for Officers staff and various stakeholders on legal, social, technical aspects of implementation of various provisions of Biological Diversity Act, 2002.
- Expert Committee for preparation of guidelines on creating structures, running administration and maintaining of accounts and other related matters pertaining to Biodiversity Management Committees
- Expert Committee on reviewing the agreements’ formats.

There is an urgent need at present to develop a strong National Biodiversity Information System, suited to the needs of our country and to serve as a referral facility for networking. Although several options are available for securing equitable sharing of benefits, arising from the use of bio-resources (and associated

Prescribed Application Forms and Fees for Seeking Approval of NBA

Application Format	Purpose	Application Fee
Form I [Sections 3 and 19, Rule 14].	Access to Bioresources/TKby foreigners/Commercial Use, Biosurvey/Bio-utilization	₹ 10,000/-
Form II [Section 4, Rule 17].	Transfer of Research Results/Data.	₹ 5,000/-
Form III [Section 6, Rule 18].	Seeking IPR	₹ 500/-
Form IV [Section 20, Rule 19].	Third Party Transfer of Bioresources	₹ 10,000/-

ITK) but there are not many case studies available as yet to provide learning experiences. Furthermore, some progress in this direction notwithstanding, there is still no adequate monitoring mechanism in place to ensure proper compliance of the contracting agreements, signed between the NBA and the users on mutually agreed terms. Another major limitation is that provisions of our national legislation on ABS do not yet have international recognition and compliance abroad.

Several National Bureaus, mandated with the conservation and sustainable use of bio-resources under the ICAR, are currently engaged in systematic registration of elite genetic resources of crop plants, livestock and fish. Over 800 elite plant genetic resources and nearly 130 elite livestock breeds have already been registered. There is need to provide legal protection to such registered elite genetic stocks by invoking relevant provisions under the Protection of Plant Varieties Act, the Biological Diversity Act and other relevant legislation and administrative measures. Some ground work has already been done but some hazy areas still remain awaiting clarity. Issues relating to beneficiary claimants and farmers' rights require more attention. These discussions need to be continued and supported to reach some meaningful conclusions and well laid out procedures. As it appears, beginning may have to be made with documenting them in relevant communities' Biodiversity Registers, duly endorsed by the concerned SBBs, and finally by the NBA, in partnership with the ICAR.

Our crop and livestock genetic resources are still evolving under *in-situ* on-farm conditions, moving gradually towards better adaptation to situations in which they are grown in the face of emerging outbreaks of pests and diseases and also non-biotic stresses. These evolutionary processes, abruptly cut off by the *ex-situ* conservation strategy, need to be continued and strengthened under the *in-situ* on-farm conditions, managed by the farming communities who are living with their bioresources under different agro-ecosystems. *In-situ* conservation and sustainable use of bioresources is strongly supported under the Biological Diversity Act. Considering that effective implementation of this Act requires joint effort and active collaboration of several union ministries of the central government and also the state governments, it is proposed that this challenging task be undertaken as a standalone national mission on 'Implementing the Biological Diversity Act for Adaptation to Climate Change'.

The Way Forward

India's Biology Diversity Act has commendable provisions for not only conservation and sustainable use of bioresources but those on fair and equitable sharing of benefits arising from their authorized use. The key bottleneck in properly implementing this national legislation appears to be the lack of adequate awareness, not only among the general public but also among the policy makers and managers alike, about the provisions of this Act bearing on access and benefit sharing. It is further compounded by poor infrastructure and little capacity building at the grassroots level. There are also not many case studies available on the subject of granting access and benefit sharing methods to learn from the relevant experiences.

There is a growing need for extending partnership to the private sector in conserving, sustainable use and managing bioresources in the country subject to suitable terms of scientific cooperation and principle of reciprocity as recommended by the Brainstorming Session on this aspect, organized in New Delhi in 2005 (Anonymous, 2005). While developing its own policy on access to and exchange of genetic resources, the ICAR make like to take suitable note of the relatively open policy adopted by some leading developed countries, formulated to promote greater use of the collected genetic resources by researchers and breeders. For example, the volume of seed samples distributed annually by the National Plant Germplasm System of the United States has expanded steadily, to a current average of about 120,000 per year, free of charge or restriction (Bretting, 2006).

Pharmacy industry and herbal food sector deserve greater attention in the context of conservation and sustainable use of raw bio-resources used by them. India has the potential of becoming a major global player in market for medicinal plants based herbal formulations, medicines and products. According to WHO, the international market of herbal products is estimated to be US \$ 62 billion which is poised to grow to US \$ 5 trillion by the year 2050, but India's share in the global export market of medicinal plants related trade is just 0.5 per cent. Out of around 6,000 plant species used in Indian systems of medicine, data on only 960 have been recorded in trade and 179 of them are used in volumes of more than 100 MT per annum (Ved and Goraya, 2008). Given the extent of biodiversity in India, a major task of all concerned, including the policy makers and planners, has to be the identification and guided development of new products with large export potential.

India has set a vision regarding its medicinal plants sector and some major policy initiatives have been taken in this direction. A new beginning may be made by promoting on-farm cultivation of medicinal and aromatic plants, focusing on priority species as reported by various high-level expert committees (Brindavanam, 2010). At the same time, the industry estimates for raw material demand should be made available well in advance so as to regulate demand-supply scenario optimally. In addition, the role of middlemen in the supply chain needs to be streamlined by making them declare their sources of supply and also the areas from where the bioresources have been collected by their primary suppliers.

The Indian government has developed some outstanding policy measures and has also enacted legislation for promoting conservation and sustainable use of country's biological resources (and associated TK) while also meeting national obligations under international agreements like CBD, ITPGRFA, and WTO-TRIPS. Though these initiatives are highly appreciable, there exists enough scope for making these measures better focused and more effective.

A promising development in this context is the adoption of Nagoya Protocol to CBD on Access and Benefit Sharing during the COP-10 meeting, held in October this year in Japan, since it is likely to provide a fillip to developing a much awaited international regime with a framework that balances access to genetic resources on the basis of PIC and MAT with the fair and equitable sharing of benefits while taking into account the important role of TK. The agreed definition of 'genetic resources', adopted under the Nagoya Protocol on ABS, now includes 'derivatives' and this augurs well with the position taken by the biodiversity-rich developing countries on this issue. However, this only provides a lead that needs to be developed further through pro-active negotiations under CBD (Schei and Tvedt, 2010). The Biological Diversity Act defines 'biological resources' as plants, animals and micro-organisms, or parts thereof, their genetic material and byproducts (excluding value added products) with actual or potential use or value, but does not include human genetic material.

The Nagoya Protocol is expected to enter into force by 2012 when the next COP meeting would be held in India. Significant developments are then likely to follow in this direction during India's presidency. This Protocol on ABS is a landmark in the international governance of biodiversity as it proposes a global

multilateral benefit sharing mechanism. The CBD had already established the concept of fair and equitable sharing of benefits as one of the three main objectives and outlined basic principles including PIC and MAT. Yet, these principles remained largely unimplemented owing largely to a range of difficulties and different views on ways of overcoming them. With the Nagoya Protocol, the fair and equitable sharing of benefits has been reaffirmed as a fundamental component of biodiversity-dealing strategies and a set of rules has been agreed upon to facilitate, promote and ensure its effective implementation. This Protocol has also brought in TK, associated with bioresources, under the ambit of benefit sharing. However, realization of benefit sharing is linked basically to provisions of national legislation and regulatory mechanisms adopted by countries providing the bioresources.

It may be noted that only those countries, who are already Contracting Parties to CBD, are eligible to sign and ratify the Nagoya Protocol. It also needs to be pointed out in this context that the text of The Nagoya Protocol is based on intense negotiations and compromises and, as a result, its content is hazy on several highly contested issues, even excluding the use of some controversial terms despite their adoption based on consensus (UNEP-CBD document, 2010 and ENB, Summary and Analysis, 2010). Considering that some of its provisions are open to interpretation, a lot will depend upon on further development of these provisions in the context of the CBD, as well as its implementation at the national level.

Next step should be 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-compliance certificate needs to be adopted as an essential attachment with applications submitted to patent offices for seeking patents on products or processes based on bio-resources and associated TK. This may be in the form of a 'certificate of origin' issued by the national authority of the provider country as the proof of CBD-compliance.

To sum up, the stage appears to be set now for embarking on a global movement for adoption of fair and equitable sharing of benefits arising from the authorized use of genetic resources and also for generating more benefits by promoting greater use of bioresources along with expanded application of modern tools and techniques

of biotechnology. It is important for India to take a lead in this direction if this movement is to make a real headway and this can be done by setting an example through more effective implementation of the national legislation on ABS and by setting up appropriate checks and balances while putting in place an efficient monitoring system.

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ANNEX I

International Treaty on Plant Genetic Resources for Food and Agriculture

List of 64 Crops Covered Under the Multilateral System

A. Food Crops (35)

Crop	Genus	Observations
Breadfruit	<i>Artocarpus</i>	Breadfruit only
Asparagus	<i>Asparagus</i>	
Oat	<i>Avena</i>	
Beet	<i>Beta</i>	
Brassica complex	<i>Brassica</i> et al.	Genera included are: <i>Brassica</i> , <i>Armoracia</i> , <i>Barbarea</i> , <i>Camelina</i> , <i>Crambe</i> , <i>Diplotaxis</i> , <i>Eruca</i> , <i>Isatis</i> , <i>Lepidium</i> , <i>Raphanobrassica</i> , <i>Raphanus</i> , <i>Rorippa</i> , and <i>Sinapis</i> . This comprises oilseed and vegetable crops such as cabbage, rapeseed, mustard, cress, rocket, radish, and turnip. The species <i>Lepidium meyenii</i> (maca) is excluded.
Pigeon Pea	<i>Cajanus</i>	
Chickpea	<i>Cicer</i>	
Citrus	<i>Citrus</i>	Genera <i>Poncirus</i> and <i>Fortunella</i> are included as root stock.
Coconut	<i>Cocos</i>	

Contd.

Crop	Genus	Observations
Major aroids	<i>Colocasia, Xanthosoma</i>	Major aroids include taro, cocoyam, dasheen and tannia.
Carrot	<i>Daucus</i>	
Yams	<i>Dioscorea</i>	
Finger Millet	<i>Eleusine</i>	
Strawberry	<i>Fragaria</i>	
Sunflower	<i>Helianthus</i>	
Barley	<i>Hordeum</i>	
Sweet Potato	<i>Ipomoea</i>	
Grass pea	<i>Lathyrus</i>	
Lentil	<i>Lens</i>	
Apple	<i>Malus</i>	
Cassava	<i>Manihot</i>	<i>Manihot esculenta</i> only.
Banana / Plantain	<i>Musa</i>	Except <i>Musa textilis</i> .
Rice	<i>Oryza</i>	
Pearl Millet	<i>Pennisetum</i>	
Beans	<i>Phaseolus</i>	Except <i>Phaseolus polyanthus</i> .
Pea	<i>Pisum</i>	
Rye	<i>Secale</i>	
Potato	<i>Solanum</i>	Section <i>tuberosa</i> included, except <i>Solanum phureja</i> .
Eggplant	<i>Solanum</i>	Section <i>melongena</i> included.
Sorghum	<i>Sorghum</i>	
Triticale	<i>Triticosecale</i>	
Wheat	<i>Triticum</i> et al.	Including <i>Agropyron</i> , <i>Elymus</i> , and <i>Secale</i> .
Faba Bean / Vetch	<i>Vicia</i>	
Cowpea et al.	<i>Vigna</i>	
Maize	<i>Zea</i>	Excluding <i>Zea perennis</i> , <i>Zea diploperennis</i> , and <i>Zea luxurians</i> .

B. Forages (29)

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

Preliminary Evaluation of Locations for Conducting Selection for Resistance to Ergot (*Claviceps purpurea*) in Rye

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Plant breeders conduct selection for resistance in environments that maximize disease development. We studied ergot resistance in rye to assess the suitability of locations as selection environment including one very favourable location for disease development. Sixty-five populations and 245 full-sib families were evaluated in six environments across three agro-climatically diverse locations (Eckartsweier, Kleinhohenheim, Oberer-Indenhof [OLI]) and 3 years. Significant genotypic and genotype-environment interaction variations were observed for ergot severity. We further partitioned interaction variation due to linear regression of environments (b , genotypic mean at a test location regressed onto average over all environments) and remainder, and also computed simple correlation (r) and coefficient of determination (r^2) between these two variables. The b and r^2 were used as measures of discrimination ability (DA) and prediction ability (PA) of test locations; respectively. Differences due to heterogeneity among b 's were significant in all experiments except one. Ergot severity was distinctly highest at OLI. But OLI had lowest DA and PA whereas Kleinhohenheim had highest values. Our study showed that OLI having higher ergot development, was not the best selection environment. More information encompassing a larger number of environments is needed.

Key Words: *Claviceps purpurea*, Discrimination ability, Ergot, Prediction ability, Rye, *Secale cereale*, Selection environment

Introduction

Plant breeders mostly select for quantitative traits. Such traits like grain yield, have complex inheritance as their phenotypic expression is controlled by several genetic factors with small, similar and supplementary effects and is also influenced by the environment and genotype-environment (GE) interactions (Falconer and McKay, 1996). The task of improving these traits is, therefore, a difficult one. In case of quantitatively inherited host-plant resistance, the pathogen is an additional factor that influences the phenotype, and the task of breeding for resistance is complicated further (Geiger and Heun 1989). The genotypes have to be evaluated under specific conditions in a wide range of environments for conducting effective selection and this leads to large expenses. The pathogen is often artificially inoculated so as to promote uniform development of disease and reduce unaccounted variation. Whatever may be the type of selection environment, the endeavor of every plant breeder is to conduct selection in an environment that promotes the identification of genotypes that perform better in the target environment. In addition to mean performance, many criteria have been advocated for the identification of desirable selection environments (Utz, 1972; Becker and Leon, 1988; Dhillon *et al.*, 1991). Mostly r or r^2 has been used where r is the simple correlation coefficient

of the genotypic performance in a test environment with that averaged over all environments; and r^2 is referred to as prediction ability (PA) of the test environment. Another criterion that has been used is the linear regression coefficient (b) of genotypic performance in the test environment on that averaged across all environments, and is referred to as discrimination ability (DA).

Ergot, caused by *Claviceps purpurea* [Fr.] Tul., is one of the most serious diseases of rye (*Secale cereale* L.). The fungus produces mycelial mass called sclerotium that replaces the kernel, and also produces toxic alkaloids that have harmful effect on the central nervous system in mammals which is known as ergotism (Mainka *et al.*, 2007). Thus, breeding for ergot resistance is an important objective in rye breeding. In two previous studies, significant quantitative variation for this trait was reported among self incompatible, fully pollen-shedding rye, among open-pollinated (OP) populations as well as full-sib (FS) families (Mirdita *et al.*, 2008; Mirdita and Miedaner, 2009). The objective of the present study was to examine the DA and PA of test environments (location x year combinations), particularly to assess the suitability of one location distinctly more favorable for disease development than others. Many studies have been conducted to evaluate the suitability of different

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locations for conducting selection for quantitative traits, but they have not been performed for quantitative disease resistance in rye, although, they are important since host and pathogen have different ecological requirements and, therefore, contribute differentially to GE interaction. All these factors affect the expression of genetic variability in an experiment.

Materials and Methods

The materials comprised 65 OP populations (indigenous and exotic populations, and cultivars registered in Germany and Poland) and 48 to 50 FS families in each of five OP populations (245 FS families in total), namely the old Polish variety Dankovskije Selekcijine (Dank. Sel.) that is a selection from a landrace, the modern Ukrainian variety Kharkovskaja (Kharkov.), the Russian strain NEM4 and two older German populations namely Halo and Carokurz, representing the Petkus and Carsten heterotic gene pools, respectively. These gene pools are being commonly used in hybrid breeding. The experiments are referred to as OP populations experiment and FS (with the name of the parent population as a prefix) experiments, respectively.

The materials were evaluated in six environments across three locations and 3 years (see Table 1). The locations were Eckartsweier (EWE, altitude 141 masl, mean annual temperature 9.9°C, mean annual precipitation 726 mm), Kleinhohenheim (KHO, altitude 440 masl, mean annual temperature 8.2°C, mean annual precipitation 700 mm) and Oberer-Lindenhof (OLI, altitude 700 masl, mean annual temperature 6.6°C, mean annual precipitation 952 mm). The OP populations were evaluated during

2002-03 and 2004-05, and FS families during 2003-04 and 2004-05 in three-row plots (0.625 m²) and six separate lattices, each with three replications. Each test entry in all experiments was separated by four wheat plots planted in a chess-board pattern to avoid plot-by-plot interference (Mirdita *et al.*, 2008).

The inoculum, a mixture of *C. purpurea* isolates, was developed and multiplied and artificial inoculations were carried out following Kirchhoff (1929) and Engelke (2002) with some modifications reported in detail by Mirdita *et al.* (2008). Conidium suspension was sprayed with a normal plot sprayer three to four times during full flowering of the entries in the evening with 2 x 10⁶ conidia ml⁻¹ and about 1,000 l suspension per ha.

The data were recorded as ergot severity (%) on dry weight basis (100 x weight of ergot sclerotia/weight of the mixture of ergot sclerotia and grain). For this, 200-500 g of grains per plot were threshed and analysed, the sclerotia were picked by hand and weighed. The logit-transformed data were subjected to lattice analysis of an experiment in each environment and analysis of variance pooled over environments. In the pooled analysis, the variation due to GE interactions was partitioned into heterogeneity of *b*'s of environments (genotypic means in an environment regressed onto means across environments) and the remainder (Utz, 1972). The *r* between genotypic means in an environment and means across all environments were computed. The *b* and *r*² were used as estimates of DA and PA, respectively. PLABSTAT, a computer package (Utz, 2001) was used for these analyses.

Table 1. Mean (Minimum) expression of ergot severity (%) of open-pollinated (OP) populations and full-sib (FS) families of five OP populations at various locations, namely Eckartsweier (EWE), Kleinhohenheim (KHO) and Oberer-Lindenhof (OLI)¹

Location (Year)	Mean (Minimum) ergot severity (%)					
	OP Populations (n = 65) ²	Halo-FS (n = 50)	Carokurz-FS (n = 48)	Dank. Sel.-FS (n = 49)	Kharkov.-FS (n = 49)	NEM4-FS (n = 49)
EWE (2002 ³ /2004)	0.66 ³ (0.24) ³	0.32 (0.11)	1.08 (0.24)	0.70 (0.07)	1.07 (0.25)	0.25 (0.05)
KHO (2002)	0.77 (0.22)					
KHO (2004)	0.78 (0.18)	0.21 (0.06)	0.83 (0.11)	0.53 (0.05)	0.25 (0.03)	0.36 (0.09)
OLI (2003)		4.19 (1.53)	7.53 (1.80)	4.34 (3.04)	3.45 (0.92)	4.14 (1.33)
OLI (2004)	6.94 (4.07)	4.42 (1.52)	6.89 (2.53)	4.95 (2.05)	7.13 (3.61)	6.09 (1.36)

¹ Adapted from Mirdita *et al.* (2008) and Mirdita and Miedaner (2009)

² *n* is the number OP populations and the number of FS families in five OP populations, namely, Halo, Carokurz, Dankovskije Selekcijine (Dank. Sel.), Kharkovskaja (Kharkov.) and NEM4.

³ At EWE OP populations were evaluated during 2002 (marked by superscript) in 2002 and FS families in 2004

Results and Discussion

There was appreciable disease development in various experiments at all locations (Table 1). In the OP populations experiment the lowest ergot severity obtained was 0.18% at KHO (2004). In FS experiments, KHO (2004) had the minimum value (0.03%) for Kharkov. In total there were five FS families (three of Kharkov. and one of Dank. Sel. at KHO, and one of NEM4 at EWE; all during 2004) which had disease severity < 0.05%. All other FS families of five populations had disease severity higher than 0.05%, the threshold limit for the acceptance of grain samples for use as human food in Germany. At OLI, means of ergot severity in individual experiments were 3 to 35 times higher than the other locations in both years.

The mean squares (MS) due to genotypes (OP populations/FS families) in the analyses of variance for each environment and pooled over environments as well as due to environments and GE interactions in the pooled analysis over environments were significant ($P < 0.01$), thereby indicating an environment-dependent response of genotypes to the pathogen (Mirdita *et al.*, 2008; Mirdita and Miedaner 2009). Thus, by using our protocol of field inoculation and experimentation, we were able to have appreciable development of the disease and to differentiate the material for their genotypic differences for host-plant resistance in all environments.

Mean ergot severity was distinctly and consistently higher at OLI (3.45-7.53%) than at the other locations (0.21-1.08%). Between EWE and KHO, the severity was higher at KHO in two experiments (OP populations and NEM4-FS) and at EWE in the other four experiments, the average across experiments being higher for EWE. All three locations have natural occurrence of ergot infestation in rye and are highly diverse for climatic conditions. This diversity affects growth and development of the fungus as well as the host and, consequently, the

pathogen's pressure and ability of the host to counter that. *C. purpurea* cannot penetrate through the glumes. Hence, its asco- and conidiospores enter the stigma when the flower is open. Cold, rainy weather during flowering delays pollination by restricting the supply of pollen and, thereby, extends the span of flowering phase. Further, wet weather is needed for the germination of ergot spores and rapid development of the fungus (Tudzinsky *et al.*, 1995). Thus, cold and rainy weather renders rye more susceptible to ergot. The weather at OLI (the location with higher elevation, lower temperature and higher rainfall) was very favourable for the development of the disease and that led to higher disease severity as compared to other locations.

The MS due to GE interactions was sub-divided into heterogeneity among b 's of environments and remainder. The analysis yielded significant MS in all experiments except that due to heterogeneity among b 's in Halo-FS experiment (analyses not shown). The results showed that the environments differed significantly for the b of genotypic means in an environment onto genotypic means across all environments, that is, the DA, in all experiments except for Halo-FS.

Considering the experiments wherein the differences among b 's explained significant portion of GE interaction variation (Table 2), KHO (2004) had always the highest estimate of DA (1.43-1.75). On the other hand OLI had the lowest DA, in four (0.61-0.84) and one (0.62) experiments during 2004 and 2003, respectively. The estimates of PA were also the highest (0.67-0.89) for KHO (2004) in all five experiments. The lowest estimates were obtained for three experiments at OLI (Dank. Sel.-FS and NEM4-FS during 2003, and Carokurz-FS during 2004). In other experiments such estimates were obtained at EWE (Kharkov-FS during 2004) and interestingly at KHO (OP populations experiment during 2003).

Table 2. Discrimination ability (DA = regression coefficient of genotypic means in an environment onto genotypic means across environments) and prediction ability (PA = square of the correlation coefficient between genotypic means in an environment and those across environments) of different environments representing years at three locations, namely Eckartsweier (EWE), Kleinhohenheim (KHO) and Oberer-Lindenhof (OLI) (Results for Halo-FS are not presented as there were no significant difference among environments for their DA)

Location (year)	Discrimination ability (b)					Prediction ability (r^2)				
	OP Populations	Carokurz-FS	Dank. Sel.-FS	Kharkov. FS	NEM4 FS	OP Populations	Carokurz FS	Dank. Sel. FS	Kharkov. FS	NEM4 FS
EWE (2002 ¹ /2004)	0.886 ¹	0.880	1.140	0.808	0.870	0.528 ¹	0.703	0.676	0.469	0.498
KHO (2002)	0.744					0.407				
KHO(2004)	1.746	1.434	1.576	1.584	1.437	0.670	0.894	0.788	0.799	0.719
OLI (2003)		0.983	0.621	1.002	0.855	0.817	0.508	0.601	0.459	
OLI (2004)	0.624	0.703	0.663	0.606	0.838	0.547	0.662	0.682	0.566	0.529

¹ At EWE, OP populations were evaluated during 2002 (marked by superscript) in 2002 and FS families in 2004

The present study indicated that, though, OLI had distinctly higher disease severity than other locations, but it did not seem to be the best location to conduct selection for ergot resistance. The genotype(s) selected at OLI may not express the same resistance across the target environment as represented by the average across all environments evaluated. This is in spite of the fact that in the FS experiments, OLI accounts for two of the four environments and thus has greater contribution than other locations in defining the target environment. By the same logic, KHO may be expected to have higher estimates of DA and PA in populations experiment. Undoubtedly, it would have been desirable to have the target environment based on a larger number of locations but the results are interesting in view of the high contribution of OLI in defining the target environment. On the whole, this study indicates KHO to be a more appropriate location for deployment as a selection environment. Thus, these results have a significant bearing on breeding for ergot resistance in rye.

Most selection experiments are conducted under conditions favorable for the expression of the traits including disease resistance. Many studies have also been conducted to examine the relationship of mean with DA, PA and related statistics. For example, for maize grain or plant dry matter yield, Weber and Vanselow (1985), Misevic and Dumanovic (1989) and Dhillon *et al.* (1991) reported that more productive locations had better discrimination and prediction, but Pollmer *et al.* (1980) did not observe any such association of DA and PA with environmental means. In conclusion, on the basis of present study OLI did not seem to be an ideal location for conducting selection for ergot resistance. Probably, pathogen pressure was higher than appropriate. Evidently it is difficult to fully elucidate the factors characterizing poor or good DA and PA because of the complex influences of many climatic and edaphic factors on host as well as pathogen. Plant breeders endeavor to have high disease resistance to impart stability of performance to the cultivars across diverse locations which include the ones with high disease pressure. But at the same time selection for resistance under extremely high disease pressure may result in loss of some desirable genes leading to poor performance in the target environment. Thus, it is a dilemma faced by the researcher. Apparently there is a need to collect larger data and undertake more critical analyses of the factors underlying the development of ergot in rye, response of genotypes to the pathogen, and relationship of ergot resistance with other agronomic traits.

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Molecular Profiling of Parents of Some Released Rice Hybrids Using SSR Markers

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SSR markers targeting (GATA)_n motifs are known to be highly polymorphic and useful in many organisms. Twenty eight germplasm of rice (*Oryza sativa* L.) involved as parents of some of the released hybrids were subjected to polymorphism based on JGT-SSRs analyses to assess the prevalence of genetic diversity. A total of 14 primers of SSRs amplified 37 polymorphic loci. The polymorphic information content ranged from 0.535 (JGT12-8.6) to 0.929 (JGT1-16.2). Prevalence of genetic diversity was revealed by (GATA)_n SSRs as range of similarity coefficient value of 0.31 to 1. The parents were grouped by subjecting the similarity values to UPGMA based SAHN clustering. Study revealed the existence of sufficient genetic variation at DNA level in the genotypes being used as parental lines. The results suggested that a relatively less number of (GATA)_n microsatellite markers can be used for the reliable estimation of genetic diversity and identification of duplicates.

Key Words: Genotypes, JGT-SSRs, Molecular diversity, Rice

Introduction

An accurate classification of parental lines into heterotic groups is essential to facilitate selection of parents and predicting the performance of F₁ hybrids. Recent studies of genetic distance analysis of rice cultivars have focused on molecular genetic markers (Naghia *et al.*, 2002). Markers based on differences in DNA sequences between individuals generally detected more polymorphism than morphological and protein based markers. Among the series of DNA markers that can be used for detecting polymorphism, SSR markers are the important class. SSR-PCR technique is a simple and quick method that combines most of the advantages of microsatellites and amplified fragment length polymorphism to the universality of Randomly Amplified Polymorphism. Most of the microsatellite loci studied so far mainly contain dinucleotide and trinucleotide motifs while very few tetranucleotide motifs have been identified (<http://www.gramene.org> and McCouch *et al.*, 2002). With the availability of whole genome sequence of rice in the public domain, it is now possible to identify the motifs of interest through in silico approaches and develop PCR-based markers. Studies have revealed that (GATA)_n containing sequences are abundant in many eukaryotic genomes (Singh, 1995). The utility of microsatellite markers targeting (GATA)_n motifs in paternity testing, genetic counseling and individual

identification has been well demonstrated (Pena *et al.* 1994). A few preliminary studies in pearl millet (Chowdari *et al.*, 1998), rice (Davierwala *et al.* 2001), sunflower (Mosges and Friedtu, 1994) and tomato (Rao *et al.* 2006) have highlighted the potential of (GATA)_n motifs in determining the genetic variability among cultivars. However, application of these markers for revealing genetic diversity is at starting stage. The objective of the present study is to detect genetic diversity among parental lines using the polymorphism developed by (GATA)_n SSR markers.

Materials and Methods

Twenty-eight genotypes [five cytoplasmic male sterile (CMS) lines and 23 restorer (R) lines representing parental lines of experimental rice hybrids] given in Table 1 were used in the present study. The leaf material of all the twenty eight genotypes were collected from Research Farm, Directorate of Rice Research (DRR), Hyderabad.

Genomic DNA from the leaf samples (25 days old seedlings) was isolated using the procedure of Zheng *et al.* (1995) with some modifications. The isolated genomic DNA was quantified using UV Spectrophotometer (Beckmann, DU 650). The isolated genomic DNA was verified for size, intactness, homogeneity and purity. Agarose 0.8% was melted to dissolve completely and

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Table 1. The lines representing parental lines of hybrids used in molecular divergence

S.No	Genotypes	Varietal Type	Genotypes	Varietal Type
1	IR 79156A	A-Line	15 1096	R-Line
2	APMS 6A	A-Line	16 IBL57	R-Line
3	PUSA 5A	A-Line	17 619-2	R-Line
4	CRMS 32A	A-Line	18 EPLT109	R-Line
5	IR 58025A	A-Line	19 SC5 2-2-1	R-Line
6	KMR 3 R	R-Line	20 SC5-9-3	R-Line
7	BR827-35	R-Line	21 SG27-77	R-Line
8	1005	R-Line	22 SG26-120	R-Line
9	611-1	R-Line	23 118	R-Line
10	612-1	R-Line	24 124	R-Line
11	GQ-25	R-Line	25 517	R-Line
12	GQ37-1	R-Line	26 R43	R-Line
13	GQ70	R-Line	27 R55	R-Line
14	GQ120	R-Line	28 R60	R-Line

the gel was casted using the gel casting plate. Genomic DNA samples of 28 rice genotypes were loaded in each well along with 2 µl of tracking dye and run at a constant voltage of 90 volts. The gel was stained using ethidium bromide and placed over an UV trans-illuminator and viewed at 300 nm. The bands appeared as orange-coloured intact bands owing to the fluorescence of ethidium bromide and the gel was photographed using ALPHA IMAGER Gel documentation System (Alpha innotech, USA).

Quantity and quality of genomic DNA

DNA was isolated from approximately 2 cm leaf bit and quantified. Approximately 3-5 µg of DNA was isolated per sample. The DNA was found to be of high molecular weight, intact and devoid of RNA.

Selection of SSR Markers Targeting (GATA)_n Motifs

A total of 24 (GATA)_n motifs with maximum possible repeat lengths were selected and primers (Table 2) were designed using the software Fast PCR (Kalendar, 2009). It was ensured that 1-2 markers were designed for each chromosome. PCR primer pairs for the selected SSR markers targeting (GATA)_n motifs were synthesized by M/s Integrated DNA technologies, USA. The list of JGT markers used for the present study is given in Table 2.

Polymerase chain reaction (PCR) amplification

The genomic DNA of the 28 rice genotypes isolated as described earlier were subjected to PCR amplification as per the procedure described by Panaud *et al.* (1996). Briefly, 10 µl reaction mixture contained 0.2 µM of each primer (both forward and reverse primers), 200 µM of deoxyribonucleotides, 50 mM KCl, 10 mM Tris HCl (pH 8.3), 1.5 mM MgCl₂, 0.1% gelatin, 40-

Table 2. Details of 24 (GATA)_n based SSR markers used in the present study

Primer name	Primer (5'-3')	Motif	Location of GATA motif
JGT01-16.2F	tgttgctgaatgattgatgataga	(GATA)11	Upstream
JGT01-16.2R	ggacctatgtggcagcaatttgaa		
JGT02-35.2F	cggggcgaatcgaggtcag	(GATA)14	Exon
JGT02-35.2R	tcgctgttgattagatgcctc		
JGT03-0.01F	ccgatgcaccaacaccctcac	(GATA)11	Intron
JGT03-0.01R	gacgcattgtgagtttgagtgat		
JGT03-26.8F	gagcgtttgtagtaagtgttcagac	(GATA)21	Upstream
JGT03-26.8R	ggcccaaccacaacacaaat		
JGT03-36.1F	gcggcaacacgaccagctt	(GATA)10	Upstream
JGT03-36.1R	catcctgagttttgagaagcaccata		
JGT04-11.5F	agggctcgtagaagtgtccaattag	(GATA)13	Upstream
JGT04-11.5R	ccgctgggtattgcctaactg		
JGT04-18.1F	cgtggcgggtatagagcgtttgta	(GATA)21	Intron
JGT04-18.1R	agcgggctcatctccatagtc		
JGT04-28.5F	ttgaatagatcgaccgttgac	(GATA)12	Upstream
JGT04-28.5R	aaaaggcagctacgtctgagc		
JGT05-7.8F	acgggtgagattaggtattgcca	(GATA)10	Intergenic
JGT05-7.8R	agttcggacaaggggagctact		
JGT06-6.8F	gagcgtttgtaggaagtttcagat	(GATA)9	Intergenic
JGT06-6.8R	ggacaaccacaagcacaccactct		
JGT06-6.9F	tggagaggagtgatgcgtaccta	(GATA)7	Intron
JGT06-6.9R	tctattggagatgaaccaaccacc		
JGT07-17.5F	cattggatgtatagccgatagctc	(GATA)9	Intergenic
JGT07-17.5R	ttgagatggtgagcggatagccac		
JGT07-22.8F	tggcgtatctaggagcgtctgt	(GATA)27	Intergenic
JGT07-22.8R	tgtaaacatttcaaaaggcactaa		
JGT07-25.2F	agcgtttgtgcatgattgtcga	(GATA)10	Intron
JGT07-25.2R	ggcagggggtacaaggactt		
JGT08-16.7F	gaaagaattgttcccacgacctc	(GATA)8	Intron
JGT08-16.7R	gctacaattgcatgctggtatgctg		
JGT09-4.8F	cgggatactaacgcaagcaaat	(GATA)8	Upstream
JGT09-4.8R	tctgcaccactaacagggaaca		
JGT10-5.7F	tatggaagcagcaagtcggag	(GATA)9	Intergenic
JGT10-5.7R	gttgatccttcacgaccacaa		
JGT11-7.8F	cggtttaggagcgtttagga	(GATA)9	Intergenic
JGT11-7.8R	atcccttgatgccactgaaattg		
JGT11-9.9F	tctggaatgtgctctggggga	(GATA)9	Upstream
JGT11-9.9R	ctagggttaggtgaccaacagtc		
JGT11-15.2F	gatcggcgttagccttttcca	(GATA)14	Intron
JGT11-15.2R	gaacagttttgctggcaacaa		
JGT11-16.3F	ggcggcgtattagcgttgta	(GATA)13	Intron
JGT11-16.3R	agggttagcccatgttaactctct		
JGT11-22.7F	ggcggcataggagtggttag	(GATA)12	Upstream
JGT11-22.7R	cgcgggtggtcgggatgag		
JGT12-8.6F	atggcagcgttaggagcgttttag	(GATA)13	Intron
JGT12-8.6R	aacgtacctaggcagcaaaattct		
JGT12-7.7F	gagcgttttagggaagttaattggac	(GATA)8	Intron
JGT12-7.7R	ggcaccgtttgatttagattattacc		

50 ng of DNA and 0.5 unit of Taq DNA polymerase (Bangalore Genei Pvt. Ltd., Bangalore). The following thermal profile was followed: Initial denaturation at 94°C for 5 minutes and subsequent 35 cycles, each with denaturation for 94°C for 30 seconds, primer annealing at 55°C for 30 seconds and primer elongation at 72°C for 1 min. The final elongation was performed at 72°C for 7 min.

Agarose gel electrophoresis of PCR products

PCR amplified products were resolved in 4% super fine resolution (SFR) agarose gels in 0.5X TBE buffer at 200V for 3.5 hrs using Submarine Horizontal Electrophoresis Unit (CBS Scientific, USA). Before loading, the PCR amplified products were mixed with 1/6th volume of gel loading dye (40% sucrose; 0.25% bromophenol blue). The sizes of amplified fragments were determined by comparing with 50 bp ladder (MBI Fermentas). The gels were stained in Ethidium Bromide (10mg/ml) for 3 min, destained in distilled water for another 2 min, placed over the UV-transilluminator and documented at 300 nm using ALPHA IMAGER gel documentation system (M/s Alpha innotech).

Data analysis

Scoring

Qualitative multistate traits that depict an array of characters were converted into binary characters (Sneath and Sokal, 1973) based on the variations present. Only the clear and unambiguous bands of SSR markers were scored. Markers were scored for the presence and absence of the corresponding band among the genotypes. The score 1 and 0 indicate the presence and absence of the bands respectively. A data matrix comprising of '1' and '0' were formed depending upon the character and this data matrix was subjected to further analysis.

Marker polymorphism

To measure the informativeness of the markers, the polymorphism information content (PIC) for each SSR marker was calculated according to the formula:

$$PIC = 1 - \sum_{i=1}^n p_i^2 - \sum_{j=1}^n p_j^2$$

Where, 'i' is the total number of alleles detected for

SSR marker and 'Pi' is the frequency of the ith allele in the set of 28 genotypes investigated and j=i+1. This formula gives us an indicator of how many alleles a certain marker has, and how much these alleles divide evenly. The PIC value was calculated using the online software- 'Polymorphism Information Content Calculator' available at www.agri.huji.ac.

Cluster analysis

The binary data matrix is subjected to cluster analysis. Sequential Agglomerative Hierarchical Non-overlapping (SAHN) clustering was performed on Squared Euclidean distance matrix and similarity matrix using Jacquard's coefficient utilizing the Unweighted Pair Group Method with Arithmetic Averages (UPGMA) method. Data analysis was done using the software NTSYSpc version 2.02 (Rohlf, 2002).

Results and Discussion

PCR Amplification Status of GATA Specific SSR Markers

Out of the 24 GATA specific SSR markers used in the present study, 5 failed to give any amplification. Out of the remaining 19 GATA specific markers amplified (Table 3), 14 were found to be polymorphic and generated a total of 37 alleles in the 28 genotypes studied. The number of alleles per SSR marker ranged from 2-4 with an average value of 2.64. The polymorphic information content (PIC), which is a measure of allelic diversity at a locus ranged from 0.535 (JGT12-8.6) to 0.929 (JGT12-8.6). Information regarding the polymorphism status of the GATA specific SSR markers is given in Table 3 along with their PIC values. Gel images of the GATA specific (JGT 3-26.8 and JGT 11-16.2) SSR markers that exhibited good polymorphism are presented in Fig.1.

Table 3. Allelic distribution of polymorphic JGT (GATA) SSR markers among 28 genotypes

Marker Name	No. of Alleles	Allele1	Allele2	Allele3	Allele4	Polymorphic information of content (PIC)	Polymorphic alleles
JGT1-16.2	3	3	5	20	-	0.929	3
JGT2-35.2	2	25	3	-	-	0.596	2
JGT3-00.1	4	7	2	16	3	0.899	4
JGT3-26.8	3	8	11	9	-	0.886	3
JGT3-36.1	3	19	4	5	-	0.833	3
JGT4-11.5	3	1	7	20	-	0.634	3
JGT4-18.1	2	24	4	-	-	0.634	2
JGT6-6.8	3	4	2	22	-	0.730	3
JGT6-6.9	3	4	23	1	-	0.768	3
JGT7-25.2	2	26	2	-	-	0.566	2
JGT9-4.8	2	12	16	-	—	0.745	2
JGT11-15.2	2	12	16	-	-	0.745	2
JGT11-16.3	3	17	7	4	-	0.877	3
JGT12-8.6	2	27	1	-	-	0.535	2

Allelic distribution of GATA specific SSR markers

Each amplicon (band) was considered as an allele in SSR analysis. The marker JGT3-0.01 generated a maximum of four alleles, while JGT1-16.2, JGT3-26.8, JGT3-36.1, JGT4-11.5, JGT6-6.8, JGT6-6.9 and JGT11-16.3 generated 3 alleles. Six of the GATA Specific markers (JGT2-35.2, JGT4-18.1, JGT7-25.2, JGT9-4.8, JGT11-15.2 and JGT12-8.6) generated 2 alleles, while JGT4-28.5, JGT5-7.8, JGT11-7.8, JGT11-9.9 and JGT11-22.7 showed only one allele (monomorphic) among the

genotypes. The allelic distribution of the 14 GATA Specific markers among the 28 genotypes is given in Table.3.

Cluster analysis

The cluster analysis was performed using Jaccard's similarity coefficient matrices calculated from GATA specific markers to generate a dendrogram of the 28 genotypes with UPGMA algorithm (Fig. 2). The similarity coefficient ranged from 0.28 to 1.00. The dendrogram

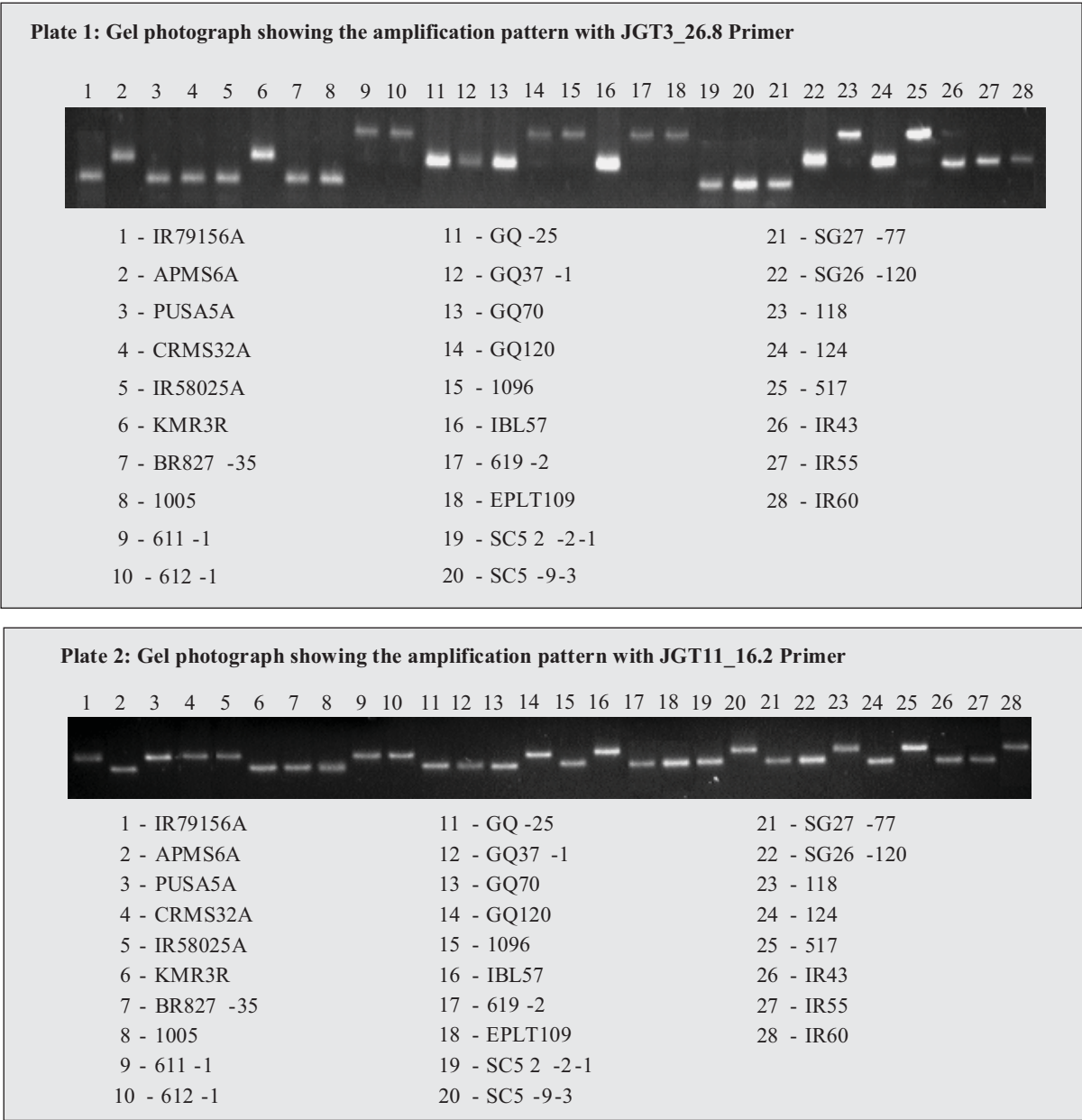


Fig. 1. Amplification pattern of (GATA) n specific SSR markers among 28 rice genotypes

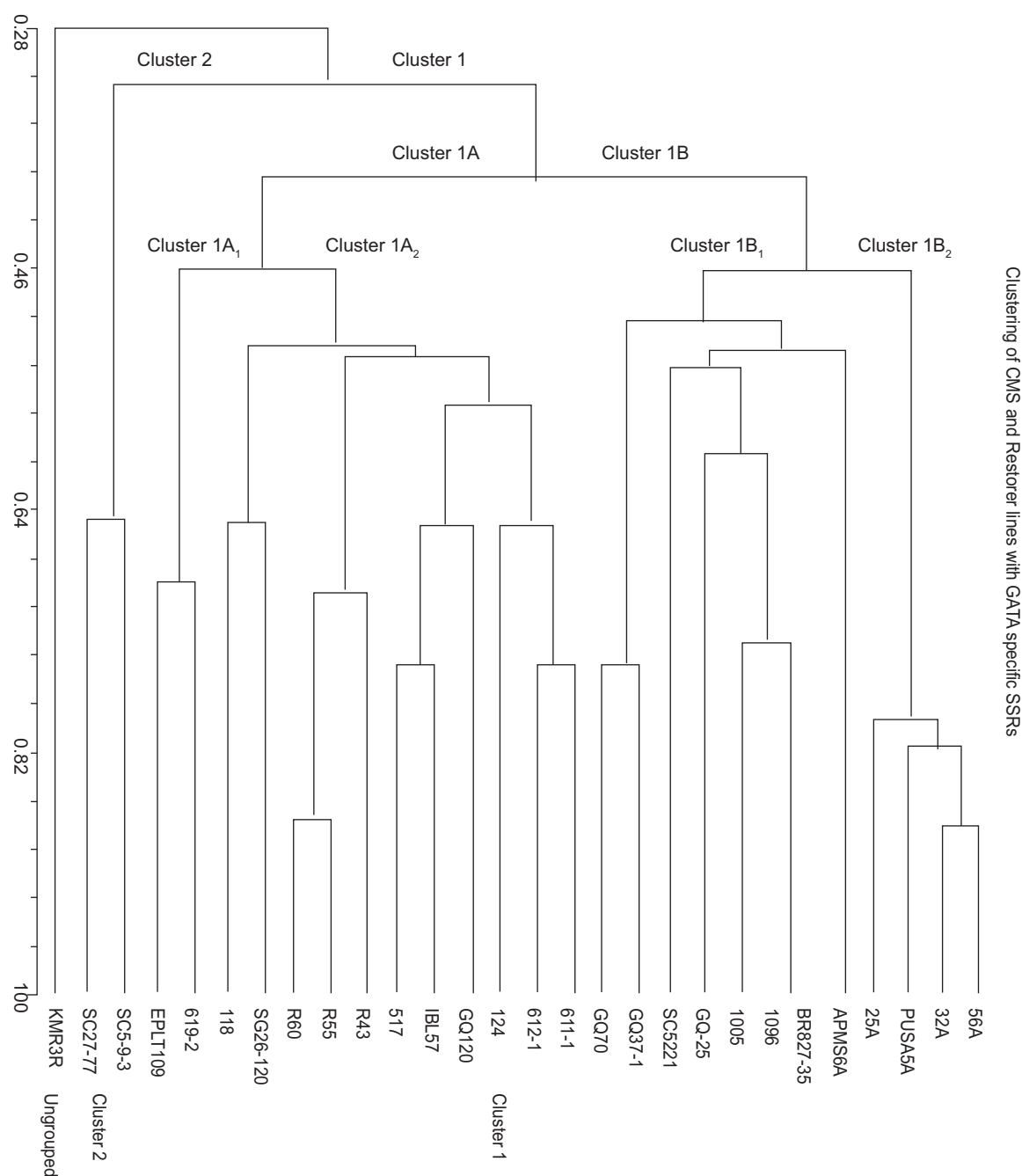


Fig. 2. Clustering of CMS and restorer lines with GATA specific SSRs

showed the grouping pattern of the 28 rice genotypes analyzed. All the 27 genotypes were grouped into two major clusters with 31.6% similarity among them, while one genotype KMR3 remain ungrouped. Two genotypes SG27-77 and SC5 9-3 were clustered in cluster 2, whereas cluster 1 divided into cluster 1A and cluster 1B. The cluster 1A was further divided into cluster 1A₁ and cluster 1A₂. In this study, the parents formed distinct subgroups from main clusters, a phenomenon which

had been noticed in other studies also (Garris *et al.*, 2005; Jain *et al.*, 2004). The cluster 1A₁ was with two genotypes EPLT 109 and 619-2, while eleven genotypes viz., 118, SG 26-120, R 60, R 55, R 45, 517, IBL-57, GQ-120, 124, 612-1 and 611-1 were clustered in the cluster 1A₂. The cluster 1B was divided into cluster 1B₁ and cluster 1B₂. The sub cluster 1B₁ had GQ-70, GQ37-1, SC5 2-2-1, GQ-25, 1005, 1096, BR 827-35 and APM 56A, whereas four CMS lines viz., IR 58025A,

PUSA5A, CRMS32A and IR 79156A were clustered under the sub cluster 1B₂. This pattern of grouping in to sub clusters corresponds to that of Glaszmann (1987) and Garris *et al.* (2005), thus, highlighting the potential of (GATA)_n motif specific microsatellite markers in genetic diversity studies.

The average similarity index based on Jaccard coefficient was 0.316, indicating a high level of diversity among the lines included in the study. The similarity coefficients ranged from (0.316) to (1.00). The representatives of similarity coefficient among the 28 rice accessions are presented in Fig. 2. The dendrogram classified rice germplasm in to two major clusters (cluster 1 and cluster 2) with 25 and 2 rice genotypes, respectively. Among the restorer parents with different names the accessions BR827-35 and 1096 with 100% similarity coefficient were collected from different sources, which may be considered as possible duplicates. Considering the grouping pattern and place of collection, GQ 37-1 and GQ 70 with 76.9% similarity; 1096 and 1005 with 73% similarity; 611 and 612-1 with 77.2% similarity; 619-2 and EPLT -109 69.7% similarity; SC59-3 and SG 27-77 66% similarity may be considered as suspected duplicates. Out of the three IRRI restorer accessions R 55 and R 60 collected from same locations were grouped together with 86.8% similarity, these two accessions can be considered as potential duplicates and R 45 can be considered as different based on grouping pattern. This is in consonance with earlier results. Olufowote *et al.* (1997) reported that the other type of DNA markers to that of RAPD gaining momentum in its usage in rice is microsatellites or SSR. The SSR markers were employed to determine the degree of relatedness and to detect duplications and seed mixtures.

However, SC5 2-2-1, SG 26-120 and SC5 9-3 collected from the same source grouped differently revealing some genetic differences between them. Similarly four genotypes (GQ-25, GQ 37-1, GQ-70 and GQ-120) collected from DRR were also grouped differently, revealing genetic differences. On the other hand accessions with same name were grouped differently like 1096 grouped with BR827-35, IBL-57 with 517, SG 26-120 with 118 and 619-2 with EPLT-109, though the place of collection was same for these collections, they are genetically different. Among the 5 CMS lines included in the study, 25A and 56A were grouped in to two clusters indicating the genetic differences.

Interestingly, two CMS lines 56A (IRRI, Philippines) and 32A (CRRI, Karnal) from different places were grouped under same cluster with 84.5% similarity. Among the 5 CMS lines APMS 6A from ANGRAU, Maruteru is different from rest of the CMS lines indicating sufficient genetic variation in producing different heterotic hybrids with different R line combinations.

The present study revealed the existence of sufficient genetic variation at DNA level in the genotypes being used as parental lines based on (GATA)_n motifs at DRR, Hyderabad. Being highly polymorphic with robust amplification, the (GATA)_n motif based microsatellite markers can be used for genetic diversity analysis and cultivar identification (Ni *et al.*, 2002). The average number of alleles and PIC value recorded for GATA markers is slightly lower than that recorded for genomic microsatellite markers in rice (Coburn *et al.*, 2002; Ni *et al.* 2002). Despite this, it is interesting to note that (GATA)_n motif specific markers exhibited good allelic diversity within cultivar groups in the present study. This diversity information will help the breeder to select diverse genotypes based on the variation at DNA level to be used in the crossing programme for realization of heterosis, identification of donor parents for useful agronomic attributes and markers linked to different polygenic traits at lower costs. By identifying 8 R lines and 1 CMS line pairs as accessions as duplicates, the present study also highlighted the presence of duplicates in R lines maintained at Directorate of Rice Research. However, it is impossible to prove to that the two accessions are genetically identical without sequencing their genomes. From germplasm management point of view, samples do not necessarily have to be completely identical in order to be considered as duplicate/redundant. Quantification of genetic diversity between samples based on screening of germplasm for large number of markers combined with passport data can be used to identify duplicate (Virk *et al.*, 1995). It can be concluded that only one of the duplicates can be selected for crossing since, it reduces the efforts for making combinations with CMS lines. The results suggested that a relatively less number of (GATA)_n microsatellite markers can be used for the reliable estimation of genetic diversity and identification of duplicates. Though (GATA)_n motifs are limited in number, PCR-based markers targeting these motifs are highly polymorphic, as evident from the present study.

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Evaluation of Castor (*Ricinus communis* L.) Germplasm for Water Use Efficiency (WUE) and Root Characters

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Sixty-four germplasm lines were sown in two root structures (30 m length, 1.5 m height and 2.4 m width on either side of central 30 cm permanent wall), thirty-two genotypes per structure replicated twice during 2006-07 at Narkhoda research farm of Directorate of Oilseeds Research, Hyderabad. Plants were grown for 100 days and observations on water use efficiency (WUE) traits, root characters and total dry matter (TDM) were recorded. Root length, root volume, root dry weight and leaf area index (LAI) showed strong positive correlation with TDM, hence lines with better root characters and TDM are considered as best lines for WUE and root characters. Fifteen lines showed root length of >195 cm, root volume of >200 cm³, root dry weight of >35 g, LAI >2.0 and TDM >250 g/plant. These lines include RG 82, RG 89, RG 122, RG 152, RG 211, RG 240, RG 272, RG 282, RG 298, RG 539, RG 627, RG 786, RG 941, RG 1667 and RG 2048.

Key Words: Castor, Root characters, TDM, Water use efficiency

Introduction

With the prediction of extreme events due to climate change, world over now there is more emphasis on breeding varieties and hybrids that can tolerate drought. As it is realized that breeding for yield *per se* is increasingly becoming difficult because of high Genotype×Environment interaction, trait based breeding is suggested. The prerequisite for such breeding programmes is identification of genotypes with one or more of such traits that impart tolerance. Among the many traits associated with drought tolerance, root characters and water use efficiency (WUE) are considered to be most relevant as the former is related to acquisition of water from soil and latter referring to efficient use of absorbed water. Improvement of these traits has been shown to increase the productivity in several species (Sheshshayee *et al.*, 2003). Therefore, an experiment was conducted to identify genotypes with better root growth and WUE traits.

Materials and Methods

Sixty-four germplasm lines with pest (Spodoptera, Semilooper, Jassids) and disease (wilt) tolerance were sown during 2006-07 in two specially constructed root structures of 30 m length, 1.5 m height and 2.4 m width on either side of central 30 cm permanent wall. Thirty-two lines were sown per structure and were replicated twice. There were four plants per replication. The spacing adopted was 90×60 cm. Recommended dose of fertilizers were applied. Plants were grown for 100 days and then

root structures were dismantled and plants along with roots were separated by using water. Observations on growth parameters viz., plant height, branches, leaf number, stem girth, WUE traits like SPAD chlorophyll meter reading (SCMR), specific leaf area (SLA) and root characters *i.e.*, root length, fresh weight, dry weight, root volume and total dry matter (TDM) were recorded. SCMR was measured using SPAD chlorophyll meter, SLA was computed by measuring leaf area and dry weight ($SLA = \text{leaf area (dm}^2) / \text{leaf dry weight (g)}$). Root volume was measured by quantifying the amount of water displaced by roots. Dried leaves which were used for measuring SCMR, SLA were powdered and these samples were sent to National facility of Isotope Ratio Mass Spectrometer (IRMS) at UAS, Bangalore for measuring ¹³C and ¹⁸O. Principal component analysis was done (Duntelman, 1994) for selecting the efficient castor genotypes with high performance in terms of shoot and root characters. In the first stage indices were developed separately for shoot and root characters using principal component analysis based on the correlation matrices. Thus, developed indices were utilized as variables for second stage principal component analysis to develop a composite index for selecting the castor genotypes. The genotypes were ranked based on the index in ascending order to select the efficient genotypes with high ranks.

Results and Discussion

The mean, range and standard deviation for different

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Table 1. Mean, range and standard deviation for different root and shoot characters in castor genotypes

Character	Plant height (cm)	Leaf number	Secondary branch number	Tertiary branch number	Stem girth (cm)	SCMR	SLA (dm ² /g)
Mean	72	23	2	2	8.5	37.0	1.76
Range	27-177	12-36	1-3	0-5	6.2-11.4	24.8-53.8	1.15-2.7
Standard deviation	37.1	5.7	0.5	1.2	1.2	5.0	0.3
Character	Root length (cm)	Root volume (cm ³)	Root dry weight (g)	LAI	TDM (g)	Root density (W/V)	Root /shoot ratio
Mean	185	169	26.7	1.8	226	0.80	13.6
Range	117-223	65-355	9.8-57.7	0.3-5.3	90-412	0.54-0.95	8.8-19.6
Standard deviation	17.6	64.1	11.1	0.84	71.2	0.09	2.5

shoot and root characters is presented in Table 1. Large genotypic variation is seen for these characters. Plant height ranged from 27 to 177 cm with an average of 72 cm. Secondary and tertiary branch number ranged from 1 to 5 with an average leaf number of 23/plant. Variation for SCMR is from 24.8 to 53.8 and for SLA it ranged from 1.15 to 2.7 dm²/g. Among different characters recorded, root length, root volume, root dry weight and leaf area index (LAI) showed strong positive correlation of >0.70 with TDM (Table 2). Different germplasm lines recorded root length ranging from 117-223 cm with an average of 185 cm; root volume differed from 65 to 355 cm³ average being 169 cm³. 10-58 g root dry weight was recorded with an average of 27 g/plant. LAI ranged from 0.3–5.3 and TDM from 90-412 g/plant. On an average, LAI of 1.8 and TDM of 226 g were recorded. The lines with better root characters and TDM are considered as best lines for WUE and root characters as these characters showed strong positive correlation with TDM.

Among the 64 lines screened, germplasm lines with >195cm root length, root volume of >200 cm³, root dry weight of >35 g, LAI >2.0 and TDM >250 g/plant and with high SCMR (>40), and low SLA (1.5) were selected and presented in Table 3. Fifteen lines which showed better growth for at least 2 to 3 shoot and root characters were selected. These lines include RG 82, RG 89, RG 122, RG 152, RG 211, RG 240, RG 272,

RG 282, RG 298, RG 539, RG 627, RG 786, RG 941, RG 1667 and RG 2048. Different shoot characters of these lines were presented in Table 4, and root characters, composite index and isotopic composition in Table 4b. Only four of these 15 lines (RG 211, RG 627, RG 941 and RG 2048) showed high SCMR (>40) and six lines showed low SLA (d" 1.6) which include RG 82, RG 89, RG 152, RG 282, RG 941 and RG 2048. These 15 lines also showed low ¹³C and high ¹⁸O values which shows their better WUE. Based on the composite index values, the top 5 genotypes include RG 152, RG 240, RG 539, RG 786 and RG 2048. These genotypes which are ranked as top ones showed efficient performance for both shoot and root growth thus confirming the composite index performed well for selecting the efficient genotypes.

Plant root system plays an important role in regulation of water uptake and extraction from deep soil layers.

Table 3. Castor lines with better root and shoot characters

Lines with	Genotypes
High Root length >195 cm	RG 34, 82, 89, 122, 152, 211, 240, 272, 282, 661, 539, 564, 627, 786, 941, 1667, 2048, 2710
High Root Volume >200 cm ³	RG 82, 89, 122, 152, 211, 240, 272, 282, 298, 539, 627, 694, 786, 941, 1667, 2048
High Root dry weight >35 g	RG 45, 82, 122, 152, 211, 240, 272, 298, 539, 627, 786, 941, 2048
High leaf area index >2.0	RG 81, 82, 117, 122, 152, 211, 240, 272, 289, 298, 539, 627, 786, 941, 2048
High total dry matter >250 g	RG 34, 45, 66, 82, 89, 90, 117, 122, 152, 211, 240, 272, 282, 297, 298, 539, 564, 627, 630, 694, 786, 941, 1667, 2048
High SPAD chlorophyll meter reading >40	RG 45, 211, 214, 226, 297, 313, 541, 627, 941, 1057, 1202, 1771, 2046, 2048
Low specific leaf area £1.5 (dm ² /g)	RG 52, 66, 78, 82, 89, 152, 282, 313, 661, 1427, 348, 357, 398, 541, 1096, 1608, 1771, 2048, 2710

Table 2. Correlation coefficients among different growth characters in castor

Characters	Mean
Root length vs TDM	0.78
Root Volume vs TDM	0.86
Root dry weight vs TDM	0.92
LAI vs TDM	0.71
SCMR vs TDM	0.04
SLA vs TDM	-0.01
SCMR vs SLA	0.011

Table 4. Plant growth characters of castor genotypes (per plant)

Germplasm lines	Plant height (cm)	Leaf number	Node number	Stem Girth (cm)	SPAD chlorophyll reading (SCMR)	Specific leaf area (SLA)	Leaf area index (LAI)	Total dry matter (TDM) (g)
RG 82	95.8	29	14	8.8	26	1.4	2.5	371
RG 89	94.8	30	15	8.9	31.2	1.5	2.4	286
RG 122	120.1	28	17	10.1	36.4	1.8	3.3	341
RG 152	145.7	21	18	10.1	36.4	1.5	2.7	389
RG 211	70.4	34	13	9.8	47.1	2.0	3.3	362
RG 240	143.1	25	17	10.7	38.8	2.7	5.3	351
RG 272	96.8	14	16	11.0	32.8	1.7	3.1	384
RG 282	84.8	29	14	9.4	38.1	1.5	2.0	315
RG 298	61.5	28	11	9.7	34.5	2.1	2.8	281
RG 539	177.3	26	21	11.4	34.9	1.93	3.5	412
RG 627	110.0	28	16	11.1	45.2	1.89	3.2	354
RG 786	120.3	27	18	10.7	34.4	1.75	2.8	333
RG 941	57.1	25	12	8.6	41.9	1.65	2.2	281
RG 1667	33.8	21	9	9.1	36.2	1.74	1.7	258
RG 2048	59.3	28	11	9.7	42.0	1.64	2.2	313
SEm ±	6.23	2.41	1.21	0.69	2.2	0.02	0.37	21.3
CD (0.05)	18.0	6.9	3.3	2.0	6.4	0.06	1.1	61.2
CV(%)	13.2	15.7	13.9	11.6	8.5	1.7	29.7	13.2

Table 5. Root characters and mass isotopes per plant in castor genotypes

Germplasm	Root characters			Isotopic composition		Composite index
	Length (cm)	Volume (cm ³)	Dry weight (g)	¹³ C	¹⁸ O	
RG 82	223	279	41.1	-26.762	28.529	
RG 89	209	203	33.9	-27.547	29.398	
RG 122	198	233	39.7	-27.018	29.326	
RG 152	218	265	59.1	-27.143	29.716	0.848
RG 211	204	206	35.7	-26.990	29.810	
RG 240	198	355	57.7	-26.306	29.419	1.037
RG 272	198	273	48	-27.541	28.287	
RG 282	198	211	33.8	-26.431	30.702	
RG 298	190	255	38.1	-26.826	29.948	
RG 539	213	317	49.4	-26.836	30.511	0.648
RG 627	203	279	47.4	-26.077	29.750	
RG 786	200	334	46.5	-25.914	30.811	0.606
RG 941	199	209	41.3	-27.137	30.068	
RG 1667	206	202	28.2	-26.098	29.652	
RG 2048	221	307	45.6	-26.701	31.021	0.730
SEm ±	11.2	19.8	4.34			
CD (0.05)	32.0	56.9	12.5			
CV(%)	8.6	16.6	23.2			

A well endowed root system is a vital mechanism of crop plants to grow under moisture deficit conditions. This in turn influences the performance of the shoot growth and has a bearing on yield potential of that genotype. Root length is an indicator of the plant's ability to absorb water from the deeper layers of soil and is influenced by better root penetrability. Among the different characters studied, root length, root volume, root dry weight and LAI showed strong positive correlation with TDM. The lines that showed better root length (>195 cm) also showed more root dry weight, LAI and TDM (Table 5). A deep rooted plant maintains leaf temperature by way of maintaining higher transpiration even under

moisture stress thus reiterates the importance of root characters. Li *et al.* (2005) have demonstrated that deep rooted rice variety exhibits significantly higher drought tolerance than shallow rooted one. Deep rooting, root length density and root distribution have been identified as drought adaptation traits. Root length and dry weight showed significant positive correlation with grain yield in stress in rice (Hanamaratti *et al.*, 2008).

Alternate approaches for measuring WUE include measuring specific leaf area (SLA), SPAD chlorophyll meter reading (SCMR). SLA is used as alternate method for estimation of genetic variability for transpiration efficiency (TE) or water use efficiency (Wright *et al.*,

1988). Similarly, SPAD reading can also provide a good estimate of leaf chlorophyll content and, hence, specific leaf nitrogen (SLN). The relation between SCMR and TE was established by Sheshshayee *et al.* (2001) in groundnut. In castor, SCMR and SLA did not show strong correlation with TDM. Only four among the 15 lines showed high SCMR (>40) and six lines showed low SLA (d'' 1.6). ^{18}O can be used as a surrogate for transpiration and stomatal conductance (gs) and high ^{18}O shows high amount of water transpired which is directly related to yield (Bindu Madhava *et al.*, 1999). Relationship between carbon isotope discrimination (CID) and WUE is studied by Farquhar and Richards (1984). Higher ^{13}C shows less WUE. The best lines identified also showed low ^{13}C and high ^{18}O values which shows their WUE. The selected fifteen lines will again be sown in field during late *rabi* along with poor root growth and WUE lines as checks by imposing stress to study their performance under field conditions.

Thus, the lines with better root length, root volume, root dry weight, LAI, TDM, high SCMR, low SLA, low ^{13}C and high ^{18}O were selected as best lines for WUE and root characters in castor.

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Association of Grain Fe and Zn Contents with Agronomic Traits in Sorghum

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Genetic variability and the association of grain Fe and Zn-contents with other agronomic traits were studied in 1,394 accessions from core germplasm maintained at the ICRISAT gene bank. A large variability for grain Fe and Zn contents were observed. The grain Fe and Zn contents of the accessions with white grains were marginally higher than those with colored grains and these white grain sorghums originated mostly from India and Zimbabwe. The Fe and Zn contents of the accessions with testa and without testa were comparable. However, endosperm texture and grain size appeared to influence grain Fe and Zn contents. Strong positive correlation between grain Fe and Zn contents and their weak association with the agronomic and grain traits indicated possibility to breed simultaneously for high grain Fe and Zn traits in varied plant agronomic backgrounds that might be suitable for different agro-climatic regions across the world.

Key Words: Iron, Micronutrient, Variability, Zinc

Introduction

Sorghum (*Sorghum bicolor* (L.) Moench) is a staple food grain in many semi-arid tropical (SAT) and tropical areas of the world because of its good adaptation to harsh environments and its good yield (Dicko *et al.*, 2006). More than 35% of sorghum is grown for direct human consumption. The rest is used primarily for animal feed, alcohol production and industrial products (FAO, 1995). Micronutrient malnutrition is primarily the result of diets poor in bio-available vitamins and minerals, mostly iron (Fe) and zinc (Zn) (Dar *et al.*, 2006). Crop varieties selected and/or bred for this purpose through a plant breeding approach will complement the existing approaches (such as other fortified foods and medical pills), and at a fraction of the cost of existing approaches. Current research focuses on identifying varieties with high Fe and Zn meeting specific agricultural and food requirements from the greater biodiversity of sorghums for their direct use and/or introgression of the traits into breeding lines to ensure health. In a set of 84 breeding lines evaluated at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, the Fe content varied from 20.1 to 37.0 mg kg⁻¹ grain and Zn content varied from 13.4 to 31.0 mg kg⁻¹ grain, indicating limited variability (Reddy *et al.*, 2005). Hence, a need was felt to explore the germplasm to identify lines with high grain Fe and Zn contents and study their associations with agronomic traits before utilization in the breeding programs.

Materials and Methods

A total of 2,974 accessions from the core collection maintained at the ICRISAT genebank representing the variability of the entire germplasm collection (about 36,774 accessions) were evaluated on Vertisols in an Augmented Design at the ICRISAT center farm, Patancheru along with four checks viz., ICSV 745, IRAT 204, Ladde Samrudhi and Paccha Jonna known for their high grain Fe and Zn contents. The material was sown on 30th November 2005. The experimental site is located at an altitude of 545 m above mean sea level with latitude of 17.53° N and longitude of 78.27° E. The site receives an average annual rainfall of 887.56 mm (average of 31 years from 1974 to 2004).

For the sake of convenience, while collecting data on plant growth and grain yield and its component traits, harvesting and processing of grain samples for Fe and Zn contents estimation, the accessions were evaluated (in contiguous blocks) as three separate groups classified based on days to 50% flowering (early: d" 65 days; medium: 66 to 80 days; late: > 80 days) in Augmented Design. The early group consisted of 1,095 accessions along with 4 checks, each repeated 11 times; the medium group consisted of 1,128 accessions along with the 4 checks, each repeated 12 times; the late group consisted of 751 accessions along with 4 checks, each repeated 8 times. Each accession was sown in one row of 2

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m length. One week after seedling emergence, the plants were thinned to maintain 10 cm spacing between plants. A fertilizer dose of 80 Kg N (half as basal and remaining half at 30 days after sowing) and 40 Kg P₂O₅ (entire as basal) was applied. Apart from this, the recommended crop production and protection packages were followed to raise a healthy crop. In each accession, the border plants were left for open-pollination and all the middle plants were selfed.

The data were collected on the traits such as days to 50% flowering, plant height (m), grain yield (t ha⁻¹), 100-grain weight (g), grain color (LB= light brown, Br= brown, DB= dark brown, Cr= cream, CW= chalky white, G= gray, R= red, W= white, Y= yellow), grain shape (C= circular, E= elliptic, NE= narrow elliptic), Grain endosperm texture (0 = 0% corneous or 100% farinaceous to 100%= 100% corneous or vitreous), Germ size (S= small, M= medium, L= large), plant agronomic aspect (taken on a 1 to 5 scale, where 1= most desirable and 5= least desirable), panicle shape (taken on a 1 to 5 scale, where 1= reverse pyramid, 2= panicle broader in the upper part, 3= symmetric, 4= panicle broader in the lower part and 5= lower part pyramidal), panicle compactness (C= compact, SC= semi-compact, SL= semi-loose, L= loose and VL= very loose), glume color (Bl= black, Br= brown, G= green, Lr= light red, P= purple, R= red, S= straw), glume coverage (0% to 100%) and presence/absence of seed sub-coat. The grain samples from some of the accessions could not be collected due to severe bird damage and in few accessions the available grains were not sufficient for estimation of Fe and Zn contents. The grain samples harvested from selfed panicles of 698 accessions of early maturity, 459 accessions of medium maturity, and 237 accessions of late maturity (making a total of 1,394 accessions), and the grain samples harvested from open-pollinated panicles of 118 accessions of early maturity, 66 accessions of medium maturity, and 30 accessions of late maturity (making a total of 214 accessions) where sufficient quantities were available. The contents of Fe and Zn in the ground grain samples (one replication per sample, random samples were duplicated) were determined by using the triacid digestion method and the Fe and Zn contents in the aliquot was determined by atomic absorption spectrometer (Sahrawat *et al.*, 2002).

Results and Discussion

Genetic variability

The Fe and Zn contents of the checks although varied, the variability was minimal as the CV% was below 15. Assuming that the variability of the check varieties was same as that of the test varieties, the trait-values of the accessions were adjusted and reported here under. A large variability for grain Fe (7.7 to 132.6 mg kg⁻¹) and Zn (15.1 to 91.3 mg kg⁻¹) contents was observed among the 1394 core accessions. The variability observed in core germplasm collection was much higher than that reported earlier, based on screening of 86 genotypes consisting of germplasm lines, hybrid parents of released/ marketed hybrids and popular varieties. In general, sorghums used as human food have white pericarp, tan plant color, straw color glumes and produce grain with medium to hard endosperms. Sorghums with brown or red color, including those with pigmented testa, are often used to produce malt and local alcoholic beverages and porridges (Rooney and Waniska, 2000). Interestingly, grain Fe and Zn contents of accessions with white grains (43.6 mg kg⁻¹ Fe and 35.1 mg kg⁻¹ Zn), which are used for human consumption in India, were marginally higher than those with colored grains (Fe content ranged from 40.4 to 42.6 ppm and Zn content ranged from 30.9 to 34.0 ppm) (Table 1). The Fe and Zn rich, white or cream colored grain sorghums originated mostly from India, Zimbabwe, Sudan and Yemen apart from other countries while those with low Fe and Zn in similar grain color background had India, Algeria, Cameroon and Sudan origin. The Fe and Zn rich, brown colored grain sorghums originated from USA, India, Spain, China, Angola and Tanzania while those with low Fe and Zn in similar grain color background had Kenya, Uganda, Mexico, Australia, Mali and Korea origin (Table 2). The Fe and Zn contents of accessions with testa (42.5 ppm Fe and 34.2 ppm Zn) and without testa (42.9 ppm Fe and 33.2 ppm Zn) were comparable (Table 1). However, endosperm texture and grain size appeared to influence grain Fe and Zn contents. While the accessions with 100% corneous endosperm had 56.2 ppm Fe and 44.3 ppm Zn contents, those with 0% to 75% corneous endosperm had less than 44.8 ppm Fe and 35.0 ppm Zn (Table 1). However, further studies are needed to confirm this. The texture of endosperm has significance in food preparations. The grains with 50% corneous endosperm are useful for

Table 1. Relationship of grain traits (colour, testa presence/absence and endosperm texture) with grain Fe and Zn contents in sorghum core germplasm collection, 2005 post-rainy season, Patancheru

Trait	# of lines	Fe (mg kg ⁻¹)		SD	Zn (mg kg ⁻¹)		SD
		Range	Mean		Range	Mean	
1. Colour of the grain							
Light Brown	29	28.8 to 63.6	41.2	8.6	21.6 to 44.4	31.8	5.7
Brown	604	7.7 to 132.6	42.6	13.4	15.8 to 91.3	34.0	8.5
Dark Brown	30	27.7 to 51.7	40.4	6.0	21.7 to 55.8	32.2	7.5
Cream	244	12.9 to 96.0	42.0	11.3	15.9 to 66.0	33.7	8.9
Chalky White	139	21.8 to 90.5	42.1	9.1	15.1 to 56.8	31.2	7.8
Gray	8	33.1 to 53.8	42.4	7.6	27.9 to 41.0	33.1	4.4
Light Red	11	31.5 to 48.1	41.6	4.8	19.8 to 29.5	30.9	9.4
Red	133	12.4 to 84.4	41.9	9.1	20.3 to 64.9	33.8	7.7
White	138	18.9 to 71.0	43.6	10.4	17.6 to 59.9	35.1	9.1
Yellow	58	22.1 to 65.6	40.9	10.6	15.7 to 52.7	30.9	8.3
2. Testa							
Present	728	7.7 to 132.6	42.5	11.7	15.7 to 66.0	34.2	8.3
Absent	666	17.6 to 128.9	42.9	11.7	15.1 to 91.3	33.2	8.7
3. Texture of the endosperm							
0 % corneous	299	20.8 to 112.4	43.4	13.2	15.8 to 91.3	34.9	9.1
25% corneous	703	7.7 to 132.6	41.7	10.3	16.0 to 63.7	33.2	7.7
50% corneous	329	15.0 to 96.0	43.2	11.3	15.1 to 66.0	33.8	9.4
75% corneous	53	24.8 to 88.6	44.8	12.4	20.0 to 55.1	35.0	8.8
100% corneous	10	48.1 to 73.9	56.2	7.8	35.1 to 53.0	44.3	5.5
4. Grain size							
Bold grain (>3.5 g 100 ⁻¹)	384	12.4 to 83.1	40.8	13.9	15.1 to 58.3	32.2	9.1
Medium grain (>2.5 g to 3.5g 100 ⁻¹)	564	19.0 to 108.4	42.6	10.2	15.9 to 66.0	33.5	8.3
Small grain (<2.5 g 100 ⁻¹)	446	7.7 to 132.6	44.4	9.3	15.8 to 91.3	35.9	7.7
Overall	1394	7.7 to 132.6	42.3	11.6	15.1 to 91.3	33.5	8.5

Table 2. Origin of germplasm lines with high and low grain Fe and Zn contents in varied grain color backgrounds

Important grain color	Micronutrient	Line*	
		High	Low
Cream	Fe	IS 8078 (Japan); IS 6413 (India), IS4622 (India), IS 2263 (Sudan)	IS 30655 (Cameroon); IS 916 (Algeria), IS 4116 (India), IS 31697 (Algeria)
	Zn	IS 2248 (India); IS 26012 (Mali), IS 28084 (Yemen); IS 27108 (Zimbabwe)	IS 5273 (India); IS 916 (Algeria); IS 23453 (India), IS 20607 (Sudan)
White	Fe	IS 25386 (Kenya); IS 30056 (Zimbabwe); IS 6975 (Sudan); IS27906 (S. Africa)	IS 16054 (Cameroon); IS 29012 (Yemen); IS 9918 (Sudan); IS 20537 (Sudan)
	Zn	IS 3790 (Taiwan); IS 24895 (Zimbabwe); IS 30056 (Zimbabwe); IS 23879 (Yemen)	IS 20537 (Sudan); IS 20552 (Sudan); IS 22381 (Sudan); IS 20502 (Sudan)
Light Red	Fe	IS 19053 (Sudan); IS 26280 (Togo); IS 22356 (Botswana); IS 20435 (Niger)	IS 22231 (Australia); IS 14433 (Lesotho); IS 20298 (Niger); IS 14869 (Cameroon)
	Zn	IS 26280 (Togo); IS 22356 (Botswana); IS 22756 (Somalia); IS 20435 (Niger)	IS 14869 (Cameroon); IS 22231 (Australia); IS 3158 (S. Africa); IS 20298 (Niger)
Red	Fe	IS 31906 (Yemen); IS 2885 (Italy); IS 28376 (Yemen); IS 26200 (Togo)	IS 16546 (Cameroon); IS 26513 (Benin); IS 13885 (S. Africa); IS 25713 (Mali)
	Zn	IS 31906 (Yemen); IS 18088 (Lebanon); IS 31984 (Yemen); IS 26200 (Togo)	IS 13585 (Uganda); IS 18745 (USA); IS 9571 (S. Africa); IS 271 (Unknown)
Yellow	Fe	IS 7881 (Nigeria); IS 22022 (India); IS 22311 (Botswana); IS 25331 (Ethiopia)	IS 21761 (Sudan); IS 24632 (Lebanon); IS 18333 (India); IS 15697 (Cameroon)
	Zn	IS 5522 (India); IS 7881 (Nigeria); IS 10973 (USA); IS 22311 (Botswana)	IS 21761 (Sudan); IS 24632 (Lebanon); IS 15697 (Cameroon); IS 24561 (Lebanon)
Brown	Fe	IS 28 (USA), IS 613 (USA); IS 6335 (India); IS 13211 (Spain)	IS 9058 (Kenya), IS 902 (Mexico); IS 22227 (Australia); IS 30520 (Korea)
	Zn	IS 6335 (India), IS 20888 (Angola); IS 30310 (China); IS 12701 (Tanzania)	IS 8891 (Uganda), IS 9058 (Kenya); IS 8084 (Uganda); IS 12380 (Mali)

*The origin of the germplasm line is given in the parentheses

preparation of 'roti' or 'chapati' (unleavened bread), the most popular food forms of sorghum grains in India, and for 'ingeri' (leavened bread), the most popular food forms of sorghum grains in some parts of Africa. Grains with more than 75% corneous endosperm are useful for preparation of 'to' the most popular food forms of sorghum grains in some parts of Africa (Anglani, 1998). The accessions with small grains (< 2.5 g 100-grain weight) had higher grain Fe (44.4 ppm) and Zn (35.9 ppm) contents than those with medium grain weight of 2.5 g to 3.5 g 100-grains (42.6 ppm Fe and 33.5 ppm Zn) and those with large grain weight of >3.5 g 100-grains (40.8 ppm Fe and 32.2 ppm Zn) (Table 1).

Association of grain Fe and Zn contents with other grain traits and agronomic traits

Correlation of grain Fe and Zn contents with agronomic and grain traits in 1394 core germplasm lines were estimated (Table 3). Fairly high correlation ($r=0.6$) between grain Fe and Zn contents suggests ample scope for simultaneous improvement of both the micronutrients. Though correlation of grain Fe and Zn contents with days to 50% flowering (0.1 for Fe and 0.2 for Zn), plant height (0.2 for Fe and 0.4 for Zn) was significant and positive, the lower magnitude of the correlation suggests near-independence of the crop growth traits and grain micronutrients contents. The results indicated that sorghum grain Fe and Zn contents can be improved in different maturity and plant stature backgrounds. Similarly, significant negative but lower magnitude of correlation of grain Fe and Zn contents with grain yield (-0.2 Fe and -0.2 Zn) and grain size (-0.1 Fe and -0.1 Zn) suggested that it is possible to enhance grain Fe and Zn contents in high yielding backgrounds with large grain. Significantly high and positive correlations were observed for grain Fe (0.9) and Zn (0.8) contents estimated from grain obtained from open-pollinated and selfed panicles.

A large variability for grain Fe and Zn contents was observed among 1394 core collection accessions. Strong positive correlation between grain Fe and Zn contents and their weak association with the agronomic and grain traits indicated possible positive outcomes from breeding simultaneously for high grain Fe and Zn traits in varied plant agronomic backgrounds that may be suitable for different regions across the world.

Table 3. Estimates of correlation of agronomic and grain traits with grain Fe and Zn contents in sorghum core germplasm collection, 2005 postrainy season, Patancheru

Trait	Fe (mg kg ⁻¹)	Zn (mg kg ⁻¹)
Days to 50% flowering	0.088**	0.207**
Plant height (m)	0.220**	0.380**
100-grain weight (g)	-0.130**	-0.143**
Grain yield (t ha ⁻¹)	-0.161**	-0.200**
Panicle shape ¹	0.063*	0.083**
Panicle compactness ²	0.214**	0.125**
Glume color ³	-0.038	-0.173**
Glume coverage% ⁴	0.278**	0.292**
Grain color ⁵	-0.016	0.002
Grain shape ⁶	-0.156**	-0.179**
Grain endosperm texture ⁷	0.071*	0.032
Germ size ⁸	0.009	0.032
Zn (ppm)	0.604**	-

n-2 = 1392; r at 5% = 0.062; r at 1% = 0.081¹Panicle shape (taken on a 1 to 5 scale, where 1= reverse pyramid, 2= panicle broader in the upper part, 3= symmetric, 4= panicle broader in the lower part and 5= lower part pyramidal), ²panicle compactness (taken on a 1 to 5 scale, where 1= compact, 2= semi-compact, 3= semi-loose, 4= loose and 5= very loose), ³glume color (taken on a 1 to 7 scale, where 1= green, 2= straw, 3= brown, 4= light red, 5= red, 6= purple, 7= black), ⁴glume coverage (taken on a 1 to 4 scale, where 1= 25%, 2= 50%, 3= 75% and 4= 100%), ⁵grain color (taken on a 1 to 9 scale, where 1= white, 2= chalky white, 3= cream, 4= yellow, 5= gray, 6= red, 7= light brown, 8= brown and 9= dark brown), ⁶grain shape (taken on a 1 to 3 scale, where 1= narrow elliptic, 2= elliptic and 3= circular), ⁷Grain endosperm texture (taken on a 1 to 5 scale, where 1= 0% corneous, 2= 25%, 3= 50%, 4= 75% and 5= 100%) and ⁸Germ size (taken on a 1 to 3 scale, where 1 = small, 2= medium, 3= large).

The accessions with high grain Fe and Zn contents are needed to be evaluated again for confirmation and simultaneously involved in the development of micronutrient-enriched cultivars with farmer-preferred traits.

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Genetic Diversity of French Bean (Bush Type) Genotypes in North-West Himalayas

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A lot of variability is available in French bean in South American continent. To breed new and better cultivars, the breeder requires a comprehensive knowledge on variability existing at the germplasm hot spots. Fifty-one French bean (bush type) genotypes of different eco-geographical origin from India and abroad were grown in replicated plots under complete randomized block design to measure the extent of diversity for further use in breeding programmes. The data recorded on 14 characters were subjected to analysis of variance. By multivariate analysis (D^2 analysis), the genetic divergence among the genotypes was quantitatively measured. The total 51 genotypes were grouped into 8 clusters by this technique. There was no relationship between clustering pattern and geographical origin. Further, the effect of genetic divergence among different genotypes, which possessed differential expression in respect of specific agronomic traits, was also worked out. Introgression of these useful gene sources from diverse clusters may prove to be useful in gene pool maintenance and will be beneficial in designing appropriate breeding strategy in future French bean improvement.

Key Words: Cluster analysis, D^2 Statistics, Diversity, French bean, Performance

Introduction

French bean is important vegetable and pulse crop belonging to family Fabaceae. It is popular among the growers and consumers because of better nutritional qualities. This vegetable not only plays an important role in human nutrition but also improve soil fertility and fits well in crop rotations because of short growing period. In the hilly regions of the country, the crop is produced during summer and rainy seasons as vegetable and fetches off-season prices to the growers in the markets in nearby plains, where the normal season of availability is spring or autumn. Therefore, to breed new and suitable planting material is always in demand. In self pollinating crops like French bean, germplasm is available in the form of a multitude of homozygous lines which can be released as genetically improved cultivars in specific ecological regions. However, for a long term crop improvement programme, a large and diverse germplasm collection is an invaluable source of parental strains for hybridization and subsequent development of improved varieties. The limiting factors resulting from normal pollination concerning biparental heredity, makes a critical choice of parents in breeding programme necessary, especially when polygenic traits are involved. Since studies on diversity are meager in this crop, the present investigation was carried out to estimate genetic divergence in French bean (bush type) genotypes including both

indigenous and exotic collections. D^2 statistics proposed by Mahalanobis (1936) offers a reliable technique to estimate the genetic divergence present in the population. These techniques measures the force of differentiation at intra cluster and inter cluster level and further helps in selecting genetically divergent parents for exploitation in hybridization programmes based on the superior mean performance. The precise information on the degree of genetic diversity and their agronomic evaluation could help in embarking upon an appropriate breeding strategy to tailor ideal genotypes, besides introgression of desirable genes from the diverse gene pool.

Materials and Methods

The experimental materials for the present study comprised of 51 genotypes obtained from different sources (Table 1). These genotypes were grown in three replications in a Randomized Block Design and spacing was maintained at 50 cm between the rows and 20 cm between the plants. The whole experiment was conducted during *Kharif* season of 2006 at the Vegetable Research Farm, Department of Vegetable Crops, Dr YS Parmar University of Horticulture and Forestry, Solan, located under the North-western Himalayan region of India. Observations were recorded on 10 randomly taken plants per replication on 14 quantitative traits such as, days to first flowering (X_1), node at which first flower appears (X_2), number

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Table 1. List of genotypes with their source

Genotype	Source	Genotype	Source
Payal	FIL India Ltd.	UHFB-19	CIAT, Colombia
IIHR-909	IIHR, Bangalore	UHFB-22	CIAT, Colombia
HAFB-3	HARP, Ranchi	UHFB-25	CIAT, Colombia
HAFB-4	HARP, Ranchi	UHFB-24	CIAT, Colombia
Arka Anoop	IIHR, Bangalore	UHFB-17	CIAT, Colombia
DWDFB-2003	UAS, Dharwad	UHFB-20	CIAT, Colombia
VLFB-2003	Almora	UHFB-12	CIAT, Colombia
VLFB-103	Almora	UHFB-11	CIAT, Colombia
EC405209	NBPGR, New Delhi	UHFB-18	CIAT, Colombia
EC405251	NBPGR, New Delhi	UHFB-10	CIAT, Colombia
PLB-44	Ludhiana	UHFB-32	CIAT, Colombia
EC8392	NBPGR, New Delhi	UHFB-33	CIAT, Colombia
Local yellow	Kinnour	UHFB-34	CIAT, Colombia
FB yellow	Ludhiana	UHFB-35	CIAT, Colombia
PLB-14	Ludhiana	UHFB-39	CIAT, Colombia
EC-8396	NBPGR, New Delhi	UHFB-40	CIAT, Colombia
CHFB-I	CHES, Ranchi	UHFB-15	CIAT, Colombia
PDR-21	IIVR, Varanasi	UHFB-03	CIAT, Colombia
EC99539	NBPGR, New Delhi	UHFB-16	CIAT, Colombia
ET-8392	NBPGR, New Delhi	UHFB-09	CIAT, Colombia
CH-812	CHES, Ranchi	UHFB-07	CIAT, Colombia
EC8391	NBPGR, New Delhi	UHFB-08	CIAT, Colombia
EC500257	NBPGR, Phagli	UHFB-28	CIAT, Colombia
EC500222	NBPGR, Phagli	Faguni	Semnis India(Pvt.) Ltd.
UHFB-23	CIAT, Colombia	Contender	Katrain, HP
		(Check)	
UHFB-26	CIAT, Colombia		

of flowers/cluster (X_3), number of pods/cluster (X_4), number of pods/plant (X_5), pod length (X_6), pod breadth (X_7), pod weight (X_8), green pod yield/plant (X_9), number of seeds/pod (X_{10}), 100 seed weight (X_{11}), seed yield/plant (X_{12}), days to first marketable maturity (X_{13}) and plant height (X_{14}). An analysis of variance and co-variance were done on the mean values of each plot. From the estimate of variance and covariance 'V' statistics, which in turn utilizes Wilk's criterion (Λ), a simultaneous test of differences between mean values of a number of correlated variables was done. Further, the analysis of genetic divergence using D^2 statistics (Mahalanobis, 1936). On the basis of the magnitude of generalized statistical distance D ($D = \sqrt{D^2}$) values, the varieties were grouped into a number of clusters as suggested by Tocher (Rao, 1952). The relative contribution of each character to the total D^2 value

between each pair of genotypes was determined following the procedures outlined by Bhatt (1970).

Results and Discussion

The analysis of variance for the 14 characters evaluated revealed significant differences among the genotypes. Using 'V' statistics, the analysis of dispersion for the test of significance of differences in the mean performance based on Wilk's criterion revealed highly significant differences between the genotypes for aggregate of 14 characters (Table 2). By using D^2 values, the 51 genotypes were clustered into 8 groups. The clustering pattern and the geographical distribution of the genotypes are presented in Table 3. A very large majority of genotypes from India and CIAT Columbia were found in cluster VII and VIII, followed by cluster V (Columbia) and cluster IV (India). The assumption of this technique is that the best parental materials may be those showing the maximum genetic divergence (Bhatt, 1970). However, the clustering pattern of bush bean genotypes did not indicate any relationship between genetic divergence and eco-geographical distribution. Cluster VII and VIII contained the geographically diverse genotypes from India and Columbia. Duddley and Davies (1960), Bhatt (1970), Dasgupta and Das (1984), Dahiya *et al.* (2002) and Gupta and Singh (2005) working with cultivars of alfalfa, Okra, Black gram and French bean respectively, also noted that genotypes are clustered in different groups irrespective of their countries of origin. Inter-cluster divergence values (D^2) between the eight clusters and their statistical distances are presented in Table 4.

The highest genetic divergence occurred between clusters IV and V ($D^2 = 86.56$), followed closely by that between clusters V and VI ($D^2 = 84.56$). However, the lowest divergence was between clusters VII and VIII ($D^2 = 22.75$). It is expected, therefore, that any cross between genotypes, namely, EC405251, PLB-44, ET-8392, EC99539 and EC8392 in cluster IV, and any

Table 2. Analysis of variance for 14 characters in French bean (Bush type)

Source	df	Mean sum of square													
		X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}
Replications	2	2.35	0.20	0.03	0.35	90.70	0.05	0.02	0.22	5055.33	0.12	10.22	150.93	0.19	1.50
Genotypes	50	257.55*	3.25*	8.31*	1.33*	189.41*	12.29*	0.41*	0.87*	6756.52*	5.12*	163.51*	1639.96*	284.17*	208.04*
Error	100	5.62	0.15	0.15	0.13	21.64	0.82	0.03	0.05	1134.24	0.26	1.92	167.70	0.77	7.20

* Significant at 5% level

• $X_1, X_2, \dots, X_{14}$ (Subscripts)

Table3. Clustering pattern of 51 genotypes of French bean on the basis of genetic divergence

Cluster	No of genotypes	Genotypes	Source
I	3	Contender, EC8396, EC500222	India
II	2	EC8391, UHFB-03	India, Columbia
III	2	Local Yellow, CH-812	India
IV	5	EC405251, PLB-44, ET8392, EC99539, EC8392	India
V	7	UHFB-26, UHFB-19, UHFB-22, UHFB-25, UHFB-24, UHFB-07, UHFB-08	Columbia
VI	2	CHFB-1, EC500257	India
VII	15	IIHR-909, HAFB-3, HAFB-4, DWDFB-2003, VLFB-2003, VLFB-103, PDR-21, UHFB-12, UHFB-18, UHFB-10, UHFB-32, UHFB-33, UHFB-35, UHFB-40, UHFB-16	India, Columbia
VIII	15	Faguni, Payal, Arka Anoop, EC405209, FB Yellow, PLB-14, UHFB-23, UHFB-17, UHFB-20, UHFB-11, UHFB-34, UHFB-39, UHFB-15, UHFB-09, UHFB-28	India, Columbia

Table 4. Average intra and inter cluster distance

Cluster	I	II	III	IV	V	VI	VII	VIII
I	16.67	51.21	43.17	39.05	59.42	50.57	35.75	36.88
II		13.55*	67.48	68.61	26.43	66.24	30.27	29.64
III			19.36**	33.31	79.83	41.89	54.33	44.63
IV				19.05	86.56**	37.40	60.85	56.36
V					15.91	84.56	31.87	36.55
VI						15.98	68.41	53.12
VII							15.53	22.75*
VIII								13.68

* Minimum Value; ** Maximum value

genotype from either V or VI will produce transgressive genetic variation within a segregating population. Further, in selecting parental materials, the important characteristics such as disease resistance, quality of produce and stability of performance should be considered. Furthermore, cluster IV had maximum cluster mean performance to days to first flowering, Number of pods per cluster, number of seeds per pod and 100 seed weight (Table 5). The genotypes included in the cluster had desirable performance for seed yield component traits. Similarly, cluster VI had genotypes with desirable number of pods/plant and days to marketable maturity. Therefore, the

Table 5. Cluster means for different characters among 51 genotypes

Characters	Cluster							
	I	II	III	IV	V	VI	VII	VIII
Days to 1 st flowering	41.73	45.03	35.75	52.94	31.33	60.13	31.79	34.92
Node at which 1 st flower appears	3.75	4.40	3.47	4.81	3.84	6.35	3.99	4.46
No. of flowers per cluster	3.97	5.40	2.97	3.51	3.31	2.64	3.76	3.42
No. of pods per cluster	3.01	2.75	2.42	3.13	1.92	2.43	2.58	2.24
No. of pods per plant	17.69	8.57	20.16	19.28	7.58	20.35	12.42	12.96
Pod length (cm)	15.31	11.15	14.07	13.83	11.95	13.24	14.15	13.69
Pod breadth (cm)	1.38	1.54	1.39	1.24	1.50	1.41	1.09	1.32
Pod weight (g)	5.49	6.76	5.97	6.27	5.99	5.55	6.07	6.13
Pod yield per plant (g)	90.41	57.79	121.28	118.64	43.18	111.97	70.29	77.80
No. of seeds per pod	5.51	3.71	3.98	5.91	4.58	5.06	5.64	5.45
100 seed weight (g)	39.40	24.67	24.57	30.46	27.14	24.32	24.68	23.23
Seed yield per plant (g)	33.82	8.03	19.13	31.49	10.85	24.51	16.40	16.36
Days to 1 st marketable maturity	55.87	58.76	48.40	67.32	45.29	75.01	44.67	47.74
Plant height (cm)	64.44	43.89	50.90	45.04	53.45	55.32	54.80	53.17

introgression between the genotypes belonging to these groups will lead to the synthesis of new gene pool which combine higher seed yield and other component traits and can act as repository for superior genetic recombinants.

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Comparative Performance of Sugarcane Genotypes against Stalk Borer (*Chilo auricilius* Dudgeon) in Punjab

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The present study was aimed at identification of the resistant/resistant clones of sugarcane against stalk borer (*Chilo auricilius*) for their exploitation in sugarcane economic breeding as the losses incurred by it to sugarcane cultivation in sub-tropical zone are upto 33% and there is no chemical control available for combating this pest in Punjab. The natural incidence of sugarcane stalk borer on 132 sugarcane genotypes/cultivars/elite clones/varieties, collected from 12 different sugarcane research centres of India, over two years has been reported. The experimental material exhibited large variations in the incidence of stalk borer ranging from 1 (Co Se 00421, Sel 18-01) to 32.91% (Co S 02258). Thirty-three genotypes showed less than five% incidence, categorized as resistant and, hence, suggested for genetic enhancement.

Key Words: Germplasm, Resistance, Stalk borer, Sugarcane

Amongst the large number of insect pests that regularly attack sugarcane crop, stalk borer (*Chilo auricilius* Dudgeon) is one of the most serious pests limiting sugarcane production especially in northern India, which can cause a loss upto 33% in cane yield and the 20.4% reduction in sucrose in juice (Jayanthi and Goud, 2002). It is active throughout the year but peak activity period is observed from July-February under Punjab conditions.

The losses caused by the borer must be minimized to increase profits but effective chemical control methods against this pest are not available and feasible (Chaudhary *et al.*, 1980). Aggravating this problem, the mechanical and cultural control methods against stalk borer are laborious and usually not followed by farmers. Hence, breeding for resistant varieties is the cheapest, reliable and most suitable method for the control of this pest. Keeping this consideration in view, the evaluation of genotypes for reaction against stalk borer was undertaken to identify promising genotypes.

Materials and Methods

The field screening was conducted on 132 sugarcane genotypes/cultivars/elite clones/varieties, collected from 12 different sugarcane research centres of India under All India Coordinated Research Programme on Sugarcane (AICRP-S). These research centres included Indian Institute of Sugarcane Research, Lucknow, Uttar Pradesh (UP); Sugarcane Breeding Institute (SBI), Coimbatore, Tamil Nadu; Chaudhary Charan Singh Haryana Agricultural University (CCSHAU), Hisar, Haryana;

Punjab Agricultural University (PAU), Ludhiana, Punjab; GB Pant University of Agriculture and Technology (GBPUAT), Pant Nagar, Uttarakhand; Rajendra Agricultural University (RAU), Pusa, Bihar; Acharya NG Ranga Agricultural University (ANGRAU), Hyderabad, AP; Orissa University of Agriculture and Technology (OUAT), Bhubaneswar, Orissa; UP Council of Sugarcane research, Shahjahanpur, UP; GS Sugarcane breeding and research institute, Seorahi, UP; Regional research station SBI, Cuddalore and Regional Agricultural Research Station, Anakappale, AP; Agricultural Research Station (ARS), Kota, Rajasthan, and advanced sugarcane breeding clones of PAU, Ludhiana, along with commercial checks. The experiment was conducted at Sugarcane research farm Ladhawal, PAU, Ludhiana, from 2004-05 to 2006-07 as per the guidelines of AICRP on sugarcane entomology. Each genotype was raised in a plot measuring 13.5 m² with 3 replications in Randomized Block Design. All the recommended package of practices of PAU, Ludhiana, for cultivation of sugarcane crop except for any insecticidal applications were followed. Parameters recorded to assess population of stalk borer at harvest were % incidence and % intensity on the basis of 25 canes/replication. Observations were recorded based on the holes in the stalk and the internal damaged portion and infestation index was calculated on the basis of following formulae

$$\text{Infestation index} = \frac{\% \text{ incidence} \times \% \text{ intensity}}{100}$$

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Results and Discussion

Stalk borer incidence varied widely among different genotypes tested in the present study as shown in Table 1. On the basis of overall comparison, no location-specific conclusions can be drawn which may be due to diverse parentage of test genotypes within the location. Moreover, the number of genotypes at one location is too less to draw conclusive interpretation (Table 2). But individual genotype information on stalk borer incidence is very useful to assess their potential for further utilization.

The comparison of the whole set of genotypes indicated wide variation for stalk borer incidence i.e. from 1.0% in Co Se 00421 and Sel 18-01 to 32.91% in Co S 02258. To accommodate the high level of variation, the genotypes were grouped into six different classes at an interval of 5% and designated as 1.0-5.0, 5.01-10.0, 10.01-15.0, 15.01-20.0, 20.01-25.0 and more than 25.01%. Thirty-three genotypes were present in the lowest incidence group of 1 to 5%, while four genotypes, namely, Co 98017, Co S 02258, Co S 88230 and Co S 96258 were grouped in maximum incidence group of >25% incidence. Rest of the 96 genotypes were grouped in four groups viz., 42 genotypes in 5.1-10%, 40 genotypes in 10.1-15.0%, 10 genotypes in 15.1-20.0% and 4 genotypes in 20.1-25.0%. The observations indicated that most of the genotypes showed lesser incidence of stalk borer during testing, only a few genotypes showed higher level of incidence in these three years 2004 to 2007 (Table 3).

Similarly, the infestation index also varied from 0 in Co Se 00421 and Sel 18-01 to 6.45 in CoS 02258. Forty genotypes showed infestation index < 0.5, 30 genotypes were in the range of 0.5-1.0, 40 genotypes were in the range of 1.0-2.0, 13 genotypes were in the range of 2.0-3.0 and 10 genotypes showed infestation index > 3.0.

The variability in the incidence of stalk borer in different genotypes has also been reported in the earlier studies. In a field study conducted in Punjab, stalk borer incidence ranged from zero to 6.7% and 17 genotypes (CoH 92, CoLk 91238, CoLk 91239, CoJ 87, CoH 92201, CoH 92202, Co 88042, S 465-94, CoS 93227, S 8846-93, S 50-94, S 93-94, S 992-94, S 161-94, CoP 96219, S 126-93 and CoS 8436) were rated comparatively resistant to stalk borer (Anonymous, 1999). Similarly, among the 24 sugarcane varieties tested for stalk borer incidence at Nayagarh, CoC 91061 found to be moderately

resistant whereas, the rest of 23 varieties were susceptible to this pest (Jena *et al.*, 1996).

In the present study genotypes CoS 8436 and CoS 767 behaved as moderately resistant against stalk borer. Similar findings have also been reported by Jaipal (1992) who found Co S 767 to be resistant to this pest amongst various sugarcane accessions and commercial hybrids evaluated.

Similarly in another screening of 15 sugarcane genotypes against *C. auricilius*, Co1148 had the highest level of stalk borer damage (7.4%) while S85-303 had the lowest (1.3%) and the genotypes S85-303 and S85-293 were least susceptible to stalk borer damage (Singh *et al.*, 1995).

The available pest management tools are inadequate to contain the losses caused by the pest. Hence, in sugarcane ecosystem varietal resistance could be a practical tool for pest management that can be fitted in the integrated pest management systems of the crop. Besides this, the resistant varieties having low pest population help in reducing the high cost of plant protection.

The promising 33 genotypes or elite clones identified in the present study are of a great significance in varietal development in sugarcane to confer insect pest resistance. Studies on parents and progeny derived from parents exhibiting a range of resistance levels for sugarcane borer (*Diatraea saccharalis*) revealed that mean percent borer-damaged internodes was higher among progeny derived from susceptible x susceptible crosses (22.8% in 1998 and 9.5%) compared to those derived from resistant x resistant crosses (20.8% in 1998 and 5.1%). Crossing a susceptible parent to a resistant parent also reduced mean percent borer-damaged internodes among the progeny compared to the susceptible parent or the susceptible x susceptible progeny and produced progeny showing transgressive segregation in both directions (Kimbeng *et al.*, 2004). Thus, the resistant genotypes identified in the present study can be further used in breeding programmes to genetically enhance resistance in sugarcane cultivars against this serious pest which can go a long way adding profitability and sustainability to the sugarcane cultivation.

A more concerted effort involving several cycles of screening and recurrent selection for resistance to borer damage is needed to identify germplasm that can withstand high levels of borer infestation.

Table 1. Reaction of different genotypes/elite clones/varieties against stalk borer at Ludhiana

S.No	Genotype	Mean incidence (%)	Mean intensity (%)	Infestation index
1	BO 128	6.46	5.20	0.34
2	BO 130	6.40	4.90	0.31
3	BO 91	4.41	5.12	0.23
4	Co 00120	4.61	12.92	0.60
5	Co 00237	4.27	7.63	0.33
6	Co 00238	6.19	11.11	0.69
7	Co 00239	6.99	9.34	0.65
8	Co 00240	8.65	19.55	1.69
9	Co 00241	6.44	14.68	0.95
10	Co 0116	7.32	7.76	0.57
11	Co 0117	11.84	9.88	1.17
12	Co 0118	11.10	10.55	1.17
13	Co 0121	11.70	10.02	1.17
14	Co 0122	7.14	7.79	0.56
15	Co 0123	15.87	15.06	2.39
16	Co 0124	9.73	7.81	0.76
17	Co 1148	11.73	16.09	1.89
18	Co 86249	19.34	13.80	2.67
19	Co 89003	24.10	22.16	5.34
20	Co 89029	4.51	4.66	0.21
21	Co 97009	13.08	15.64	2.05
22	Co 98014	4.00	7.10	0.28
23	Co 98017	28.36	12.99	3.68
24	Co 99015	23.75	15.66	3.72
25	Co 99016	13.01	17.21	2.24
26	Co A 93081	11.68	21.39	2.50
27	Co C 90063	9.75	21.35	2.08
28	Co H 110	12.26	14.22	1.74
29	Co H 115	8.38	5.43	0.46
30	Co H 117	8.79	12.72	1.12
31	Co H 118	13.38	13.46	1.80
32	Co H 119	18.81	20.07	3.78
33	Co H 92201	21.15	8.10	1.71
34	Co H 92202	4.23	7.69	0.33
35	Co J 64	13.12	11.66	1.53
36	Co J 83	9.53	8.53	0.81
37	Co J 85	6.72	11.26	0.76
38	Co J 88	11.69	11.54	1.35
39	Co J 89	2.38	1.80	0.04
40	Co J 99192	16.58	13.53	2.24
41	Co Lk 9412	9.84	8.93	0.88
42	Co Lk 9606	2.42	3.11	0.08
43	Co Lk 9616	10.18	17.05	1.74
44	Co Lk 9705	5.16	5.16	0.27
45	Co Lk 9707	3.61	2.55	0.09
46	Co Lk 9709	4.30	5.01	0.22
47	Co Lk 9710	6.76	8.21	0.55
48	Co Lk 97169	10.81	9.11	0.98
49	Co Pant 01215	6.80	12.99	0.88
50	Co Pant 01216	9.57	10.50	1.00
51	Co Pant 02217	7.61	12.86	0.98
52	Co Pant 02218	7.81	10.11	0.79
53	Co Pant 84211	10.88	5.11	0.56
54	Co Pant 84212	8.14	7.99	0.65
55	Co Pant 90223	7.24	6.01	0.44
56	Co Pant 99213	12.65	8.89	1.12
57	Co Pant 99214	10.79	8.86	0.96
58	Co Pk 1122	9.21	8.22	0.76
59	Co Pk 174	6.06	15.49	0.94
60	Co Pk 59	7.56	2.80	0.21
61	Co Pk 78	8.41	7.59	0.64
62	Co S 00221	8.21	15.26	1.25
63	Co S 00257	12.05	11.12	1.34
64	Co S 01256	12.10	8.81	1.07
65	Co S 01268	9.89	19.35	1.91

Contd.

Table 1 Contd.

S.No	Genotype	Mean incidence (%)	Mean intensity (%)	Infestation index
66	Co S 02252	5.40	6.50	0.35
67	Co S 02258	32.91	19.59	6.45
68	Co S 02264	9.23	12.19	1.13
69	Co S 767	9.35	6.22	0.58
70	Co S 8436	12.29	4.97	0.61
71	Co S 88230	26.90	18.90	5.08
72	Co S 94257	11.02	12.10	1.33
73	Co S 95258	2.62	1.11	0.03
74	Co S 96258	28.33	12.86	3.64
75	Co S 96275	12.93	14.61	1.89
76	Co S 97248	7.15	6.86	0.49
77	Co S 98259	4.66	8.44	0.39
78	Co Se 00421	1.00	0.10	0.001
79	Co Se 92423	1.85	0.66	0.01
80	Co Se 95422	10.32	9.63	0.99
81	Sel 761-98	11.74	12.34	1.45
82	Sel 842-98	10.55	15.50	1.64
83	Sel 906-98	2.13	5.74	0.12
84	Sel 922-98	10.45	14.74	1.54
85	Sel 928-98	14.21	12.61	1.79
86	Sel 943-98	11.93	10.62	1.27
87	Sel 95-98	9.77	12.70	1.24
88	Sel 17-00	10.89	16.61	1.81
89	Sel 18-00	8.21	6.10	0.50
90	Sel 19-00	2.90	0.35	0.01
91	Sel 21-00	6.60	0.89	0.06
92	Sel 22-00	6.92	5.60	0.39
93	Sel 24-00	4.41	0.69	0.03
94	Sel 25-00	11.18	18.82	2.10
95	Sel 28-00	19.20	13.87	2.66
96	Sel 49-00	16.44	14.72	2.42
97	Sel 56-00	19.49	11.84	2.31
98	Sel 63-00	2.63	0.90	0.02
99	Sel 64-00	9.36	10.17	0.95
100	Sel 67-00	6.95	16.92	1.18
101	Sel 68-00	7.55	16.43	1.24
102	Sel 69-00	4.65	9.11	0.42
103	Sel 70-00	3.35	10.94	0.37
104	Sel 77-00	8.11	8.50	0.69
105	Sel 11-01	10.73	12.44	1.33
106	Sel 12 -01	17.06	25.28	4.31
107	Sel 17-01	11.65	8.85	1.03
108	Sel 18-01	1.00	0.10	0.001
109	Sel 56-01	17.48	14.65	2.56
110	Sel 61-01	2.32	25.00	0.58
111	Sel 69-01	10.16	15.12	1.54
112	Sel 1046-03	10.01	8.23	0.82
113	Sel 1059-03	10.50	11.44	1.20
114	Sel 112-03	20.10	19.56	3.93
115	Sel 113-03	9.32	23.45	2.19
116	Sel 140-03	1.14	2.10	0.02
117	Sel 145-03	1.44	0.50	0.01
118	Sel 147-03	1.33	2.36	0.03
119	Sel 149-03	10.51	9.58	1.01
120	Sel 152-03	11.05	12.21	1.35
121	Sel 164-03	1.04	0.31	0.003
122	Sel 174-03	20.00	22.80	4.56
123	Sel 187-03	10.01	10.23	1.02
124	Sel 281-03	1.23	2.90	0.04
125	Sel 33-03	10.10	10.80	1.09
126	Sel 49-03	2.03	3.20	0.06
127	Sel 50-03	1.50	2.50	0.04
128	Sel 589-03	3.10	6.30	0.20
129	Sel 806-03	2.40	5.68	0.14
130	Sel 902-03	10.10	10.89	1.10
131	Sel 91-03	4.26	22.41	0.95
132	Sel 945-03	10.40	18.90	1.97

Table 2. Regional distribution of genotypes evaluated against stalk borer at Ludhiana

S.No.	Location	Series	Total No. of genotypes evaluated	<5 % incidence		>15 % incidence	
				No.	Per cent	No.	Per cent
1	Bihar and Orissa	BO	3	1	33.3	0	0
2	Tamil Nadu (Coimbatore)	Co	22	4	18.18	5	22.73
3	Andhra Pradesh (Anakapalli)	Co A	1	0	0	0	0
4	Kerala (Cuddalore)	Co C	1	0	0	0	0
5	Haryana (Karnal)	Co H	7	1	14.29	2	28.57
6	Punjab (Jalandhar)	Co J	6	1	16.67	1	16.67
7	UP (Lucknow)	Co Lk	8	3	37.5	0	0
8	Uttarakhand (PantNagar)	Co Pant	9	0	0	0	0
9	Rajasthan (Kota)	Co Pk	4	0	0	0	0
10	UP (Shahjahanpur)	Co S	16	2	12.5	3	18.75
11	UP (Seorahi)	Co Se	3	2	66.67	0	0
12	Punjab (Ludhiana 1998)	Sel	7	1	14.29	0	0
13	Punjab (Ludhiana 2000)	Sel	17	5	29.41	3	17.65
14	Punjab (Ludhiana 2001)	Sel	7	2	28.57	2	28.57
15	Punjab (Ludhiana 2003)	Sel	21	10	47.62	2	9.52
Total			132	32	24.24	18	13.63

Table 3. Percent incidence of Stalk borer in different genotypes

Range (%)	No. of genotypes
1.0-5.0	33
5.01-10.0	42
10.01-15.0	40
15.01-20.0	10
20.01-25.0	4
>25.01	4

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Genetic Analysis for Seed Cotton Yield and Fibre Quality Traits in Cotton (*Gossypium hirsutum* L.)

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Adoption of modern rotor spinning system by textile industry has increased demand for high fibre strength cottons. Most of the presently developed *G. hirsutum* cultivars have low fibre strength. Thus, there is an urgent need to develop improved cultivars having high yield and superior fibre quality, especially high fibre strength to meet the requirements of modern textile industry. Strain P 56-4 identified for high fibre strength was crossed with low fibre strength variety RS 2013 during 2005-06. Crosses were made during 2006 to obtain 6 generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) which were evaluated at IARI, New Delhi during 2007-08. Additive, dominance and epistatic gene effects were important for seed cotton yield, boll number, boll weight, ginning outturn, seed index and plant height. Dominance gene effects and epistasis were important for 2.5% span length and fibre elongation, and epistatic effects were important for monopodial branches, uniformity ratio and fibre strength. Heterosis breeding approach may be followed to exploit dominance and epistatic gene effects for high yield and superior fibre quality.

Key Words: Cotton, Fibre quality, Heterosis, Seed cotton yield

Introduction

Cotton is an important commercial crop in India and plays a key role in the national economy. The total cotton production of the country has shown tremendous improvement since 2003-04 and recorded an all time high production of 315 lakh bales from an area of 9.55 m hectares during 2007-08 with an average lint yield of 560 kg/ha. The productivity of cotton in India was still one of the lowest among the major cotton growing countries of the world and was also significantly lower than the world average of 794 kg/ha during 2007-08. It is, therefore, important to use the genetic variability available for different traits effectively and efficiently to increase production and productivity. Modernization of textile industry has increased the demand for high fibre strength cottons as the high speed rotor spinning reduces yarn strength by about 20-25%. Besides genetic improvement of seed cotton yield, the genetic improvement of fibre quality traits has also become essential in order to meet the requirements of the modern textile industry. Proper understanding of nature of gene action for yield and fibre quality parameters is therefore important to exploit the available genetic variability. The estimates of components of variance also have a strong bearing on the choice of breeding methods to be followed to achieve the objectives of a breeding programme. High

additive gene effects are useful in the development of pure lines. On the other hand dominance and epistatic gene effects are useful to exploit hybrid vigour. The present investigation was therefore taken up at Indian Agricultural Research Institute (IARI), New Delhi, during 2005-08 to estimate gene effects for yield and fibre quality traits by generation mean analysis.

Materials and Methods

Contrasting parents ('P 56-4' and 'RS 2013') for fibre quality traits, especially for fibre strength and fibre length, were used in this investigation. The mean fibre strength of 'P 56-4' was 27.8 g/tex as compared to 19.3 g/tex of 'RS 2013'. Its mean 2.5% span length was 28.2 mm and micronaire value was 3.9. In contrast, 'RS 2013' showed mean fibre length of 25.4 mm and micronaire value of 4.4. Crosses were made between 'P 56-4' and 'RS 2013' during 2005 to obtain F_1 . During 2006-07, the F_1 (P 56-4 x RS 2013) was advanced to F_2 generation through selfing and crosses were also made to obtain BC_1 and BC_2 generations, besides making 'P56-4' x 'RS 2013' crosses to obtain F_1 . The 6 generations P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 were evaluated in a field trial during 2007-08 at the research farm of IARI, New Delhi. The parents P 56-4 (P_1), RS 2013 (P_2) and F_1 were planted in 2 row plots; BC_1 and BC_2 in 4 row plots and F_2 in 8 row plots with 3 replications. The row

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length was 4.2 m accommodating 15 plants, spaced 30 cm apart. The row-to-row spacing was 75 cm. All the recommended agronomic and plant protection practices were followed to raise a good crop. Data were recorded on randomly selected 10 plants each in 2 parents and F_1 , 20 plants each in back cross generations (BC_1 , BC_2) and 40 plants in F_2 generation in each replication. Observations were recorded on important traits like seed cotton yield/ plant, ginning percent, boll number, boll weight, seed index, number of monopodial and sympodial branches, plant height and fibre quality traits namely 2.5% span length, uniformity ratio, fibre strength, micronaire value and fibre elongation. The generation means were calculated by taking the average over all the replications for each generation. To test the adequacy of the additive-dominance model, the individual scaling tests given by Mather (1949) as well as joint scaling test by Cavalli (1952) were used. First simple additive-dominance model consisting of mean 'm', additive component [d] and dominance component [h] was tried and adequacy of the model was tested by the chi-square test. When this model failed to explain variation among generation means, successively non-allelic parameters, i.e., additive $\times$ additive [i], additive $\times$ dominance [j] and dominance $\times$ dominance [l] were included in the model. Thus all possible models with different combinations of epistatic parameters were tried to identify the best fit model with minimum non-significant value of the chi-square and maximum number of significant parameters as suggested by Mather and Jinks (1982).

Results and Discussion

The scaling tests, joint scaling test and best fit model for yield and yield components are given in Table 1 and for fibre quality traits in Table 2. The scaling test detected the presence of epistasis for all the characters included in this study as the values for at least one or more scales 'A', 'B', 'C' and/or 'D' were significant. After the scaling test failed, the joint scaling test was applied, in which Chi-square values were also found significant for all characters except for micronaire value. This suggested the presence of epistasis for all characters except for the micronaire value. The three parameter model thus identified both additive [d] and non additive [h] components of variance as important for fibre fineness. Significance of different components detected by three parameter model for seed cotton yield, ginning outturn, boll number, boll weight, seed index, number of monopodia and sympodia, plant height, and fibre quality traits 2.5% span length, uniformity ratio, fibre strength and fibre elongation is of little value due to inadequacy of the model. The model involving m, [d], [h], [i], [j] and [l] with all parameters significant was adequate for seed cotton yield, boll number and boll weight, and opposite signs for [h] and [l] components suggested the presence of duplicate type of epistasis for these characters. Components [d], [h] and [i] were significant for ginning outturn, [d], [h], [i] and [l] for

Table 1. Estimates of different scaling tests, joint scaling test and genetic components in the best fit model for yield and yield components in the cross P 56-4 $\times$ RS 2013

Parameter	Seed cotton yield	Ginning out-turn	Boll number	Boll weight	Seed index	No. of monopodia	No. of sympodia	Plant height (cm)
Scaling test								
A	-82.42** $\pm$ 9.42	0.31 $\pm$ 0.61	-15.47** $\pm$ 3.69	-0.84** $\pm$ 0.10	-0.13 $\pm$ 0.24	0.20 $\pm$ 0.23	-2.83** $\pm$ 1.32	22.75** $\pm$ 4.87
B	-238.48** $\pm$ 19.92	1.18** $\pm$ 0.49	-57.37** $\pm$ 4.92	0.14 $\pm$ 0.10	-0.40** $\pm$ 0.18	-1.57** $\pm$ 0.24	3.07** $\pm$ 1.04	31.70** $\pm$ 4.72
C	-6.89 $\pm$ 15.25	3.90** $\pm$ 0.74	-2.63 $\pm$ 6.30	0.71** $\pm$ 0.23	1.29** $\pm$ 0.40	-0.90** $\pm$ 0.45	-1.93 $\pm$ 2.05	36.70** $\pm$ 7.91
D	-157.00** $\pm$ 12.49	-1.21** $\pm$ 0.47	-35.10** $\pm$ 3.82	-0.70** $\pm$ 0.12	-0.91** $\pm$ 0.23	-0.23 $\pm$ 0.22	1.08 $\pm$ 1.01	8.87 $\pm$ 4.69
Joint scaling test								
m	80.00** $\pm$ 2.26	32.67** $\pm$ 0.12	34.22** $\pm$ 0.76	3.00** $\pm$ 0.02	7.87** $\pm$ 0.04	3.22** $\pm$ 0.07	16.19** $\pm$ 0.34	146.59** $\pm$ 0.77
[d]	-6.13** $\pm$ 2.35	1.23** $\pm$ 0.12	2.01** $\pm$ 0.76	-0.61** $\pm$ 0.02	-1.48** $\pm$ 0.04	-0.40** $\pm$ 0.07	-0.87** $\pm$ 0.32	-22.54** $\pm$ 0.78
[h]	3.63 $\pm$ 3.68	0.90** $\pm$ 0.20	3.96** $\pm$ 1.59	0.61** $\pm$ 0.04	0.35** $\pm$ 0.07	-0.78** $\pm$ 0.13	-0.96 $\pm$ 0.63	-9.62** $\pm$ 1.67
χ^2	217.06**	30.22**	149.77**	89.73**	17.29**	47.48**	19.18**	69.43**
Best fit model								
m	75.05** $\pm$ 3.34	32.45** $\pm$ 0.16	33.24** $\pm$ 1.32	3.09** $\pm$ 0.05	7.73** $\pm$ 0.09	2.87** $\pm$ 0.09	16.23** $\pm$ 0.39	137.01** $\pm$ 1.76
[d]	-75.46** $\pm$ 10.56	-0.76** $\pm$ 0.35	-22.15** $\pm$ 2.77	1.02** $\pm$ 0.06	1.37** $\pm$ 0.14	-0.23 $\pm$ 0.13	2.98** $\pm$ 0.64	26.54** $\pm$ 3.09
[h]	316.64** $\pm$ 25.25	3.43** $\pm$ 0.96	69.90** $\pm$ 7.83	2.02** $\pm$ 0.25	2.14** $\pm$ 0.47	-0.42 $\pm$ 0.46	-2.93 $\pm$ 2.13	-22.12** $\pm$ 9.55
[i]	314.01** $\pm$ 24.98	2.42** $\pm$ 0.94	70.20** $\pm$ 7.64	1.40** $\pm$ 0.24	1.81** $\pm$ 0.47	0.47 $\pm$ 0.44	-2.17 $\pm$ 2.03	-17.75 $\pm$ 9.38
[j]	-156.06** $\pm$ 21.70	0.87 $\pm$ 0.75	-41.90** $\pm$ 5.76	0.99** $\pm$ 0.12	-0.27 $\pm$ 0.29	-1.77** $\pm$ 0.30	5.90** $\pm$ 1.49	8.95 $\pm$ 6.39
[l]	-634.91** $\pm$ 44.90	-0.93 $\pm$ 1.59	-143.03** $\pm$ 12.73	-2.10** $\pm$ 0.33	-2.34** $\pm$ 0.69	-1.83** $\pm$ 0.68	2.40 $\pm$ 3.29	72.22** $\pm$ 14.68

*, **P $\leq$ 0.05 and 0.01, respectively

Table 2. Estimates of different scaling tests, joint scaling test and genetic components in the best fit model for fibre quality parameters in the cross P 56-4 × RS 2013

Parameter	2.5% Span length (mm)	Uniformity ratio (%)	Fibre strength (g/tex)	Micronaire value	Fibre elongation
Scaling test					
A	1.85**±0.43	-1.50*±0.58	3.02**±0.55	-0.01±0.11	0.08±0.04
B	-2.01**±0.49	-1.82**±0.58	-3.84**±0.49	0.28**±0.14	-0.25**±0.05
C	1.36±0.70	-2.15±1.36	0.73±0.82	0.19±0.20	0.05±0.09
D	-0.76*±0.34	-0.59±0.59	-0.77±0.43	0.04±0.11	-0.06±0.04
Joint scaling test					
m	26.28**±0.10	53.21**±0.18	24.96**±0.10	4.11**±0.03	6.21**±0.02
[d]	-1.75**±0.10	-0.59**±0.15	-3.35**±0.10	0.28**±0.03	-0.06**±0.02
[h]	0.34±0.22	1.23**±0.37	0.28±0.22	0.28**±0.06	0.12**±0.03
÷2	54.38**	12.02**	120.88**	4.58	27.67**
Best fit model					
m	26.26**±0.11	53.77**±0.27	24.87**±0.15	4.23**±0.04	6.26**±0.01
[d]	0.10±0.25	0.38±0.25	0.26±0.31	-0.16*±0.07	0.03±0.02
[h]	2.20**±0.73	1.77±1.26	1.60±0.91	0.22±0.22	0.26**±0.09
[i]	1.53*±0.68	1.17±1.19	1.55±0.87	-0.07±0.21	0.12±0.08
[j]	-3.86**±0.55	-0.32±0.65	-6.86**±0.64	0.29±0.16	-0.34**±0.07
[l]	-1.69±1.23	-4.50**±1.69	-2.36±1.47	0.34±0.35	-0.29*±0.14

*, **Pd"0.05 and 0.01, respectively

seed index, [d], [h] and [l] for plant height, [d] and [j] for number of sympodia, and [j] and [l] for number of monopodia indicating the importance of additive and/or dominance gene effects and epistasis for different traits. Dominance gene effects and epistasis were found significant for fibre quality traits, such as components [h] and [j] for 2.5% span length, [h], [j] and [l] for fibre elongation. Epistatic effects like components [l] for uniformity ratio and [j] for fibre strength were significant. Duplicate type of epistasis was also indicated for ginning outturn, seed index, number of monopodia, 2.5% span length, uniformity ratio, fibre strength and elongation. In the present study additive, non additive and epistatic gene effects were important for seed cotton yield and yield components, *i.e.*, boll number, boll weight, ginning outturn, seed index and plant height. Additive and epistatic effects were important for number of sympodial branches. Non-additive gene effects and epistasis be involved in the inheritance of 2.5% span length and fibre elongation and epistatic effects were important for monopodial branches, uniformity ratio and fibre strength. The involvement of additive, non additive and/or epistatic effects in different yield components and fibre quality characters has also been reported by other workers (Ahuja *et al.*, 1999; Singh and Singh, 2001; Patel *et al.*, 2007). Singh *et al.*, 2008 have also

reported that additive as well as non additive gene effects were important in the inheritance of seed cotton yield, boll number, boll weight, ginning outturn and 2.5% span length. These findings are similar to the work reported in this study. They also reported different magnitude of gene effects in different crosses. It is, therefore, important to select a specific breeding strategy for a particular cross to achieve improvement in desired characters. It is also clear from the present study that besides the additive and non additive gene effects there is involvement of epistatic effects in most of the traits. It is thus important to take into consideration gene interactions in addition to additive or non additive gene effects to formulate the right breeding strategies for genetic improvement of seed cotton yield and fibre quality traits.

The study suggests heterosis breeding approach to exploit dominance and epistatic gene effects to obtain high yield and superior fibre quality.

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Studies on Variability, Heritability and Genetic Advance for Fruit Yield and its Component Traits in Early Segregating Generation in Bhendi [(*Abelmoschus esculentus* (L.) Moench)]

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An experiment was undertaken to study phenotypic and genotypic coefficients of variation, heritability and genetic advance in three double crosses and four single crosses F_2 population of okra. The analysis of variance revealed highly significant differences for the populations under study for the characters. The estimate of phenotypic and genotypic coefficients of variation were moderate to high for all the characters except days to first flowering, stem diameter (in double cross), fruit length and 100 seed weight. Heritability and genetic advance were also high for all the characters indicating the involvement of additive type of gene action in controlling these characters, hence, selection could be effective.

Key Words: *Bhendi*, Coefficient of Variation, Genotypes, Heritability

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] or *Bhendi* is an important vegetable crop cultivated throughout the world and is a native of tropical Africa. It is grown in tropical and sub-tropical parts of the world. India is the largest producer of okra covering an area of 3.91 lakh ha with an annual production of 39.7 lakh tonnes (Anon, 2004). Tender fruits are used as vegetable, eaten boiled or in culinary preparation as sliced and fried pieces. It has good nutritional value, particularly vitamin C (30 mg/100 g), calcium (90 g/100 g) and iron (1.5 mg/100 g) in the edible fruit.

Okra belongs to family Malvaceae with $2n=8x=72$ or 144 and amphidiploid in nature. It is a self pollinated crop, however occurrence of out crossing to an extent of 4 to 19 per cent by insect has been reported which renders considerable genetic diversity.

Bhendi is one vegetable crop where heterosis has been exploited successfully. Yield plateau seems to have been reached in heterotic hybrids. In order to break this barrier there is a need to develop truly potential inbred line which in combination can produce really novel hybrids with desirable maximum heterosis. Among the various approaches for developing inbred lines, selection in potential segregating population is an important one. But then, the key to success lies in developing the really promising potential segregating populations. In this regard the segregating populations developed from double cross combinations involving parents with desired diversity may prove to be better than segregating

population derived from single cross combination. As it is known the double cross combination generated employing two single cross combination which are diverse may produce the desired double cross combination. Such segregating population may serve as good source populations for identifying promising pure line varieties.

Improvement of any character depends on the magnitude of variability present in the population. The desirable variability provides valuable information regarding selection of diverse parents to be used in hybridization programme. Estimates of heritability can serve to identify the factors which can be used as indicators for high yield during selection. Keeping these things in view, the study was planned to assess genetic variability with heritability and genetic advance so as to select superior genotypes in early segregating populations.

Materials Aand Methods

The experimental material for present investigation consisting of 13 potential F_1 hybrids viz., BH 1, BH 2...BH 13 along with popular check Arka Anamika were evaluates in randomised block design (RBD) with three replications during *Kharif* 2005. The plot size was four rows each of 5 m length with a spacing of 60 cm $\times$ 30 cm. All recommended cultivation practices were followed to raise good healthy crop. Observations were recorded on five competitive plants for fifteen quantitative characters viz., days to first flowering, plant height (cm), number of branches per plant, internodal length (cm), stem diameter (cm), number of nodes at first flowering,

fruit length (cm), fruit diameter (cm), fruit weight (g), number of seeds per fruit, number of fruit per plant, pedicel length (cm), number of ridges per fruit, 100 seed weight (g) and fruit yield per plot (kg). The data was subjected to Mahalanobis (1936) D^2 statistics to assess the genetic diversity between hybrids. The hybrids were grouped in to different clusters following the Touchers' method (Rao, 1952).

Three double crosses (BH 2×BH 10, BH 2×BH 12 and BH 2×BH 13) were developed which represent maximum single cross hybrid diversity to be chosen as parents for developing double cross hybrids. These double cross hybrids were selfed to obtain F_2 populations during summer 2006. Simultaneously, the single cross hybrids involved in the generation of double cross hybrids were also selfed to derive F_2 populations. Then F_2 population of three double crosses and four single crosses, F_1 parental hybrids of three double crosses and four single crosses along with checks were evaluated in RBD with three replications during *Kharif* 2006. The plot size was two rows each for single and double cross hybrids, sixteen rows each for single and double cross F_2 population and two rows each of commercial and local checks. Row length was 6m length with a spacing of 60×30 cm. Observation were recorded on five competitive plants in each population for above mentioned characters. The data was subjected for analysis of genotypic and phenotypic coefficients of variation using the formulae suggested by Burton and Devane (1953). Broad sense heritability was calculated as per Hanson *et al.* (1956). Genetic advance was estimated by the method suggested by Johnson *et al.* (1955).

Results and Discussion

The analysis of variance for fifteen quantitative characters (Table 1) indicated the existence of highly significant differences among populations for all the characters studied. The data on mean, range, phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as per cent over mean were characterwise presented in Table 2. In single crosses F_2 population, the fruit yield per plant varied from 135.52 to 652.18 with an average mean of 340.03 g. This trait exhibited high mean PVC (31.40), GCV (26.61) heritability (72.26) and GAM (46.59). In double crosses F_2 population the yield per plant ranged from 123.93 to 759.0 with an average of 341.16 g. The double crosses also exhibited high PVC (32.38), GCV (27.44), heritability (81.71) and GAM (50.46)

Table 1. Analysis of variance (ANOVA) in respect of 16 characters in 3 double cross hybrids

S. No.	Characters	Mean sum of squares Genotypes
	Degrees of freedom	8
1	Days to first flowering	2.78**
2	Days to 50 per cent flowering	2.74**
3	plant height (cm)	48.05**
4	Number of branches per plant	0.58**
5	Inter nodal length (cm)	1.53**
6	Stem diameter (cm)	0.01**
7	Number of nodes at first flowering	0.22**
8	Pedicel length (cm)	0.24**
9	Fruit length (cm)	0.57**
10	Fruit diameter (cm)	0.07**
11	Number of ridges per fruit	0.57**
12	Seeds per fruit	71.00**
13	100 seed weight (g)	0.16**
14	Average fruit wt (g)	2.88*
15	Fruits per plant	6.83**
16	Yield per plant (g)	2397.35*

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

For days to first flowering, the mean value in low (43.83) in double cross F_2 compared to single cross F_2 (44.05). It showed low PCV (7.41 and 7.84) and GCV (7.26 and 7.29) and GAM (14.69 and 13.99), respectively, in both single and double crosses.

The plant height ranged from 55.0 to 153.5 cm with mean value of 103.25 cm in single crosses and it was 64.33 to 168.0 with mean value of 113.35 cm in double crosses. High PCV (16.92 and 17.26), GCV (16.66 and 16.94), heritability (96.27 and 96.34) and GAM (33.78 and 34.27) were noticed in both crosses. The mean value was high in double crosses compare to single crosses.

The number of branches per plant ranged from 0 to 4.3 with mean value of 1.43 and 1.44, respectively, in single and double crosses. Very high PCV (61.56 and 62.30), GCV (51.18 and 50.93), heritability (69.71 and 66.91) and GAM (87.87 and 85.79), respectively, observed in both single and double crosses.

The internodal length, the important fruit yielding character ranged from 6.25 to 15.25 with an average mean of 10.48 cm in single crosses. The mean value of double crosses ranged from 6.93 to 14.67 with average of 11.09 cm. Moderate PCV and GCV and high heritability and GAM were observed for this character.

Not many differences were seen for stem diameter in both single and double crosses. In single crosses this trait exhibited range from 0.60 to 2.27 cm with mean of 1.11 cm. This trait exhibited high PCV (25.20), GCV

Table 2. Estimates of genetic variability for quantitative characters in single and double cross F₂ populations of bhendi

S.No	Character	Genotype	Mean	Range	PCV%	GCV%	h ² %	GAM%
1	Days to first flowering	SC F2						
		BH-2	43.52	39 to 52.00	7.03	6.80	93.56	13.55
		BH-10	43.94	40 to 56.00	7.53	7.30	93.92	14.57
		BH-12	43.93	40 to 56.00	7.42	7.38	98.96	15.13
		BH-13	44.81	41 to 56.00	7.64	7.56	98.02	15.43
		Mean	44.05	40 to 55.00	7.41	7.26	96.12	14.67
		DC F2						
		BH-2 X BH-10	43.52	38 to 53.00	7.51	6.78	81.53	12.62
		BH-2 X BH-12	43.08	39 to 50.00	6.26	5.73	83.68	10.80
		BH-2 X BH-13	44.89	40 to 57.00	9.74	9.36	92.41	18.54
		Mean	43.83	39 to 53.33	7.84	7.29	85.87	13.99
2	Plant height (cm)	SC F2						
		BH-2	106.92	55.00 to 152	15.29	15.18	98.49	31.03
		BH-10	103.73	65.00 to 146	16.25	15.77	94.13	31.51
		BH-12	98.51	40.00 to 158	20.09	19.75	96.66	39.99
		BH-13	103.83	60.00 to 158	16.05	15.94	98.59	32.60
		Mean	103.25	55.00 to 153.5	16.92	16.66	96.27	33.78
		DC F2						
		BH-2 X BH-10	111.47	61.00 to 162	17.12	16.64	94.54	33.34
		BH-2 X BH-12	116.97	75.00 to 175	15.97	15.68	96.45	31.72
		BH-2 X BH-13	111.62	57.00 to 167	18.69	18.50	98.03	37.74
		Mean	113.35	64.33 to 168	17.26	16.94	96.34	34.27
3	Number of branches	SC F2						
		BH-2	1.43	0.00 to 4	56.01	50.86	82.46	95.15
		BH-10	1.50	0.00 to 5	68.13	54.09	63.04	88.48
		BH-12	1.34	0.00 to 4	67.29	55.20	67.28	93.26
		BH-13	1.43	0.00 to 3	54.82	44.56	66.06	74.60
		Mean	1.43	0.00 to 4	61.56	51.18	69.71	87.87
		DC F2						
		BH-2 X BH-10	1.60	0.00 to 5	59.76	49.78	69.38	85.41
		BH-2 X BH-12	1.40	0.00 to 4	63.08	51.99	67.94	88.28
		BH-2 X BH-13	1.31	0.00 to 4	64.06	51.01	63.40	83.67
		Mean	1.44	0.00 to 4.333	62.30	50.93	66.91	85.79
4	Internodal length (cm)	SC F2						
		BH-2	11.09	6.50 to 15.2	17.60	17.30	96.64	35.04
		BH-10	10.12	5.20 to 14.5	19.30	17.77	84.75	33.69
		BH-12	10.66	6.90 to 15.0	16.76	14.19	71.67	24.74
		BH-13	10.05	6.40 to 16.3	16.62	14.63	77.51	26.53
		Mean	10.48	6.25 to 15.25	17.57	15.97	82.64	30.00
		DC F2		to				
		BH-2 X BH-10	11.64	7.60 to 15.2	17.11	16.22	89.81	31.66
		BH-2 X BH-12	10.84	6.60 to 14.5	15.39	14.49	88.65	28.10
		BH-2 X BH-13	10.79	6.60 to 14.3	18.09	16.71	85.32	31.79
		Mean	11.09	6.93 to 14.67	16.86	15.80	87.93	30.52
5	Stem diameter (cm)	SC F2						
		BH-2	1.20	0.43 to 2.4	35.28	33.02	87.60	63.67
		BH-10	1.13	0.70 to 2.1	22.97	17.28	56.58	26.77
		BH-12	1.06	0.60 to 2.4	22.52	18.42	66.87	31.02
		BH-13	1.06	0.67 to 2.2	20.01	11.39	32.41	13.36
		Mean	1.11	0.60 to 2.275	25.20	20.03	60.86	33.71
		DC F2						
		BH-2 X BH-10	1.13	0.67 to 2.3	18.98	11.15	34.48	13.48
		BH-2 X BH-12	1.08	0.64 to 1.622	17.36	9.63	30.76	11.00
		BH-2 X BH-13	1.15	0.73 to 1.8	16.36	8.99	30.16	10.17
		Mean	1.12	0.68 to 1.907	17.57	9.92	31.80	11.55

Contd.

Table 2. Contd.

S.No	Character	Genotype	Mean	Range	PCV%	GCV%	h ² %	GAM%
6	Number of nodes at first flowering	SC F2						
		BH-2	2.59	1.00 to 5	33.37	25.41	57.97	39.85
		BH-10	2.52	1.00 to 4	26.76	22.15	68.50	37.76
		BH-12	2.58	1.00 to 5	30.90	23.95	60.10	38.25
		BH-13	2.55	1.00 to 6	33.67	21.32	40.11	27.82
		Mean	2.56	1.00 to 5	31.17	23.21	56.67	35.92
		DC F2						
		BH-2 X BH-10	2.35	1.00 to 7	36.86	27.24	54.59	41.45
		BH-2 X BH-12	2.29	1.00 to 5	34.41	26.15	57.77	40.95
		BH-2 X BH-13	2.51	1.00 to 6	35.81	28.41	62.97	46.44
		Mean	2.38	1.00 to 6	35.69	27.27	58.44	42.95
7	Fruit length (cm)	SC F2						
		BH-2	13.46	9.70 to 21.30	13.41	12.65	88.92	24.57
		BH-10	13.96	9.88 to 18.75	13.86	12.78	84.96	24.26
		BH-12	14.15	9.75 to 20.68	16.06	15.48	92.90	30.73
		BH-13	13.20	9.98 to 17.38	10.96	8.86	65.39	14.76
		Mean	13.69	9.83 to 19.53	13.57	12.44	83.04	23.58
		DC F2						
		BH-2 X BH-10	13.64	9.62 to 18.68	12.71	11.91	87.80	22.99
		BH-2 X BH-12	14.36	9.78 to 19.92	15.61	14.87	90.82	29.20
		BH-2 X BH-13	13.34	10.15 to 18.60	11.65	10.37	79.32	19.03
		Mean	13.78	10.00 to 18.24	12.16	10.67	76.55	19.35
8	Fruit diameter (cm)	SC F2						
		BH-2	1.69	1.02 to 2.68	16.75	15.56	86.27	29.76
		BH-10	1.73	0.90 to 2.62	19.06	17.60	85.31	33.49
		BH-12	1.64	1.10 to 2.46	15.31	11.97	61.13	19.28
		BH-13	1.62	0.10 to 2.42	19.18	17.96	87.69	34.65
		Mean	1.67	0.78 to 2.545	17.58	15.77	80.10	29.30
		DC F2						
		BH-2 X BH-10	1.58	0.80 to 2.84	23.47	21.84	86.57	41.85
		BH-2 X BH-12	1.72	1.02 to 3.4	31.37	24.94	63.20	40.84
		BH-2 X BH-13	1.65	0.98 to 2.98	20.65	20.64	99.95	42.56
		Mean	1.65	0.93 to 3.073	25.16	22.48	83.28	41.75
9	Fruit weight (g)	SC F2						
		BH-2	17.74	10.30 to 31.75	21.28	18.73	77.46	33.96
		BH-10	17.70	9.80 to 35.00	25.16	23.52	87.37	45.29
		BH-12	16.24	9.20 to 28.26	21.09	19.41	84.74	36.81
		BH-13	16.45	9.50 to 29.30	22.08	18.39	69.37	31.55
		Mean	17.03	9.70 to 31.08	22.40	20.01	79.74	36.90
		DC F2						
		BH-2 X BH-10	17.21	10.00 to 24.40	21.30	20.00	87.64	34.72
		BH-2 X BH-12	18.75	8.30 to 32.00	22.83	20.38	77.84	33.40
		BH-2 X BH-13	16.57	8.30 to 30.00	25.09	22.21	78.36	40.51
		Mean	17.51	8.87 to 28.80	23.07	20.86	81.28	36.21
10	Number of seeds per fruit	SC F2						
		BH-2	57.80	30.00 to 102	17.63	15.80	80.40	29.19
		BH-10	54.10	40.30 to 80	13.45	12.00	79.70	22.08
		BH-12	56.28	20.00 to 110	17.89	15.95	79.42	29.28
		BH-13	55.87	23.00 to 87	15.91	13.78	75.03	24.60
		Mean	56.02	28.33 to 94.75	16.22	14.38	78.64	26.29
		DC F2						
		BH-2 X BH-10	54.69	40.26 to 88	16.27	15.09	85.99	28.83
		BH-2 X BH-12	54.69	39.26 to 110	18.21	17.22	89.42	33.54
		BH-2 X BH-13	55.89	40.20 to 120	15.57	14.55	87.32	28.01
		Mean	55.09	39.91 to 106	16.68	15.62	87.58	30.12

Contd.

Table 2. Contd.

S.No	Character	Genotype	Mean	Range	PCV%	GCV%	h ² %	GAM%
11	Number of fruits per plant	SC F2						
		BH-2	19.42	10.00 to 32	22.13	19.18	75.11	34.24
		BH-10	20.39	10.00 to 39	22.37	19.43	75.42	34.76
		BH-12	20.36	10.00 to 37	21.62	20.19	87.17	38.83
		BH-13	19.87	6.00 to 30	21.62	18.26	71.28	31.75
		Mean	20.01	9.00 to 34.5	21.94	19.26	77.24	34.90
		DC F2						
		BH-2 X BH-10	22.69	8.00 to 32	21.13	20.00	89.64	39.02
		BH-2 X BH-12	19.09	8.00 to 32	22.49	20.05	79.43	36.80
		BH-2 X BH-13	19.25	7.00 to 34	24.44	22.35	83.67	42.12
		Mean	20.34	7.67 to 32.67	22.69	20.80	84.25	39.31
12	Pedicel length(cm)	SC F2						
		BH-2	3.05	1.20 to 4.5	24.23	21.26	87.73	43.79
		BH-10	3.24	2.00 to 4.5	18.30	9.97	54.48	20.53
		BH-12	3.52	2.15 to 4.52	16.06	5.66	35.24	11.66
		BH-13	3.72	2.24 to 6.68	21.31	16.77	78.66	34.54
		Mean	3.38	1.90 to 5.05	19.97	13.41	64.03	27.63
		DC F2						
		BH-2 X BH-10	3.58	1.60 to 5.2	19.75	13.66	69.16	28.14
		BH-2 X BH-12	3.31	1.86 to 5.12	22.25	14.45	64.93	29.77
		BH-2 X BH-13	3.53	2.13 to 6.24	21.95	17.11	77.91	35.24
		Mean	3.47	1.86 to 5.52	21.32	15.07	70.67	31.05
13	Number of ridges per fruit	SC F2						
		BH-2	5.46	5.00 to 7.9	11.13	11.05	98.57	22.61
		BH-10	5.49	5.00 to 8	13.81	13.27	92.41	26.28
		BH-12	5.40	5.00 to 8.6	14.26	13.94	95.55	28.07
		BH-13	5.41	5.00 to 8.6	14.71	14.27	94.16	28.53
		Mean	5.44	5.00 to 8.275	13.48	13.13	95.17	26.37
		DC F2						
		BH-2 X BH-10	5.48	5.00 to 8.6	14.66	13.92	90.15	27.22
		BH-2 X BH-12	5.55	5.00 to 8.2	15.35	15.29	99.17	31.36
		BH-2 X BH-13	5.46	5.00 to 8.6	14.26	13.50	89.67	26.33
		Mean	5.50	5.00 to 8.467	14.76	14.24	93.00	28.31
14	100 Seed weight (g)	SC F2						
		BH-2	6.94	6.56 to 7.26	2.02	1.61	63.87	2.65
		BH-10	7.20	6.69 to 8.6	4.90	4.07	69.20	6.98
		BH-12	6.98	6.50 to 8.5	4.02	3.13	60.64	5.03
		BH-13	6.90	6.05 to 7.52	3.53	2.91	67.58	4.92
		Mean	7.00	6.45 to 7.97	3.62	2.93	65.33	4.89
		DC F2						
		BH-2 X BH-10	7.19	6.67 to 7.8	4.20	4.11	96.01	8.30
		BH-2 X BH-12	7.08	6.56 to 7.8	3.52	3.34	89.72	6.51
		BH-2 X BH-13	6.99	6.56 to 7.6	2.39	1.82	58.03	2.86
		Mean	7.09	6.60 to 7.733	3.37	3.09	81.25	5.89
15	Yield per plant (g)	SC F2						
		BH-2	344.60	136.20 to 674.3	31.93	27.26	72.87	47.94
		BH-10	355.57	161.84 to 700	32.59	27.52	66.10	41.30
		BH-12	330.85	160.00 to 638	29.76	27.41	84.85	52.01
		BH-13	329.11	83.22 to 596.4	32.59	27.52	65.23	45.13
		Mean	340.03	135.32 to 652.18	31.40	26.61	72.26	46.59
		DC F2						
		BH-2 X BH-10	356.33	112.16 to 840	32.74	28.64	92.49	54.75
		BH-2 X BH-12	355.12	142.88 to 747	32.65	25.60	74.56	45.54
		BH-2 X BH-13	312.04	116.76 to 690	31.77	28.07	78.06	51.08
		Mean	341.16	123.93 to 759	32.38	27.44	81.70	50.46

SC – Single cross, DC – Double cross

(20.03), heritability (60.86) and GAM (63.07). In double crosses the range was 0.68 to 1.90 cm with mean of 1.12 cm but it exhibited low PCV, GCV, heritability and GAM (17.57, 9.92, 31.80 and 11.55, respectively).

The number of nodes at first flowering varied from 1 to 5 with a mean value of 2.56 in single crosses and it varied from 1 to 6 with mean of 2.38 in double crosses. High PCV (31.17 and 35.69), GCV (23.21 and 27.27), GAM (35.92 and 42.95) were observed for single and double crosses, respectively.

The mean fruit length was almost same in both single and double crosses (13.69 and 13.78, respectively). PCV, GCV, high heritability and GAM (13.57 and 12.16, 12.44 and 10.67, 83.04 and 76.55 and 23.58 and 19.35) observed for single and double crosses population, respectively.

Fruit diameter was almost same in single and double crosses F_2 population. In single crosses it varied from 0.78 to 2.54 with an average mean of 1.67 and its PCV (17.58), GCV (15.77), heritability (80.00) and GAM (29.30) were high. The double crosses F_2 populations showed the range from 0.93 to 3.07 with mean of 1.65. Its PCV, GCV, heritability and GAM (25.16, 22.48, 83.48 and 41.75, respectively) were high.

Similarly, the fruit weight was almost same in both crosses. In single crosses it varied from 9.70 to 31.08 with the mean of 17.03 and in double crosses it showed 8.87 to 28.80 with mean of 17.51. This character showed high PCV, GCV, heritability and GAM (22.40 and 23.07, 20.01 and 20.86, 79.74 and 81.28 and 36.90 and 36.21) in single and double crosses, respectively.

Number of seeds per fruit observed moderate PCV (16.22 and 16.68), GCV (14.38 and 15.62) and heritability (78.64 and 87.58) and high GAM (26.29 and 30.12) in both single and double crosses, respectively.

The most important yield attributing character the number of fruits per plant ranged from 9.0 to 34.5 with mean of 20.01 and exhibited high PCV (21.94), GCV (19.26), heritability (77.24) and GAM (34.90) in single crosses. In double crosses it varied from 7.67 to 32.67 with mean of 20.34. High PCV (22.69), GCV (20.80), heritability (84.25) and GAM (39.31) were observed.

Pedicle length ranged from 1.90 to 5.05 with mean of 3.38 in single crosses and it varied from 1.86 to 5.52 with mean of 3.47 in double crosses. It recorded moderate PCV (19.97 and 21.32), GCV (13.41 and 15.07)

and heritability (64.03 and 70.67) and high GAM (27.63 and 31.05) in single and double crosses, respectively. Similarly, the number of ridges per fruit recorded moderate PCV (13.48 and 14.76) and GCV (13.13 and 14.24), high heritability (95.17 and 93.00) and GAM (26.37 and 28.31) in both the crosses. The mean 100 seed weight recorded 7.00 g and 7.09 g, respectively, in single and double crosses. It showed very low PCV (3.62 and 3.37), GCV (2.93 and 3.09) and GAM (4.89 and 5.89) in both the crosses.

In the present investigation it was observed that the double crosses populations exhibited higher mean than the single crosses for most of the characters studied. Hence, selection can be more effective in double cross F_2 population. Similar results were reported by Jaiprakashnarayan (2003) in 66 genotypes of Okra. Higher variability were recorded for fruit yield per plant and its components traits except days to first flowering, stem diameter, fruit length and 100 seed weight in both populations. Similar results were also reported by Sahoo *et al.* (1990) and Hazra and Basu (2000) in 45 F_2 populations in single cross chilli. The presence of high variability indicates presence of more variation in the population to select superior segregants.

The heritability estimates helps in effective selection for a particular character. The study show that all the characters exhibited high heritability and GAM. The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. Based on variability, heritability along with genetic advance, it could be concluded that improvement by direct selection in bhendi is possible for traits like plant height, number of branches, intermodal length, fruit length, fruit diameter, number of fruit per plant and fruit yield per plant.

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Variability in Bael (*Aegle marmelos* Correa) Genotypes from Orissa

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Survey was conducted in different part of Orissa to assess the existing natural diversity in bael seedling trees and to identify the superior genotype with desirable horticultural traits. Observations on morphological and physico-chemical parameters of fruit were recorded in 21 promising genotypes. All the genotypes showed considerable variations with respect to physico-chemical characters assessed. The genotypes CHBI-13 and CHBI-14 were found promising with respect to pulp weight (86.04 and 86.92%) and skull thickness (2.32 and 2.22 mm). The CHBI-13 also had higher fruit weight (2.915 kg) and found superior over other genotypes. The minimum seed number was counted in CHBI-15. The maximum Total Soluble Solids (40.43 °Brix) of fruit was recorded in CHBI-20 whereas the TSS/acid ratio was maximum (107.08) in CHBI-7.

Key Words: Bael, Genotypes, Physico-chemical Characters, Seedling

Introduction

Bael (*Aegle marmelos* Correa) is one of the important under utilized indigenous fruit crop of India. It belongs to family Rutaceae. The fruit has been known in India since the pre historic era. It is a sacred tree dedicated to Lord Shiva and is mentioned in Vedic literature and Ramayana. Fruits are widely and abundantly available in forests of Orissa especially *Dhenkanal*, *Angul*, *Bolangir* and *Rayagadha* districts. So far there is no organized and systematic orcharding of this fruit crop has been taken in India (Kumar *et al.*, 1994). It can easily be grown on eroded soil and adverse climatic conditions where most of the other fruits can not be grown. Bael fruits are popular due to its medicinal and nutritional properties and regarded as 'Amrit Phal' in cure of diarrhoea and dysentery. All part of tree (stem, bark, root, leaves and fruits) at different maturity stages has one or the other use. It is also used in the preparation of Ayurvedic medicines since ancient times (Rai *et al.*, 1991). In India, it is found in wild form in sub-Himalayan tract and in dry deciduous forest of central and southern Indian region (Pandey *et al.*, 2005) since pre-historic times and, therefore, a large number of landraces are available in the different diversity regions. A wide range of diversity of bael tree has been noticed in dry sub-tropical belt of north India. The plains of Bihar and plateau regions of Jharkhand have wide distribution of bael genotypes particularly in dry, undulating/forest lands. Bael cultivars have been identified and found

useful for commercial cultivation i.e., Narendra Bael-5, NB-7 and NB-9 from Narendra Dev University of Agriculture and Technology, Kumarganj, Faizabad (Pareek and Nath, 1996); Pant Aparna, Pant Sujata, Pant Shivani and Pant Urvashi from GB Pant University of Agriculture & Technology Pant Nagar, Nainital (Singh *et al.*, 2000) and CISH-B1 and CISH-B2 from Central Institute for Sub-tropical Horticulture, Lucknow (Pathak *et al.*, 2002). The location specific genotypes of bael need to be identified and evaluated in iso-climatic regions to develop good cultivars on one hand and known by local people for high degree of variability with regards to qualitative characters are on the verge of extinction due to urbanization and industrialization. Therefore, there is an immediate need to conserve them for the use of posterity (Rai *et al.*, 1991). Central India has high level of variability in bael. Therefore, a survey was conducted in parts of Orissa state with a view to identify superior genotypes for various horticultural traits.

Materials and Methods

Survey of bael growing region was conducted in *Dhenkanal*, *Angul*, *Bolangir* and *Rayagadha* district of Orissa during April, 2007 and 2008 and was undertaken both in cultivated as well as forests as per the method suggested by Gupta and Rai (1996). Efforts were made to select only regular, prolific bearing, dwarf type with thin skull, less seed and fibre, pest and disease free healthy trees with prolific bearing fruit of good size and shape. A total of 21 genotypes having desirable

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fruit characteristics and bearing behaviour were identified. The method of random sampling after gathering information about a particular genotype was followed. Five fruit were randomly collected from all the direction of each genotype to record the morphological and qualitative characters. The extent of variations in physico-chemicals traits of fruit from different locations were recorded. The physical attributes viz., fruit weight, length, diameter, skull thickness, number of seeds, seed weight and seed size were estimated/measured following standard procedure. The fruit yield/tree was measured by calculating the number of fruits per tree and multiplying by the average fruit weight. The Total Soluble Solids (TSS) of fruits was estimated by Hand Refractometer and presented in terms of ° Brix. The titratable acidity expressed in terms of percentage of citric acid was recorded by titrating 2 ml juice against N/10 NaOH using phenolphthaleine indicator (AOAC, 1960). The pH was estimated by pH meter. The data were statistically analyzed as per the method given by Gomez and Gomez (1984) using randomized block design.

Results and Discussion

Growth and fruit yield

The data on trunk cross sectional area of tree at 30 cm height, fruit yield and its attributes are presented

in Table 1. The trunk cross-sectional area of tree varied from 325.85 to 1789.97 cm². The highest trunk cross-sectional area of tree was recorded in CHBI-21 and minimum in CHBI-1. Fruit number/tree increased with increasing the trunk cross-sectional area of tree. There is positive and linear relationship between trunk cross-section area and fruit number. Maximum fruit number was recorded in CHBI-21 followed by CHBI-20 and CHBI-19. The fruit weight was maximum in CHBI-13 which was at par with CHBI-1 and CHBI-11. Fruit weight has been considered as one of the desirable character for selection in bael (Pandey *et al.*, 2008). The fruit yield was maximum in CHBI-13 and it was superior over other genotype collected from the region. The fruit length and diameter was maximum in CHBI-13 followed by CHBI-1, CHBI-14 and CHBI-7. The skull weight was minimum in CHBI-19 genotype but lowest per cent of skull weight and skull thickness and the highest pulp recovery percentage was observed in CHBI-14. The thinner skull and maximum pulp per cent is considered to be the good quality characters for bael fruit (Rai *et al.*, 1991). Similar variations in fruit weight, fruit size, pulp weight, skull thickness were also recorded in various bael genotypes (Pandey *et al.*, 2008; Nath *et al.*, 2003; Singh *et al.*, 2000). The seed number and weight significantly varied in different

Table 1. Vegetative growth and physical characters of bael fruits collected from Orissa

Genotypes	TCA (cm ²)	No. of fruits/ tree	Fruit Wt. (g)	Fruit yield (Kg/pl)	Fruit size (cm)		Skull characters		Pulp wt. (g)	Pulp (%)	Skull (%)	No. of seed/ fruit	Seed Wt/ fruit (g)	Seed size (mm)	
					Length	Diameter	Weight	Thickness						Length	Diameter
CHBI-1	325.85	34	2695	91.63	16.3	16.9	417.84	2.87	2277.16	84.49	15.51	152	18.97	9.20	7.90
CHBI-2	336.11	35	0860	30.10	13.1	10.1	210.20	2.45	649.80	75.55	24.45	140	15.32	8.70	6.50
CHBI-3	367.85	40	1425	57.00	13.6	13.8	429.58	2.36	995.42	69.85	30.15	104	14.90	9.32	7.61
CHBI-4	389.81	45	1125	50.62	13.2	11.2	325.20	2.46	799.80	71.09	28.91	108	15.12	8.70	7.90
CHBI-5	548.05	47	1490	70.03	14.1	13.5	283.80	2.88	1206.20	80.95	19.05	107	9.38	8.40	6.63
CHBI-6	717.97	48	1350	64.80	14.3	12.6	410.30	2.67	939.70	69.60	30.40	112	15.43	8.20	6.57
CHBI-7	733.17	50	2310	115.5	15.4	16.7	490.10	3.42	1819.90	78.78	21.22	131	10.33	7.34	6.78
CHBI-8	738.17	57	1450	82.65	12.5	11.2	415.40	2.87	1034.60	71.35	28.65	125	12.67	7.12	6.56
CHBI-9	795.54	64	1830	117.12	14.1	15.1	436.15	2.76	1393.85	76.16	23.84	121	7.93	7.20	6.18
CHBI-10	811.53	67	1295	86.76	13.9	13.1	395.50	2.68	899.50	69.45	30.55	105	12.45	8.49	7.88
CHBI-11	820.68	75	2085	156.37	15.2	16.5	429.26	2.88	1655.74	79.41	20.59	175	16.73	9.67	7.28
CHBI-12	827.68	78	1645	128.31	15.3	13.6	405.70	2.78	1239.30	75.33	24.67	145	13.34	7.50	6.89
CHBI-13	877.08	85	2915	247.75	17.2	17.8	406.93	2.32	2508.07	86.04	13.96	120	19.12	7.07	9.60
CHBI-14	910.81	92	1800	165.60	15.5	14.5	235.35	2.22	1564.65	86.92	13.08	130	24.40	7.12	8.35
CHBI-15	997.93	112	1065	119.28	14.3	12.5	219.76	2.59	845.24	79.36	20.64	68	7.87	8.76	6.45
CHBI-16	1052.10	120	1005	120.00	12.5	12.1	217.18	2.63	787.82	78.90	21.10	132	15.83	7.12	8.23
CHBI-17	1449.88	125	1675	209.37	13.5	14.7	298.69	2.95	1376.31	82.16	17.84	156	21.80	7.60	7.20
CHBI-18	1471.43	135	1370	184.95	13.1	12.5	345.23	2.89	1024.77	74.80	25.20	123	14.50	8.23	7.34
CHBI-19	1672.63	136	1060	144.16	11.1	12.2	204.88	2.50	855.12	80.67	19.33	133	11.72	7.54	6.34
CHBI-20	1780.97	140	0700	98.00	10.7	10.3	206.22	2.52	493.78	70.54	29.46	99	9.66	8.76	6.45
CHBI-21	1789.97	152	0930	141.36	12.9	11.6	273.83	2.98	656.17	70.55	29.45	85	11.85	9.12	6.78
CD at 5%	—	—	540.1	—	1.2	1.1	124.45	0.31	530.4	8.24	6.23	55.19	5.67	0.67	0.59

CHBI: Central Horticulture Bael, Trunk cross-sectional area (TCA) : $\text{Girth}^2 / 4 \text{ p}$

genotypes. The maximum seed number was counted in CHBI-11 followed by CHBI-17 and CHBI-1 and the minimum seed number was found in CHBI-15. Whereas seed weight was estimated maximum in CHBI-14 and minimum in CHBI-15. The maximum seed length was measured in CHBI-11 but diameter was maximum in CHBI-13. The lower seed number and weight is the preferred character for selection of superior genotypes in bael (Rai *et al.*, 1991). The above observations revealed that while selecting superior bael genotypes, pulp content, seed number and size and skull thickness should be given more importance rather than fruit weight (Pandey *et al.*, 2005; Majumdar, 1975).

Fruit quality characters

Variations in fruit quality characters among different genotypes were observed and presented in Table 2. The TSS varied from 31.45 to 40.43 ° Brix in different genotypes. The significantly superior value was obtained in CHBI-20 followed by CHBI-17. The minimum TSS value was recorded in CHBI-2. The highest titratable acidity was estimated in CHBI-10 followed by CHBI-12 and CHBI-8. The TSS:acid ratio was maximum in CHBI-7 followed by CHBI-19 and CHBI-20. The pH of fruit juice was maximum in CHBI-8 and minimum in CHBI-13. The variations in quality parameters of bael were also recorded by Jauhari *et al.*, 1969; Pandey *et al.*, 1986; Pandey *et al.* 2005; Pandey *et al.*, 2008. Based on morphological and quality characters of fruits for the consecutive two years, it was concluded that CHBI-13, CHBI-14 and CHBI-15 and CHBI-20 genotypes were most promising. The scion shoot of these genotypes have been collected and grafted plants are being established in germplasm block at Central Horticultural Experiment Station, Bhubaneswar.

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Table 2. Quality characters of bael germplasms collected from Orissa

Genotypes	TSS (° B)	Acidity (%)	TSS/acid ratio	pH
CHBI-1	32.24	0.43	74.97	4.77
CHBI-2	31.45	0.39	80.64	4.74
CHBI-3	32.76	0.40	81.90	5.11
CHBI-4	33.34	0.41	81.30	5.40
CHBI-5	34.56	0.42	82.28	5.20
CHBI-6	35.89	0.38	94.44	4.86
CHBI-7	38.55	0.36	107.08	5.15
CHBI-8	36.36	0.44	82.63	5.45
CHBI-9	36.98	0.36	102.72	4.21
CHBI-10	38.74	0.50	77.48	5.32
CHBI-11	37.56	0.36	104.33	5.12
CHBI-12	38.41	0.45	85.35	4.34
CHBI-13	38.78	0.40	96.95	4.17
CHBI-14	38.87	0.41	94.80	4.50
CHBI-15	38.25	0.36	106.25	5.13
CHBI-16	36.43	0.37	98.45	4.63
CHBI-17	40.21	0.43	93.51	5.20
CHBI-18	37.65	0.39	96.53	5.43
CHBI-19	38.35	0.36	106.52	5.23
CHBI-20	40.43	0.38	106.39	4.65
CHBI-21	31.56	0.40	78.90	4.49
CD at 5%	3.35	0.08	16.07	0.09

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Genetic Divergence and Gene Source Studies in *Terminalia arjuna* Bedd.

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Studies on genetic divergence for 19 parameters were conducted with 50 accessions of *Terminalia arjuna*. Analysis of variance showed difference among accessions for all the traits studied. Based on the relative value of the magnitude of divergence value all the accessions were grouped into 9 clusters. Intra cluster distance was maximum for cluster VI (3.27) followed by 3.21 in cluster IV. The maximum inter cluster distance was 24.60 between cluster V and VI indicating high genetic divergence among accessions of these two groups. Maximum contribution towards the divergence was 44.73% by proline followed by protein (38.94%), reducing sugar (5.31%) and non-reducing sugar (3.76%). Gene sources for higher lamina length (Acc. 225); lamina width (IC 382333); low internodal distance (IC 410837), high protein (IC 560422) and low phenol (IC 3263888) were identified for future improvement programme.

Key Words: Cluster, D² analysis, Gene source, *Terminalia arjuna*

Introduction

Terminalia arjuna Bedd. commonly known as *Arjun* is a multi-purpose tree. It is of immense economic importance in various industries like pharmaceutical, timber, paper, soap, match industry, food, fodder and fuel. Besides, the foliage of the tree is primary food for tropical tasar silkworm *Antheraea mylitta* D. It is extensively distributed in tropical forests all over India on the banks of river, streams and dry water course (Anonymous, 1982). Considering the diverse uses of plant, it is essential to develop superior clones of this species through breeding. Genetic improvement of any species is primarily depends on the extent and magnitude of genetic variability among collection for different important traits. Based on the requirement it is essential to identify genetically divergent genotypes among the collected germplasm to select suitable parents for breeding programme. Studies on divergence analysis in *T. arjuna* germplasm are not reported so far. The present study was aimed to determine the genetic divergence in 50 germplasm accessions available in the field gene bank at Central Tasar Research and Training Institute (TR&TI), Ranchi. This will help in arranging the accessions into homogenous groups for further utilization in breeding programme to develop clones with desirable characteristics and identification of gene source for different traits.

Material and Method

The present study was carried out in 50 accessions of *T. arjuna* established under *ex situ* condition at clonal gene bank of CTR&TI, Nagri, Ranchi, Jharkhand, India

(123° 4' N and 85° 88' E, altitude-708 m SL). Data was collected from 4 plants in each accession of uniform age of 5 years. Stomatal studies were conducted by applying a thin layer of quick fix on the abaxial leaf surface. The dried layer was peeled out from the surface containing the impression of stomata. The thin layer was then kept on the slide and covered with the cover slip and observed under Olympus microscope. The size and number of stomata was calculated with the help of occulometer pre-calibrated with stage micrometer. Chloroplast number/stomata was counted of 3rd and 5th leaf of a twig in descending order from the fully opened leaf at the top using ventral surface peeling of freshly collected leaf sample. The peels were stained and mounted in 2% potassium iodide-iodine solution following the method of Dwivedi *et al.* (1986). Estimation of phenol, chlorophyll a, b and total chlorophyll, reducing and non-reducing sugar, proline and protein was done as per the methods given by Mahadevan and Sridhar (1974).

Data on growth traits viz., lamina length, lamina width, petiole length, internodal distance leaf weight, moisture content and moisture retention capacity(%) was recorded from 5 branches of 4 clones from the leaf located at 6, 7 and 8th node. For internodal distance, length of longest shoot from each clone was measured and the total number of nodes was counted. Thereafter, shoot length was divided by the number of nodes for calculating the internodal distance. Leaf moisture and moisture retention capacity in harvested leaves were calculated following the method reported earlier (Suryanarayana *et al.*, 2006). Multivariate analysis for

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Table 1. Range, mean, standard error and co-efficient of variance for different characters in *Terminalia arjuna*

Parameter	Range	Mean	SE±	CV%
Lamina length (cm)	9.22-16.32	13.10	0.53	7.02
Lamina width (cm)	3.70-6.72	4.84	0.07	2.53
Petiole length (cm)	0.23-0.72	0.54	0.05	18.06
Internodal distance (cm)	1.55-2.68	2.08	0.02	2.00
Single leaf weight (gm)	1.09-2.08	1.64	0.07	7.45
Moisture content	62.58-78.57	67.51	0.15	0.40
Moisture retention capacity (%)	61.44-76.64	65.23	0.03	0.09
Frequency of stomata (mm ²)	193.93-524.18	381.34	7.07	3.21
Stomata length (µm)	22.73-30.83	26.08	0.85	5.70
Stomata width (µm)	12.36-17.46	15.46	0.66	7.42
Number of chloroplast in guard cells	7.66-11.00	8.63	0.54	10.90
Phenol (µg/mg)	0.34-4.51	1.89	0.04	4.41
Chlorophyll a (mg/g)	0.58-1.56	1.08	0.04	7.95
Chlorophyll b (mg/g)	0.39-1.68	0.86	0.03	7.74
Total Chlorophyll (mg/g)	0.88-3.49	1.93	0.02	1.98
Reducing sugar (µg/mg)	2.64-14.41	7.40	0.03	0.75
Non- Reducing sugar (µg/mg)	4.27-14.62	8.24	0.04	0.96
Proline (µ mol/g)	14.55-71.11	43.73	0.08	0.35
Protein (mg/g)	10.11-35.93	20.59	0.04	0.37

the estimation of genetic distance among all the accessions was carried out by using Mahalanobis D² statistic analysis as suggested by Mahalanobis (1936) and clustering of genotypes was done by the method of Tocher (Rao, 1952).

Results and Discussion

Analysis of variance showed significant differences among accessions for all the traits studied. It indicated existence of genetic variability in the accessions (Table 1). Based on the relative value of the magnitude of divergence of the 50 accessions were grouped into 9 clusters (Table 2). The maximum genotypes were grouped in cluster I (17) followed by cluster II (14); VI (7); IV (6); V (2) and one each in cluster III, VII, VIII and IX. Intra cluster distance was maximum for cluster VI (3.27) followed by 3.21 in cluster IV. However, cluster III, VII, VIII and IX had no intra cluster distance as they were represented by a single genotype. The maximum inter cluster distance (24.60) was observed between cluster V and VI indicating high genetic divergent accessions of these two groups. Minimum inter cluster distance (3-21) was observed between cluster III and IV showing their close proximity. However, in all cases inter cluster distances were greater than the intra cluster distances indicating the presence of genetic diversity among the accessions between different clusters (Table 3).

The cluster means indicated substantial variation among 9 clusters (Table 4). Maximum lamina width was in cluster V which represents 2 accessions collected from Andhra Pradesh and Uttar Pradesh. Frequency of stomata and width of stomata was minimum in cluster

III representing only 1 accession (IC 382306). Accessions in cluster IX showed minimum internodal distance. Cluster V showed lower phenol content in the leaf whereas, cluster VI had maximum chlorophyll b and non-reducing sugar content in the leaf. Moisture content and moisture retention capacity was higher in cluster

Table 2. Cluster composition in *T. arjuna*

Cluster No.	No. of accessions	Accession number and source
I	17	382334, 382330, 410840; Uttarakhand 410797, 326375, 410795; Maharashtra 210, 214, 225, 212, 410830, 410779, 410780; Jharkhand 410748, 382303, 382300; Andhra Pradesh 410863; Chhattisgarh
II	14	560439, 560451; Uttar Pradesh 410781, 355582, 410827, 381646, 381644, 381639, 118; Jharkhand 560423; Maharashtra 410752; Andhra Pradesh 382333; Uttarakhand 410859, 410865; Chhattisgarh
III	01	382306; Andhra Pradesh
IV	06	410806, 560424; Maharashtra 410838; Uttarakhand 410866; Chhattisgarh 410755; Andhra Pradesh 381641; Jharkhand
V	02	560452; Uttar Pradesh 410754; Andhra Pradesh
VI	07	135, 381635; Jharkhand 560422, 560418, 326382, 326388; Maharashtra 560436; Uttar Pradesh
VII	01	410858; Chhattisgarh
VIII	01	410806; Maharashtra
IX	01	410837; Jharkhand

Table 3. Inter and Intra-cluster distances of accessions in gene pool

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	1.76								
II	7.13	2.20							
III	3.08	7.68	0.0						
IV	4.39	8.64	1.51	3.21					
V	3.47	14.56	4.48	6.52	0.75				
VI	14.93	6.08	10.54	11.26	24.60	3.27			
VII	7.50	3.86	12.07	12.96	13.75	13.46	0.0		
VIII	12.69	6.28	12.18	14.58	16.88	11.60	7.64	0.0	
IX	11.29	13.75	3.57	4.58	13.34	10.67	21.52	19.39	0.0

VIII. Higher values of lamina length, petiole length, chlorophyll a, total chlorophyll, reducing sugar and total protein were recorded in cluster IX. Maximum contribution towards total divergence was 44.73% by proline followed by protein (38.94%). On the contrary the others characters have given very little or no contribution to total divergence for enabling clear discrimination of the genotypes (Table 4).

The results indicated that geographical distribution and genetic divergence did not follow the same pattern. The grouping of genotypes of different geographical locations into one cluster may be due to presence of some common genes controlling the most important characters through modifying effect of micro and macro environment affecting genetic diversity. Another feature that genotypes from same location were placed in separate cluster indicating wide diversity among genotypes from same location. This shows that the geographical diversity may not necessarily be related to genetic diversity in this

species. The present findings are in agreement with Srivastava *et al.* (2007) and Dwivedi and Mitra (1996) in apricot and litchi, respectively. Thus, the complex composition of clusters indicates that geographical diversity is important but not the sole factor determining the genetic diversity (Murthy and Arunachalam, 1966). The geographical diversity has been disproved to be an index of genetic diversity in mulberry (Rajan *et al.*, 1997; Tikadar *et al.*, 2003); pearl millet (Singh *et al.*, 1981) and in black gram (Das and Dasgupta, 1984).

Based on the analysis, accessions with gene source for some of the important qualitative and quantitative parameters have been identified (Table 5). Gene source for lamina length Acc. 225; lamina width IC382333 and internodal distance in IC410837, whereas IC560422, IC326388 and IC560452 are gene source for protein, phenol and proline respectively. Since, leaf quality (sugar and protein contents, and moisture retention capacity) is the major factor in determining the silk yield, accessions

Table 4. Mean performances of the clusters with respect to different characters

Parameter	Cluster									
	I	II	III	IV	V	VI	VII	VIII	IX	Contribution %
Lamina length (cm)	13.31	13.17	12.87	12.52	12.92	12.92	13.47	13.10	13.93	0.0
Lamina width (cm)	5.15	4.68	4.09	4.56	5.38	4.82	3.70	4.49	5.12	0.0
Petiole length (cm)	0.56	0.57	0.54	0.54	0.50	0.50	0.47	0.54	0.62	0.0
Internodal distance (cm)	2.22	2.10	2.25	1.88	1.89	2.01	1.91	2.32	1.55	0.0
Single leaf weight (gm)	1.66	1.61	1.17	1.64	1.74	1.80	1.10	1.65	1.49	0.0
Leaf moisture (%)	67.34	66.78	70.21	66.60	73.44	66.42	67.96	78.57	67.97	0.0
Moisture retention capacity %	64.59	64.97	66.49	64.76	69.24	64.61	65.24	76.64	66.96	6.69
Frequency of stomata (mm ²)	400.53	398.98	215.80	363.10	406.77	319.21	483.88	263.20	483.14	0.08
Stomata length (µm)	25.70	26.43	27.57	25.67	27.47	25.98	25.77	26.70	26.47	0.0
Stomata width (µm)	15.69	15.34	13.07	15.77	15.23	14.89	14.60	17.47	17.37	0.0
Number of chloroplast in guard cells	8.45	8.71	9.00	8.83	7.83	8.71	8.67	10.33	8.33	0.0
Phenol (µg/mg)	2.05	1.87	1.75	2.20	1.11	1.31	1.24	4.51	1.48	0.16
Chlorophyll a (mg/g)	1.00	1.08	1.11	1.15	1.01	1.19	1.04	1.24	1.32	0.0
Chlorophyll b (mg/g)	0.80	0.95	0.79	0.85	0.59	0.99	0.59	0.98	0.94	0.0
Total chlorophyll (mg/g)	1.73	2.04	1.96	1.98	1.58	2.21	1.45	2.20	2.44	0.33
Reducing sugar (µg/mg)	7.93	6.55	7.78	8.82	9.19	5.42	10.92	3.85	12.03	5.31
Non- Reducing sugar (µg/mg)	8.30	8.77	6.34	6.54	6.33	10.17	8.84	4.59	5.64	3.76
Proline (µmol/g)	54.83	27.25	61.88	61.30	68.38	28.62	20.17	20.63	65.78	44.73
Protein (mg/g)	14.73	20.46	24.11	24.24	12.53	32.84	11.92	20.48	35.73	38.94

Table 5. Gene donors for some important characters in *Tarjuna* accessions

Character	Potential	Accession
Lamina length (cm)	16.32	Acc. 225
Lamina width (cm)	6.72	IC 382333
Internodal distance (cm)	1.55	IC 410837
Leaf moisture (%)	78.57	IC 410806
Reducing sugar (µg/mg)	14.41	IC 381641
Non-Reducing sugar (µg/mg)	14.62	IC 326382
Proline (µ mol/g)	71.11	IC 560452
Protein (mg/g)	35.93	IC 560422
Phenol (µg/mg)	0.34	IC 326388

showing high mean values contributing in leaf quality will be utilized for future selection and breeding for superior varieties.

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Germplasm Evaluation of Low-chill Pears (*Pyrus* spp.) for Vegetative, Reproductive and Fruit Quality Parameters in Tarai Area of Uttarakhand

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Twenty-one low-chill pear germplasm were evaluated for plant growth, fruit yield and fruit quality parameters at Horticulture Research Centre, Patharchatta, G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, during 2001-02 to 2003-04 for various vegetative, reproductive and yield parameters. The mean performance values for tree height (10.0 m) and trunk girth (56.8 cm) indicated larger values for Pant Pear-18 and LeConte, respectively. The maximum canopy spread (5.1 m) was recorded in *Pyrus pashia* and Pant Pear-18, respectively. Among fruit quality traits maximum fruit weight was recorded in Pant Pear-3 (11.3 g), fruit length in China (8.7 cm), TSS in LeConte (15.2%), acidity in Tumaria (0.37), total sugar in LeConte (9.1%) and fruit yield in Pant Pear-3 (26.5 q/ha) during the study. The variability observed in the pear germplasm can be used for the genetic improvement of fruit yield and quality.

Key Words: Evaluation, Fruit quality, Fruit yield, Low-chill pear, *Pyrus* spp.

Introduction

The productivity of pear in Asian countries is 6.6 t/ha, while in India, it is nearly 6.00 t/ha (Gemman, 2002). Pear is one of the few fruit crops that are adaptable to wide variety of climatic conditions. The agro-climatic conditions of Uttaranchal in foothill of Sivalik range of Himalaya are well suited for the cultivation of low chill pears. Considerable variation occurs in the adoption of pear cultivars in a particular set of agro-climatic conditions due to variability in macro and micro-climate. The availability of cultivar variability is a pre-requisite for breeding of any fruit crop. Particular attention is desirable on improvement of agronomic and pomological characteristics, such as tree vigour, productivity, appearance, quality and yield. Knowledge of heritability of main characteristics is very important for the successful breeding work. The first step is long-term evaluation of varieties in the field, in genebanks or in cropping plantations. The second step has to be the testing of parents and populations (Fischer, 2009). *Pyrus* is genetically quite diverse, with considerable variability in morphological and physiological adaptations (Lombard and Westwood 1987; Bell *et al.*, 1996). European and Asian pear breeders have utilized this variability to develop high quality cultivars with large size and attractive appearance that are well adapted to local conditions (Hancock and Lobos, 2008). Pear cultivar Gola, Tumaria and Bagugosha are the promising cultivars of Uttarakhand. Therefore, the collected pear germplasm at Horticulture

Research Centre, Patharchatta, GB Pant University of Agriculture and Technology, Pantnagar, Uttarakhand were evaluated for their performance in terms of plant growth, fruit yield and fruit quality.

Materials and Methods

Twenty-one experimental trees comprising 12 to 13 years old bearing trees of 13 pear seedling selections (Pant Pear-1, Pant Pear-2, Pant Pear-3, Pant Pear-4, Pant Pear-5, Pant Pear-6, Pant Pear-7, Pant Pear-9, Pant Pear-10, Pant Pear-13, Pant Pear-15 and Pant Pear-18), six varieties (Patharnakh, Smith, Kieffer, Tumaria, China, LeConte and Thumb Pear) and two rootstocks (Mehal and Sand Pear) were planted at 5×5 m distance in square system. The experimental site is situated in the foothills of the Shivalik ranges of the Himalaya at 29°N latitude and 79.3°E longitude and at an altitude of 243.84 metres above mean sea level. The experiment was carried out in a randomized block design with three replications and each treatment had four trees/replication. The data on tree growth, yield and fruit quality were recorded. The physicochemical parameters were analyzed as per the method described in AOAC (1970). Growth parameters and physical fruit quality was determined following Mahajan *et al.* (2002). The TSS of the fruit juice was estimated with the help of hand refractometer by adjusting at 20°C by temperature correction chart. The sugar was assessed by the method of Lane and Eynon (1943). Titrable acidity was determined with the standard alkali

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solution and expressed in terms of malic acid.

Results and Discussion

Vegetative Parameters

All the parameters were recorded and analyzed by taking Patharnakh as standard germplasm for the evaluation (Table 1). Tree height of the plants varied from 4.0 m (Pant Pear-13) to 10.0 m (Pant Pear-18) among the selected germplasm. Significant difference was observed in all the selected germplasm for tree height as compared to Patharnakh. Maximum trunk girth of 56.9 cm in Patharnakh and minimum of 19.3 cm in Pant Pear-6 was recorded with no significant difference amongst Patharnakh with Pant Pear-1, Mehal, Kieffer and LeConte. Mean value for the canopy spread varied from 0.5 m (Pant Pear-6) to 5.1 mm (Mehal). Pant Pear-3, Pant Pear-18 and Mehal showed no significant difference for canopy spread with reference to Patharnakh whereas all other selected germplasm were significantly different from Patharnakh. Tree habit showed that majority plants (Pant Pear-1, Pant Pear-2, Pant Pear-4, Pant Pear-5, Pant Pear-6, Pant Pear-9, Pant Pear-10, Pant Pear-15, Patharnakh, Smith, Sand Pear, Le Conte and Thumb Pear) were upright in growth, whereas, others were spreading (Pant Pear-3, Pant Pear-7, Pant Pear-13, Pant Pear-18, Tumaria and China). Drooping (Kieffer) and weeping (Mehal) types of plants were also recorded. Vigour

of the tree varied from extremely weak (Pant Pear-10, Kieffer) to weak (Pant Pear-13 and China), intermediate (Pant Pear-1, Pant Pear-5, Pant Pear-18, Patharnakh, Sand Pear and LeConte), vigorous (Pant Pear-2, Pant Pear-3, Pant Pear-6, Pant Pear-7, Pant Pear-15, Mehal, Smith and Thumb Pear) and very vigorous (Pant Pear-4, Pant Pear-9 and Tumaria), respectively. The findings were in agreement with Prakash (2000) and Singh *et al.* (2001).

Reproductive Parameters

Data indicated (Table 2) that early flowering was recorded in the germplasm of Pant Pear-1 (8-10 February), Pant Pear-2 (8-11 February), Pant Pear-4 (6-8 February), Pant Pear-5 (8-9 February), Pant Pear-10 (7-9 February), Pant Pear-13 (8-10 February), Pant Pear-18 (8-10 February), Patharnakh (7-9 February), Smith (7-9 February) and Sand Pear (5-8 February) whereas, late flowering was recorded for Pant Pear-7 (14-17 February), Pant Pear-9 (19-21 February), Pant Pear-3 (20-22 February), Pant Pear-6 (22-24 February), Mehal (14-16 February), Kieffer (20-21 February), Tumaria (25-27 February), China (24-26 February), LeConte (22-25 February) and Thumb Pear (22-26 February). In the early flowering groups flowering varied from 5th to 10th February, whereas in the late flowering groups varied from 14th to 21st March. The end of Flowering in early groups was recorded from 1st to 8th March whereas in the late group the

Table 1. Vegetative parameters of *Pyrus* spp. germplasm

Germplasm	Tree habit	Tree vigour	Tree height (m)	Trunk girth (cm)	Canopy spread (m)
Pant Pear-1	Upright	Intermediate	8.7	55.8	4.0
Pant Pear-2	Upright	Vigorous	7.6	47.9	4.0
Pant Pear-3	Spreading	Vigorous	9.2	50.0	5.0
Pant Pear-4	Upright	Very Vigorous	7.7	46.3	4.3
Pant Pear-5	Upright	Intermediate	6.1	39.4	2.9
Pant Pear-6	Upright	Vigorous	4.8	19.3	0.5
Pant Pear-7	Spreading	Vigorous	6.9	45.5	4.1
Pant Pear-9	Upright	V Vigorous	8.2	24.9	1.0
Pant Pear-10	Upright	Extremely weak	6.1	46.1	4.2
Pant Pear-13	Spreading	Weak	4.0	28.2	2.6
Pant Pear-15	Upright	Vigorous	5.5	20.5	1.1
Pant Pear-18	Spreading	Intermediate	10.0	50.0	5.1
Patharnakh	Upright	Intermediate	9.7	56.9	5.0
Mehal	Weeping	Vigorous	9.1	55.9	5.1
Smith	Upright	Vigorous	9.3	54.1	4.5
Kieffer	Drooping	Extremely weak	4.5	56.0	4.7
Tumaria	Spreading	V Vigorous	8.8	53.3	4.4
China	Spreading	Weak	7.6	50.3	3.9
Sand Pear	Upright	Intermediate	8.2	50.3	4.0
Le Conte	Upright	Intermediate	6.6	56.8	3.5
Thumb Pear	Upright	Vigorous	7.6	43.5	3.6
SEm±	—	—	0.1	0.4	0.4
LSD (P= 0.05)	—	—	0.2	1.2	0.4

PNN = Pyrifirm narrow neck; M = medium; V = very

Table 2. Reproductive parameters of *Pyrus* spp. germplasm

Genotypes	Date of flower setting	Date of end of flowering	Date of full bloom	Date of fruiting	Date of harvest	Duration of bloom (days)
Pant Pear-1	8-10 Feb	3-8 Mar	16-20 Feb	5-10 Mar	4-7 Jul	5
Pant Pear-2	8-11 Feb	3-7 Mar	15-18 Feb	5-11 Mar	5-7 Jul	4
Pant Pear-3	20-22 Feb	12-16 Mar	28-2 Mar	15-18 Mar	25-30 Jul	4
Pant Pear-4	6-8 Feb	2-6 Mar	14-17 Feb	5-8 Mar	3-8 Jul	4
Pant Pear-5	8-9 Feb	3-5 Mar	17-19 Feb	6-9 Mar	4-8 Jul	3
Pant Pear-6	22-24 Feb	18-21 Mar	28-3 Mar	20-23 Mar	2-5 Aug	4
Pant Pear-7	14-17 Feb	4-7 Mar	22-25 Feb	6-10 Mar	6-9 Aug	4
Pant Pear-9	19-21 Feb	15-18 Mar	27-1 Mar	17-21 Mar	3-6 Aug	3
Pant Pear-10	7-9 Feb	4-7 Mar	14-17 Feb	6-9 Mar	3-7 Aug	4
Pant Pear-13	8-10 Feb	3-7 Mar	16-18 Feb	5-10 Mar	4-8 Jul	5
Pant Pear-15	22-24 Feb	17-21 Mar	2-6 Mar	20-24 Mar	24-30 Jul	5
Pant Pear-18	8-10 Feb	2-7 Mar	16-19 Feb	3-9 Mar	4-9 Jul	4
Patharnakh	7-9 Feb	2-6 Mar	14-17 Feb	4-8 Mar	2-8 Jul	4
Mehal	14-16 Feb	8-11 Mar	22-25 Feb	11-15 Mar	25 Jul- 2 Aug.	4
Smith	7-9 Feb	2-5 Mar	15-17 Feb	4-8 Mar	4-8 Jul	3
Kieffer	20-21 Mar	14-18 Mar	27-30 Mar	16-20 Mar	30 Jul- 6 Aug.	5
Tumaria	25-27 Feb	18-21 Mar	9-11 Mar	20-23 Mar	2-7 Aug	3
China	24-26 Feb	16-18 Mar	8-10 Mar	19-21 Mar	1-6 Aug	3
Sand Pear	5-8 Feb	1-6 Mar	13-16 Feb	3-9 Mar	1-6 Aug	4
Le Conte	22-25 Feb	19-22 Mar	6-9 Mar	22-25 Mar	2-7 Aug	4
Thumb Pear	22-26 Feb	20-23 Mar	5-8 Mar	23-25 Mar	4-9 Jul	4

end was recorded from 4th to 23rd March. Full bloom in early germplasm was recorded from 3rd to 15th March with 3-5 days full bloom duration. While in late germplasm full bloom varied from 6th to 30th March with full bloom duration also of 3-5 days. Among the early flowering germplasm fruit set was recorded from 3rd to 11th March whereas in the late flowering germplasm fruit set varied from 6th to 25th March. The findings were in agreement with Mann and Singh (1985), Kumar (1996), Prakash (2000) and Singh *et al.* (2001).

Morphological fruit quality

The data (Table 3) revealed significant variation amongst the pear germplasm for various parameters. All the data recorded for different germplasm was compared with Patharnakh, perhaps the standard low chill germplasm. Mean value of fruit weight varied significantly from 34.2 g (Mehal) to 113.3 g (Pant Pear-3). Significant difference in germplasm was recorded for Pant Pear-3, Pant Pear-5, Pant Pear-10, Pant Pear-13, Mehal, Smith, Sand pear and Thumb pear with respect to Patharnakh. Whereas, other germplasm exhibited no significant difference for the fruit weight. Fruit length mean value varied from 4.3 (Mehal) to 8.7 cm (China). All the germplasm under study showed significantly different fruit weight and width with respect to Patharnakh except LeConte. Mean value of fruit width varied from 4.8 cm (Pant Pear-4 and Pant Pear-10, respectively) to 7.0

cm (Patharnakh). Four types of fruit shape were recorded during the study. Round (Pant Pear-2, Pant Pear-4, Pant Pear-10, Pant Pear-13, Pant Pear-18, Patharnakh, Smith, Mehal and Thumb Pear), globose (Pant Pear-7), pyriform (Pant Pear-1, Pant Pear-3, Pant Pear-5, Pant Pear-6, Pant Pear-9, Pant Pear-15, Smith, Kieffer, Tumaria and Sand Pear) and pyriform with narrow neck (LeConte and China). Among the smooth, medium rough and rough surfaces, smooth surface was recorded for Pant Pear-3, Pant Pear-6, Pant Pear-7, Pant Pear-9, Pant Pear-15, Tumaria, China LeConte and Thumb Pear, whereas medium rough for Pant Pear-1, Pant Pear-2, Pant Pear-4, Pant Pear-5, Pant Pear-18, Patharnakh, Kieffer and Sand Pear and rough for Pant Pear-10, Pant Pear-13, Mehal and Smith. Pant Pear-3, Pant Pear-6, Tumaria, China, LeConte and Thumb Pear recorded very high pulp juiciness. Whereas, high (Pant Pear-1, Pant Pear-5, Pant Pear-7, Pant Pear-9, Patharnakh and Kieffer), medium (Pant Pear-2, Pant Pear-4, Pant Pear-15, Pant Pear-18, Smith and Sand Pear) and less (Pant Pear-10, Pant Pear-13 and Mehal) were observed in the germplasm. Pulp taste of the selected germplasm varied from acidic (Pant Pear-10 and Mehal) to sub acidic (Pant Pear-9 and Kieffer) to medium sweet (Pant Pear-3, Pant Pear-4, Pant Pear-18, Smith and Sand Pear); Pant Pear-1, Pant Pear-5, Pant Pear-6, Pant Pear-7, Pant Pear-13, Pant Pear-15, Patharnakh and Thumb Pear were sweet. Pant Pear-2, Tumaria, China and LeConte were

Table 3. Fruit quality and yield of *Pyrus* spp. germplasm

Germplasm	Fruit shape	Pulp juice	Pulp taste	Gritt cells	Fruit surface texture	Pulp texture	Fruit weight (g)	Fruit length (cm)	Fruit width (cm)	TSS %	Acidity	Total Sugar	Yield (q/hac)
Pant Pear-1	Pyriform	High	Sweet	M	M rough	Soft	89.2	5.1	5.0	10.2	0.27	6.4	16.8
Pant Pear-2	Round	M	Highly sweet	M	M rough	Soft	90.8	5.4	5.2	11.0	0.23	7.0	18.2
Pant Pear-3	Pyriform	V high	M sweet	Low	Smooth	Melting	113.3	6.6	6.3	14.3	0.17	9.0	26.5
Pant Pear-4	Round	M	M sweet	M	M rough	M	85.8	5.1	4.8	10.3	0.27	6.4	18.3
Pant Pear-5	Pyriform	High	Sweet	M	M rough	Soft	106.7	5.2	5.2	13.5	0.27	7.3	19.5
Pant Pear-6	Pyriform	V high	Sweet	Low	Smooth	Soft	115.8	6.5	6.0	14.6	0.26	8.3	23.8
Pant Pear-7	Globose	High	Sweet	M	Smooth	Soft	91.7	6.3	6.0	12.5	0.18	8.0	18.7
Pant Pear-9	Pyriform	High	Sub acidic	Low	Smooth	Soft	94.2	7.1	6.3	13.4	0.18	8.1	20.7
Pant Pear-10	Round	Less	Acidic	High	Rough	M	52.5	5.0	4.8	10.3	0.27	6.6	12.7
Pant Pear-13	Round	Less	Sweet	High	Rough	M	56.7	5.3	5.3	10.2	0.26	7.0	11.7
Pant Pear-15	Pyriform	M	Sweet	M	Smooth	Soft	85.8	6.3	6.1	12.2	0.27	7.3	15.9
Pant Pear-18	Round	M	M sweet	M	M rough	Soft	89.2	6.4	6.3	12.3	0.28	7.3	18.1
Patharnakh	Round	High	Sweet	M	M rough	Soft	93.3	7.6	7.0	12.4	0.25	8.0	19.5
Mehal	Round	Less	Acidic	High	Rough	Hard	34.2	4.3	5.0	9.1	0.24	6.1	10.2
Smith	Round	M	M sweet	M	Rough	M	78.3	6.3	6.1	10.9	0.27	7.0	17.1
Kieffer	Pyriform	High	Sub acidic	M	M rough	M	85.8	6.4	6.3	11.0	0.28	8.3	18.5
Tumaria	Pyriform	V high	Highly sweet	Low	Smooth	Melting	97.5	7.9	6.6	14.5	0.37	8.9	19.3
China	PNN	V high	Highly sweet	Low	Smooth	M	100.8	8.7	6.6	14.3	0.36	8.2	20.5
Sand Pear	Pyriform	M	M sweet	High	M rough	M	72.5	5.0	5.1	14.2	0.27	8.0	13.9
Le Conte	PNN	V high	Highly sweet	Low	Smooth	Soft	98.3	7.9	6.7	15.2	0.17	9.1	19.5
Thumb Pear	Round	V high	Sweet	Low	Smooth	Soft	104.2	5.3	6.6	14.9	0.27	8.9	19.6
SEm±	—	—	—	—	—	—	3.6	0.4	0.3	0.8	0.51	0.4	2.3
LSD (P=0.05)	—	—	—	—	—	—	9.9	0.3	0.3	0.2	0.29	0.3	4.03

M=Medium; V=Very

highly sweet. Grittiness varied in the selected germplasm from low (Pant Pear-3, Pant Pear-6, Pant Pear-9, Tumaria, China, LeConte and Thumb Pear) to medium (Pant Pear-1, Pant Pear-2, Pant Pear-4, Pant Pear-5, Pant Pear-7, Pant Pear-15, Pant Pear-18, Patharnakh, Smith and Kieffer) and high (Pant Pear-10, Pant Pear-13, Mehal and Sand Pear). Melting, soft, medium and hard, melting types of pulp texture were recorded for selected germplasm. Melting type of pulp was observed in Pant Pear-3 and Tumaria and soft pulp in Pant Pear-1, Pant Pear-2, Pant Pear-5, Pant Pear-6, Pant Pear-7, Pant Pear-9, Pant Pear-15, Pant Pear-18, Patharnakh, LeConte and Thumb Pear. Medium pulp texture was recorded in Pant Pear-4, Pant Pear-10, Pant Pear-13, Smith, Kieffer, China and Sand Pear. Hard pulp texture was observed in Mehal only. The findings were in agreement with Prakash (2000) and Singh *et al.* (2001),

Chemical fruit quality and yield parameters

TSS (%) variation was recorded from 9.1% (Mehal) to 15.2% (LeConte). All the germplasm differed significantly with Patharnakh except Pant Pear-7, Pant Pear-15 and Pant Pear-18. The difference in acidity (%) was significant with maximum (0.37%) recorded in Tumaria and minimum (0.17%) in Pant Pear-3 with no significant difference amongst other selected

germplasm. Selected germplasm varied in sugar from 6.1% (Mehal) to 9.1% (LeConte). No significant difference was observed amongst Pant Pear-6, Pant Pear-7, Pant Pear-9, China and Sand pear. Whereas other selected germplasm differed significantly with Patharnakh. The highest fruit yield was recorded in Pant Pear-3 (26.5 q/ha) and the lowest in Mehal (10.2 q/ha). Significant fruit yield difference was recorded for Pant Pear-3, Pant Pear-6, Pant Pear-10, Pant Pear-13, Mehal and Sand pear as compared to Patharnakh. The findings were in conformity with Mann and Singh (1985), Kumar (1996), Prakash (2000) and Singh *et al.* (2001),

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SHORT COMMUNICATION

Genetic Variation in Pearl Millet Germplasm**D Lakshmana*¹, BD Biradar¹, D Madaiah² and RB Jolli¹**¹AICRP on Pearl Millet, Regional Agricultural Research Station, University of Agricultural Science, Bijapur-586 101, Karnataka²Zonal Agricultural Research Station, Mudigere-577 132, Karnataka

A study was conducted during 2005, among 105 pearl millet germplasm lines to assess the genetic variability present among the genotypes for different quantitative traits in relation to yield. High phenotypic coefficient of variation and genotypic coefficient of variation was observed high for ear length, ear girth, plant height, grain yield/plant and productive tillers/plant. High estimate of broad sense heritability coupled with high genetic advance as per cent of mean was registered for grain yield/plant, plant height, ear length and ear girth. The genetic variances for these traits are probably indicates better scope for improvement of these traits through direct selection.

Key Words: Genetic advance, Germplasm, Heritability, Phenotypic coefficient variation

Pearl millet is an important staple food crop of millions of people living in harsh environment and predominantly grown in arid and drier semi-arid regions of the world. Genetic reconstruction of a plant type is required for developing high yielding varieties by incorporating and improving yield components characters. Therefore, evaluation of germplasm for genetic variability is essential for present as well as for future crop improvement programmes. Moreover, proper utilization of germplasm requires testing of genetic potential under local conditions under targeted environment for which the breeding programme is aimed. Hence, the present study was taken up during 2005 to assess genetic variability in pearl millet germplasm to identify genetically diverse and agronomically superior genotypes.

The experimental material comprised of 105 diverse pearl millet germplasm lines collected from different geographical regions of India and abroad and were grown during *khari*f season of 2005 in a Randomized Block Design with three replications at Regional Agricultural Research Station, Bijapur, Karnataka. Each germplasm entry was sown in two rows of 4 meter length with a spacing of 50 cm between rows and 15 cm between plants with in the row. The recommended packages of practices were followed to raise the crop. Five plants were taken at random from each replication for all the entries to recorded observations on 12 characters viz., days to 50% flowering, days to maturity, plant height, ear length, ear girth, flag leaf area, peduncle length,

ear weight, grain yield/ear, grain yield/plant and 1000-seed weight. The phenotypic and genotypic coefficients of variations were computed as suggested by Burton (1952). Heritability estimates were computed as suggested by Hanson *et al.* (1956) and expected genetic advance as per the formulae given by Johnson *et al.* (1955).

Analysis of variance for 105 pearl millet germplasm lines for 12 quantitative characters revealed that the mean squares were highly significant for all the characters under study, indicating greater diversity among the germplasm lines (Table 1). Some of the genotypes were identified as desirable genotypes like IP-12901, 10085, 9140 and 6460 for early maturing, IP-10945, 10914, 15273, 7440 for ear length, IP-8389, 15899, 9246 and 9140 for more number of productive tillers/plant and genotype IP-13875, 10839, 12768, 5275, 4779, 13875 and IP-18742 for more ear weight/ear. Genotypes like IP-5275, 10839, 14778, 4779, 16690, 13875, 18742, 7468 and IP-7838 were identified as high yielding genotypes. IP-11211, 10839, 16690, 13875, 19388, 18742 and 13154 were recognized as more than 1000-seed weight genotypes (Table 2).

Significant variance due to genotypes and wide range of variability for all the characters were observed among the germplasm, suggesting ample scope for improvement through selection. The phenotypic coefficient of variation (PCV) though was higher than genotypic coefficient of variation (GCV) for all the characters under study (Table 3) but the narrow difference between PCV and

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Table 1. Analysis of variance for 12 quantitative characters in 105 pearl millet germplasm lines

Sources of variation	df	Days to 50% flowering	Days to maturity	Plant height (cm)	Prod. tillers/plant	Ear girth (cm)	Ear length (cm)	Flag leaf area (cm ²)	Peduncle length (cm)	Ear weight/ear (g)	Grain yield/ear (g)	Grain yield/plant (g)	1000-grain weight (g)
Replication	2	0.37	4.91	51.00	0.14	0.02	3.60	1.96	14.47	25.40	22.06	47.20	1.59
Treatment	104	17.72**	18.55**	464.46**	0.31**	3.47**	41.00**	430.00**	22.15**	8**	65.23**	623.99**	10.01**
Error	208	5.84	4.25	114.68	0.03	0.08	1.34	7.92	1.36	7.23	2.68	16.81	0.17
S.E.(diff.)		1.70	0.79	7.57	0.12	0.20	0.82	1.99	1.99	11.90	1.15	2.89	0.29
C.D. @ 5%		3.36	1.56	14.92	0.24	0.39	1.61	3.92	1.63	3.75	2.28	5.71	0.58
C.D @ 1%		4.44	2.05	19.68	0.32	0.52	2.13	5.17	2.14	4.94	3.01	7.53	0.77

** Significant at 1 % level

GCV indicated that environmental effect was slightly less for most of the characters. High values of GCV and PCV were obtained for the characters like ear length, ear head girth, plant height, grain yield per plant and productive tillers per plant, indicating variation for these characters contributed markedly to the total variability. Further, narrow range of difference between PCV and GCV indicated that any selection pressure operated on these characters may help to realize improvement at early generation (Table 3). High PCV and GCV values were reported in pearl millet by Kunjir and Patil (1986a) for plant height, productive tillers/plant and ear length, Lakshmana *et al.* (2003) for grain yield/plant and Borkhataria *et al.* (2005) for ear girth and grain yield/plant.

Heritability in conjunction with genetic advance is more effective and reliable in predicting resultant effect of selection and based on which, selection procedures can be evaluated. The results of present study on heritability (%) in broad sense for 12 characters revealed that all traits except days to flowering and days to maturity are highly heritable whereas days to 50% flowering and days to maturity showed moderate heritability. Burton (1952) suggested that genetic variation along with the heritability estimates would give a better idea about the expected efficiency of selection, characters possessing high GCV along with the high heritability will be evaluated in a selection programme. The results of present study on heritability (%) in broad sense for 12 characters revealed that all traits except days to flowering and days to maturity are highly heritable. Ear length, ear head girth, and plant height, grain yield/plant and productive tillers/plant recorded high estimates of GCV coupled with high heritability. However, the values of genetic advance suggested that real progress could be made only for a few characters such as ear head length, ear head girth and grain yield/plant. Similar observation were reported by earlier workers viz., Berwar *et al.* (2001)

for plant height; Solanki *et al.* (2002) and Lakshmana *et al.* (2003) for grain yield per plant. Moderate heritability accompanied with low or medium to low genetic advance for the days to 50% flowering and days to maturity indicated the involvement of non-additive gene action in the expression of these characters and moderate heritability is expressed due to favourable influence of the environment rather than genotypes. These results

Table 2. Potential genotypes identified for most important yield attributing parameters in pearl millet germplasm

Characters	Potential genotypes
Days to maturity (80-85 days)	IP-12901, 10085, 9140, 6460, 10394, 13154, 8429, 9416, 17144, 7449, 13840, 9301, 12091, 6445
Ear length (cm) >5 cm	IP-17028, 15257, 14038, 17979, 17978, 10945, 15710, 11503, 10914, 10839, 15364, 15273, 14497, 16196, 7440, 14644, 15364, 18621, 186251, 16197, 16690, 13875, 17144, 12682, 19246, 18800, 8069
Ear weight/ear (g) 30 g	IP-10394, 10820, 15256, 17493, 10811, 10085, 15681, 15257, 14942, 17690, 8229, 8429, 5275, 15710, 11211, 11503, 10914, 10839, 14778, 4779, 18621, 18625, 16197, 16690, 13875, 12779, 12768, 10339, 19388, 18742, 13154
Grain yield/ear (g) >70 g	IP-5256, 9416, 10811, 15681, 17690, 17978, 5275, 11211, 10914, 10839, 4779, 18625, 16690, 13875, 10339, 18742, 13154
Grain yield/plant (g) 70 g	IP-9140, 9286, 3799, 10394, 10811, 15681, 17978, 5275, 112411, 10839, 14778, 16196, 9301, 4779, 18625, 16690, 13875, 12779, 18742, 18657, 13154, 12901, 4169, 7468, 6545, 6451, 7838
1000-seed weight (g) >12 g	IP-9140, 9286, 15857, 15899, 9149, 15817, 10085, 17753, 8229, 6417, 5275, 14026, 11211, 10839, 9301, 4779, 16690, 13875, 12779, 19388, 18742, 13154, 16449, 13137, 12474, 6545, 4511

Table 3. Mean, range and other variability parameters for 12 quantitative characters in 105 pearl millet germplasm lines

Characters	Range	Mean	Variance		Coefficient of variation		h ² (bs)	Genetic advance	Genetic advance (as % mean)
			σ ² p	σ ² g	PCV	GCV			
Days to flowering	44.33	50.32	9.80	3.96	6.22	3.96	40.40	2.60	5.61
Days to maturity	81.67-92.33	86.82	9.01	4.76	3.45	2.51	52.83	3.26	3.75
Plant height (cm)	147.97-206.27	174.98	231.27	116.59	8.69	6.17	50.41	15.79	9.02
Productive tillers/plant	1.47-2.90	2.16	0.12	0.09	16.43	14.27	75.40	0.54	25.00
Ear length (cm)	5.60-11.00	7.75	1.21	1.13	14.21	13.73	93.4	2.10	27.09
Ear girth (cm)	15.67-31.00	23.76	14.69	13.35	16.14	15.38	90.8	7.14	30.08
Flag leaf area (cm ²)	54.97-118.20	81.43	148.62	140.69	14.97	14.57	94.6	23.65	29.04
Peduncle length (cm)	17.33-28.37	21.97	8.29	6.93	13.11	11.98	83.5	4.93	22.43
Ear weight/ear	32.93-72.10	48.80	70.88	63.64	17.25	16.35	89.7	15.49	31.74
Grain yield/ear (g)	17.30-38.47	26.06	23.53	20.84	18.62	17.52	88.5	8.81	33.80
Grain yield/plant (g)	30.70-85.33	60.14	219.20	202.39	24.62	23.66	92.3	28.02	46.59
1000-seed weight (g)	6.37-13.70	9.44	3.45	3.29	19.69	19.18	94.9	3.61	38.24
σ ² p-Phenotypic variance			σ ² g- Genotypic variance				GAM-Genetic advance over mean		
PCV-Phenotypic coefficient of variation			GCV-Genotypic coefficient of variation				h ² (bs)-Heritability in broad sense		
GA-Genetic advance									

were similar to the findings of Navale *et al.* (1991) for days to 50% flowering and Berwal *et al.* (2001) for days to maturity in pearl millet.

Heritability estimates along with genetic advance are more useful than heritability alone in predicting the effectiveness of selection. Further, the heritability estimates coupled with expected genetic advance as per cent of mean indicate the mode of gene action in choosing an appropriate breeding methodology. Some characters like grain yield per ear and 1000-grain weight had high heritability with moderate genetic advance and thus could serve as an index for selection, for high grain yield per plant. These results are in line with findings of Dang *et al.* (1985) and Kunjir *et al.* (1986) who reported high heritability for 1000-grain weight in pearl millet. High estimates of genetic advance as per cent of mean coupled with high estimates of heritability was observed for grain yield/ plant, 1000-seed weight, grain yield/ ear, ear weight and ear length. These characters are likely to provide high selection response, owing to their high transmissibility (Saxena and Singh, 2001). High estimates of genotypic coefficient of variation, heritability and genetic advance as per cent of mean indicate the predominance of additive gene action in controlling these characters and simple directional selection may be effective to improve these characters (Roopa Lavanya, 2006). The study revealed substantial genetic variability in the germplasm collection and a scope for improvement through selection.

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SHORT COMMUNICATION

D² Analysis for Fruit Yield and Quality Components in Tomato (*Lycopersicon esculentum* Mill.)**Sanjeev Kumar^{1*}, Puja Rattan², Jag Paul Sharma² and RK Gupta¹**¹*Division of Vegetable Science & Floriculture, Faculty of Agriculture*²*Directorate of Research, Sher-e-Kashmir University of Agricultural Sciences and Technology, Jammu-180 009, J & K*

Forty-nine tomato genotypes collected from different parts of Jammu region, Indian Institute for Vegetable Research, Varanasi and National Bureau of Plant Genetic Resources, New Delhi, India were studied using Mahalanobis D² Statistics to elucidate the genetic divergence for fruit yield, quality and their contributing characters. The genotypes were grouped into ten clusters by Toucher's method. The cluster I contained highest number of genotypes (13) followed by cluster VII (8), cluster III (7) and cluster IV (7). The cluster IX and X consisted of one genotype each. The intra cluster distance was highest in cluster IV (D=14.90) which accommodated promising genotypes namely RCMT-2, Pant T-8, and CTS-05-35-3 (SPS) having large, round, red fruits with good yield potential. Cluster VI (D=13.81) and cluster VIII (D=13.09) ranked second and third. Sufficient variation in these clusters indicates scope of genetic improvement through hybridization of genotypes available within the cluster. Lowest intra-cluster distance was observed in cluster IX and X (D=0.00). Highest inter-cluster distance was observed between cluster IX and X (D=68.99) followed by cluster III and X (D=66.29). Sufficient genetic distance was also observed between the clusters V and III, IX and V and VI and IX. The genotypes which fall in diverse clusters namely PAU 2374, 127-1 Sel., VR 35, PAU 2372, Tomato 169, VR 415, Punjab Chuhara, RCMT 1, Pant T-10; DT-2 and CTS-05-16, KS 229, ATL-02-39 and VTG 85, with high inter-cluster distance may be utilized in heterosis as well as in recombination breeding programme to develop heterotic hybrids. Cluster mean analysis indicated cluster II, IV, V and IX accommodated tall genotypes while clusters II, V and X were characterized by higher number of fruits per plant. Pericarp thickness was maximum in cluster III, IV and II. Total soluble solids which is a processing trait was available in genotypes belonging to cluster II and X. Cluster X gave the highest gross yield as well as marketable yield followed by cluster V and II. The genotypes in cluster II, V and X could serve as direct source for development of high yielding open pollinated varieties.

Key Words: Divergence, Genotype clustering, Tomato, Yield

Tomato (*Lycopersicon esculentum* Mill.) is one of the most important vegetable crops in India as well as around the world. It finds a very important role in every kitchen with enormous role in food and nutritional security. It also has a very important and significant position in the post harvest industry. Going by its commercial importance, there is utmost need to develop newer varieties/genotypes/hybrids with disease resistance, heat tolerant and processing traits. For this purpose the breeders choose genetically distant parents, genetic diversity plays an important role in breeding vegetables, because hybrids derived from the lines of diverse origin display more heterosis than those between closely related strains. Estimation of genetic divergence also allows breeders to eliminate some parents in downsizing the gene pool available and concentrate their efforts in a smaller number of hybrid combinations (Fuzzato *et al.*, 2002). Among the various methods identified/developed

to study the genetic divergence in the genotypes, the Mahalanobis D² (Mahalanobis, 1936) is reliable and most frequently used. D² analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different components to the total divergence, both at the inter- and intra-cluster levels. Keeping these points in mind, the present study was undertaken to know the magnitude of diversity in the available germplasm for yield and quality components and to identify the diverse parents so as to develop the heterotic crosses.

The present investigation was undertaken in the experimental farm of the Division of Vegetable Science and Floriculture, FOA, Chatha, SKUAST (J&K), India, during February-May, 2008. The research farm is situated at 33°55' North latitude and 74°58' East longitude at an elevation of 332 m above mean sea level. The place

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experiences cool winters and very hot summers with average rainfall. Agroclimatically, the location represents Zone IV of the state of Jammu & Kashmir, India, and is characterised by humid, tropical climate.

The experimental material comprising of forty-nine tomato genotypes collected from different parts of Jammu region by Indian Institute for Vegetable Research, Varanasi and National Bureau of Plant Genetic Resources, New Delhi, and maintained in the Division of Vegetable Science and Floriculture, SKUAST (J&K), were grown in randomized block design with three replications during 2008. The seedlings were transplanted on 26th February, 2008 and were spaced at 75 cm row to row and 45 cm plant to plant. There were 15 plants in each entry/replication. All the recommended cultural practices were followed to raise a healthy crop. Data was recorded on 7 randomly selected plants per entry per replication for various horticultural characters namely total number of fruits per plant, average fruit weight (g), gross yield (g), marketable yield (g), marketable number of fruits per plant, plant height (cm) and 5 randomly selected fruits were taken per entry per replication for quality characters namely fruit shape index, pericarp thickness (mm), number of locules per fruit and total soluble solids (%). The data was analysed as per method given by Mahalanobis (1936). Criteria Toucher (Rao, 1952) was used for determining the groups and clustering was done accordingly. Average inter- and intra-cluster distances were estimated as per method given by Singh and Chaudhary (1985).

Forty-nine genotypes were grouped into 10 clusters on the basis of D^2 values, indicating adequate genetic diversity for selecting superior and diverse parents which can be exploited for any breeding programme. The perusal of data (Table 1) depicted that cluster I had the maximum number of genotypes (13) followed by cluster VII with

Table 1. Clustering pattern of 49 genotypes of tomato based on D^2 statistics

Clusters	Number of genotypes	Name of genotypes and serial number
I	13	HADT-294, VTG 90, CO 3, CTS-06-02, NDT 9, VTG 106, RUCH-1-1 Sel., CO 3-1 Sel., NTH-2003-1 Sel., ARTH-3 Sel., CTS-05-30-2 Sel., CTS-06-19, Improved Shalimar
II	2	CTS-05-35-2 (SPS), Pant T-7
III	7	VR 35, PAU 2372, Tomato 169, VR 415, Punjab Chuhara, RCMT 1, Pant T-10
IV	7	ATL-01-19, PAU 2371, Arka Vikas, Local 2707, CTS-05-35-3 (SPS), Pant T-8, RCMT 2
V	2	CTS-05-16-1 Sel., DT-2
VI	3	KS 229, ATL-02-39, VTG 85
VII	8	ARTH-3-1, 127-1 Sel., CTS-05-16-2-1 Sel., CTS-05-16-1-2 Sel., EC 521041, KS 227, VTG 86, VR 20
VIII	5	EC 538151-3 Sel., CTS-05-24-1 Sel., EC 538151-2 Sel., EC 251581-1 Sel., JTP-02-07
IX	1	PAU 2374127-1
X	1	Sel.

8 genotypes and cluster III and cluster IV with 7 genotypes in each cluster. The clustering pattern indicated that there was no association between genetic diversity and geographical diversity. These results are similar to the findings of Peter and Rai (1976), Rai *et al.* (1998), Joshi and Kohli (2003) and Singh *et al.* (2008). On the other hand, the genotypes that originated in one region had been distributed into different clusters, indicating that genotypes with same geographic origin could have under gone change for different characters under selection. This could be due to selection pressure, genetic drift and introduction, which help in creating more diversity rather than genetic distance.

The intra- and inter-cluster values (Table 2) showed that cluster IV recorded maximum intra-cluster distance (14.90) followed by cluster VI (13.81) and cluster VIII (13.09), revealing considerable genetic divergence among

Table 2. Average intra (bold) and inter cluster distance values

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	(12.24)	38.75	22.66	18.77	54.55	45.34	27.36	35.62	29.74	62.30
II		(11.11)	44.75	34.12	39.29	26.17	28.02	19.28	48.76	49.74
III			(11.20)	29.42	59.07	50.69	35.52	42.21	19.39	66.29
IV				(14.90)	51.23	41.29	19.95	30.30	35.14	59.41
V					(10.36)	30.43	47.20	41.33	62.12	30.52
VI						(13.81)	36.16	28.08	54.21	42.82
VII							(12.60)	22.81	40.40	55.99
VIII								(13.09)	46.39	51.16
IX									(00.00)	68.99
X										(00.00)

Table 3. Cluster mean for different quantitative characters in 49 diverse genotypes of tomato (*Lycopersicon esculentum*)

Characters	Total number of fruits	Average fruit weight	Gross yield	Marketable yield	Marketable number of fruits/plant	Plant height	Fruit shape Index	Pericarp thickness	Number of locules/ fruit	Total soluble solids
Cluster										
I	28.00	37.96	1045.56	894.35	24.05	79.46	0.91	0.47	3.19	4.28
II	116.80	18.72	1959.50	2076.80	124.75	133.00	0.82	0.53	3.00	5.88
III	18.60	36.23	643.80	574.71	16.71	84.50	1.09	0.56	2.50	4.49
IV	42.60	37.94	1323.56	1109.25	35.38	95.14	0.88	0.56	3.29	4.21
V	160.50	22.24	3318.50	2807.53	137.25	110.00	0.94	0.43	3.00	4.53
VI	59.70	45.18	2619.57	2216.35	50.67	69.00	1.02	0.48	2.33	4.42
VII	48.40	35.99	16.11.39	1383.57	41.71	77.63	0.88	0.41	2.94	4.68
VIII	68.70	34.30	2005.95	1721.90	58.60	75.90	1.09	0.44	3.20	4.56
IX	11.50	35.50	407.05	283.20	8.00	95.00	0.92	0.40	3.00	3.40
X	147.30	28.69	4158.34	3208.04	113.33	77.50	0.90	0.35	2.50	5.40

the genotypes of the cluster. The parents within the cluster can be chosen for hybridisation programme. The relative distance of each cluster from other cluster *i.e.*, inter-cluster distance showed greater divergence between cluster IX and cluster X *i.e.*, $D = 68.99$ followed by cluster III and cluster X ($D = 66.29$) and cluster I and cluster X ($D = 62.30$), indicating greater diversity between genotypes belonging to respective pairs of cluster. The cluster I and cluster IV had the least genetic distance *i.e.*, $D = 18.77$.

The cluster means of genotypes (Table 3) revealed considerable genetic differences between the groups. Cluster II, for plant height (133.00) and total soluble solids (5.88); cluster III [VR 35, PAU 2372, Tomato 169, and cluster VIII for fruit shape index (1.09) and pericarp thickness (0.56); cluster IV [ATL-01-19, PAU 2371, Arka Vikas, Local 2707, CTS-05-35-3 (SPS), Pant T-8, RCMT 2], for pericarp thickness (0.56) and number of locules/fruit (3.29); cluster V [CTS-05-16-1 Sel., DT-2], for total number of fruits per plant (160.50) and marketable number of fruits/plant (137.25) and cluster X [127-1 Sel.], for gross yield (4158.34) and marketable yield (3208.04) registered highest mean values for two characters each. Remaining characters were low in performance.

The inferences drawn from inter-cluster distances may be used to select genetically diverse and superior genotypes. Intercrossing of genotypes from these diverse clusters may result in wide array of variability for having effective selection for these characters. These results are in accordance with Singh and Singh (1976) and Singh *et al.* (2008). Intercrossing of divergent groups would lead to greater opportunity for crossing over, which

may release hidden variability by breaking linkage (Thoday, 1969). Hence, these genotypes might be used in single as well as multiple crossing programmes for development of promising hybrids. On the basis of mean value for economic traits and placement in distantly located clusters, the varieties RCMT-1, Pant T-10, DT-2 and Selection-127-1 are suitable both as open-pollinated varieties and as parents to be used in hybridization programme.

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SHORT COMMUNICATION

Correlation and Path Coefficient Analysis of the Components of Yield in Sunflower Cultivars (*Helianthus annuus* L.)

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Genetic variability, character association and path analysis between seed yield and its contributing traits were studied in 22 genotypes of sunflower. Highly significant differences between genotypes were recorded for all the characters studied. A slight increase of genotypic correlation coefficients over phenotypic correlation coefficient was noticed for all the character combinations. All the examined characteristics except days to 50% flowering, % filled seeds, 100-seed weight and oil content were significantly and positively associated with seed yield. Since, plant height, head diameter, head weight and number of seeds/head are intercorrelated among themselves, selection for these traits will result in increased seed yield. Path coefficient analysis revealed that among all the traits studied, stem diameter at mid height and head weight contributed most directly to seed yield. All other yield contributing traits had sizeable influence on seed yield indirectly only through stem diameter at mid height and total head weight.

Key Words: Correlation, Path analysis, Sunflower

High seed yield and oil content are definitely the major criteria in sunflower breeding. However, breeders often encounter problems with these characteristics because of their low heritability and high responsiveness to genotype/environment interaction. Seed yield and oil content are complex characteristics which are affected by different factors which may act individually or collectively. More information are needed to clarify the relations between these characteristics and plant and seed characteristics. The experiments discussed in this paper were undertaken in order to obtain information about correlation, direct and indirect effects of biomorphological characteristics on seed yield and oil content in sunflower.

The material comprised of 22 genotypes of sunflower were collected from the Division of Genetics, Indian Agriculture Research Institute (IARI), New Delhi and were evaluated in a randomized block design experiments with three replications at Research Farm of Kisan (PG) College, Simbhaoli, Ghaziabad, during rainy season 2007. Each genotype was assigned to two row plots of 3 m length with inter- and intra-row spacing of 75 cm and 30 cm, respectively. Recommended agronomic practices were followed to raise a good crop. Data were collected on five randomly selected competitive plants from each plot on growth, yield and oil content. Oil content was estimated by the

Pulsed Nuclear Magnetic Resonance Spectrometer (NMR) technique (Tiwari *et al.*, 1974). Phenotypic and genotypic correlation coefficients for all characters combinations were computed following Al-Jibouri *et al.* (1958). Path coefficient analysis was carried out according to Dewey and Lu (1959) by partitioning the genotypic correlation coefficients into direct and indirect effects.

The analysis of variance for different characters is presented in Table 1. The critical perusal of the table revealed that highly significant genotypic differences were observed for all the characters under study. A slight increase of genotypic correlation coefficients over phenotypic correlation coefficients was noticed for all the character combinations indicating that though there is a strong inherent association between many traits studied, the phenotypic expression of the association is reduced under the influence of environment (Sivaram, 1986). Singh and Labana (1990) reported such higher genotypic correlation coefficients over phenotypic correlation coefficients in sunflower. The relative magnitude of genotypic and phenotypic correlations suggests that phenotypic selection can be reliable as the underlying cause of association has a genetic basis.

Seed yield/plant was significantly and positively correlated with number of leaves/plant, plant height, stem diameter at top height, stem diameter at mid height, head diameter, head diameter of sterile area, weight of

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Table 1. Estimates of genetic constraints (for variability) for sixteen characters in 22 genotype of sunflower

Characters	Range	Heritability (bs)	Genetic advance	Genetic advance over mean	Coefficient variability	Difference GCV	PCV-GCV PCV
D.F. 50%	50.83-64.67	0.76	6.55	11.90	6.65	7.65	1.00
NL/P	13.67-23.83	0.49	3.22	17.12	11.82	16.84	5.02
PH	69.70-131.90	0.55	21.76	22.64	14.81	19.97	5.16
SDTH	1.93-3.40	0.35	0.35	12.86	10.46	17.62	7.16
SDMH	2.53-4.30	0.42	0.60	17.91	13.58	21.08	7.50
HD	5.60-10.47	0.39	1.44	18.34	14.31	22.95	8.64
HDSA	1.10-3.87	0.51	0.90	35.43	23.99	33.45	9.46
TWH	32.67-192.50	0.59	62.21	63.54	40.01	51.91	11.90
NS/H	82.33-213.33	0.61	58.30	43.81	27.17	34.71	7.54
PFS	62.10-80.73	0.24	3.74	5.15	5.07	10.28	5.21
100SW	8.17-16.33	0.62	3.58	28.66	17.65	22.38	4.73
SY/P	4.00-22.90	0.72	9.45	86.06	49.83	59.46	9.63
OC%	43.37-54.43	0.68	4.86	10.26	6.06	7.38	1.32
LL	10.53-22.63	0.60	3.95	27.39	17.13	22.06	4.93
LB	6.43-16.17	0.59	3.34	35.34	22.37	29.12	6.75
LA	50.73-257.57	0.61	68.83	68.29	42.59	54.72	12.13

head, number of seeds/head, leaf length, leaf breadth and leaf area. Singh and Labana (1990) and Doddamani *et al.* (1997) observed similar positive significant correlations for these traits. On the other hand, Patil *et al.* (1996) reported that there was a negative correlation between seed yield and head diameter. Furthermore, some researchers could not find correlations between seed yield and certain characteristics (Natali and Saikh, 1970; Varshnay and Singh, 1977).

As a rule, the plants with a large size of heads also had a large number of seeds/head as illustrated by the highly significant positive correlation between the head diameter and the number of seeds/head (+0.441*). There were positive but non significant correlations between the head diameter and the weight of 100 seeds.

The poor association of seed yield with days to 50 per cent flowering suggests that duration of photosynthetic activity is not a limitation in sunflower. Therefore, reducing the length of growing period without affecting final seed yield is at the realm of sunflower breeding. Gowda (1994), Patil *et al.* (1996) and Doddamani *et al.* (1997) also reported poor association between seed yield and days to flowering.

The positive significant correlation observed between plant height and seed yield is justifiable and is in agreement with results reported by Patil *et al.* (1996) and Doddamani *et al.* (1997). Tall plant supporting many leaves as illustrated by highly significant positive association between plant height and number of leaves per plant could increase total biomass production through increased carbon fixation which can ultimately be partitioned to reproductive organs. Thus, the number

of internodes, which are sites of leaf initiation, should remain constant during breeding for shorter plant types. From the foregoing, it may be concluded that an intensive selection for plant height, head diameter, total weight of head and number of seeds per head will automatically improve seed yield in sunflower. Again, since all these four traits are intercorrelated among themselves, selection in any one of the traits will result in improvement of other traits, thereby finally increasing the seed yield.

With regard to one important quality character, oil content, the breeder facing real challenge, since oil content is not significantly related to any of the yield components mentioned above, the selection of these traits will not influence the oil content. However, oil content is negatively correlated not only with seed yield, but also with number of leaves/plant. Hence, there is every chance of reduction in oil content if selection process is exerted on these traits in the positive side. Therefore, a compromise has to be arrived at to have an optimum oil content without sacrificing the seed yield. Among the other characters, % filled seeds and 100-seed weight showed non-significant but positive association with seed yield and thereby, suggesting the possibilities of improving these characters independent of seed yield.

Since, we could not establish the cause and effect relationships between the examined yield components and seed yield per plant on the basis of simple correlation coefficients, we processed the data by the path-coefficient analysis which enabled the partitioning of the direct and indirect effects of individual yield components and identification of yield components applicable as selection criteria in sunflower breeding. Partitioning of genotypic

correlations of other characters with yield into direct and indirect effect revealed that stem diameter at mid height (0.515) and head weight (0.471) had maximum direct effect on seed yield. The correlation coefficients recorded for these characters, being most important components of yield, should be given more weightage during selection process. Patil *et al.* (1996) also observed high positive direct effect of stem diameter at mid height and head weight on seed yield. The direct effect of stem diameter at top height, plant height, head diameter of sterile area and leaf breadth was negative on seed yield per plant, but their significant positive correlations with seed yield was due to their respectively high and moderate indirect effects through stem diameter at mid height. Similar findings were reported by Doddamani *et al.* (1997). Oil content, the only trait which showed negative association with seed yield had low positive direct effect. But its positive influence on seed yield was mainly due to high positive indirect effect through stem diameter at mid height. Even the traits which had no significant association with seed yield, viz., days to 50% flowering and 100-seed weight had moderate indirect influence on seed yield through diameter at mid height.

The above findings revealed that increase in seed yield can be achieved through increase in stem diameter and mid height. All the characters exhibited their indirect effect mostly through stem diameter at mid height. Hence, it may be concluded that more seeds developed when sufficient nutrients were supplied through a thicker stem measured in terms of the stems diameter at mid height. Variations at genotypic level were also quite high for

most of the traits indicating sufficient scope for selection. The magnitude of GCV and PCV were comparatively higher for seed yield/plant, leaf area, total weight of head and number of seeds/head as compared to other characters.

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SHORT COMMUNICATION

Response of Germplasm Lines towards PEG-induced Drought Stress in Cotton (*Gossypium hirsutum* L. and *Gossypium arboreum* L.)

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Key Words: Germination, *Gossypium*, Osmoticum, Polyethylene glycol

Cotton (*Gossypium* spp.), a major fibre crop of India, often encounters moisture stress during seed germination especially under rainfed cultivation in Central and South zones. Breeding for drought tolerance has always been a challenging goal in cotton research. The germplasm which is rich in diversity may be a potential source for identifying lines tolerant to moisture stress. In percent study, 22 lines of cotton genlarm were screened for drought-stress tolerance.

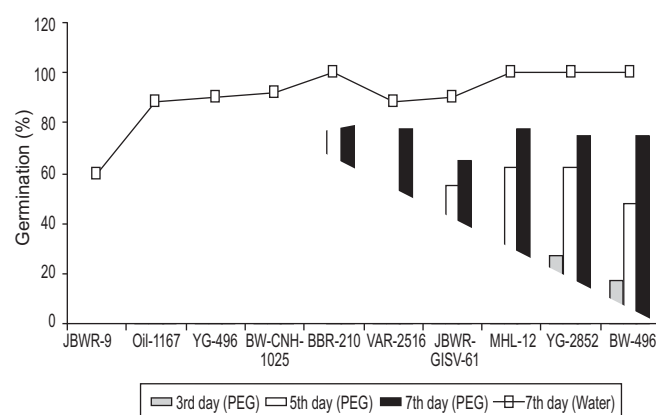
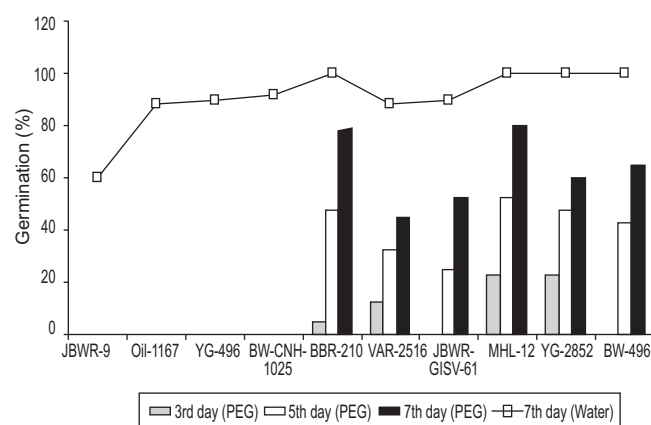
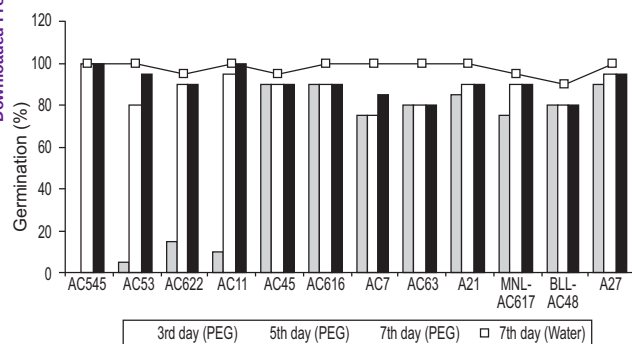
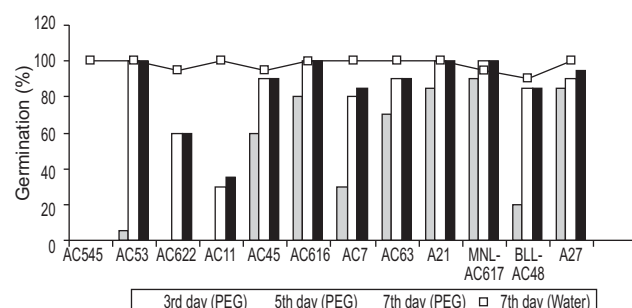
Ten germplasm lines belonging to *G. hirsutum* (Oil-1167, JBWR-9, MHL-12, JBWR-GISV-61, VAR-2516, BW-496, BBR-210, BW-CNH-1025, YG-496, YG-2852) and 12 lines belonging to *G. arboreum* (6506-A21, 6507-A27, 6519-AC-7, 6522-AC11, 6556-B66-AC48, 6559-AC53, 6563-AC63, 6579-AC545, 6583-AC616, 6584M11-AC617, 6589-AC622 and AC-45) were used to investigate their capacity to survive under different polyethylene glycol (PEG) concentrations and early vigor. The seeds were collected from the germplasm curator, Central Institute of Cotton Research (CICR), Nagpur, and multiplied under field conditions. The seeds were observed for seed index and tested for initial germination as per the ISTA standards by rolled towel method (Table 1). Simulated water deficit stress was created using two concentrations (15% and 20%) of PEG 6000. One hundred seeds of each line were washed and surface sterilized with 0.1% HgCl₂ followed by thorough washing under tap water twice. Fifty seeds/replication/line were plated in each petri plate lined with filter paper soaked in equal volume of PEG solutions along with a control set maintained in double distilled water. Four replications were maintained for each treatment. Later they were kept in an incubator for 7 days at 25 °C. To account for any change in PEG solution, it was changed at 2 days interval. The treatments were replicated four times. The observation on germination was made daily. Seeds were considered to be germinated when radical became 2 mm long. Rate of germination was assessed by counting the number of seeds germinated each day.

Comparisons between treatments and lines were made using the data on the 3rd, 5th and 7th day of seed plating.

Simulated water deficit stress using PEG solutions, adversely affected germination especially, in *G. hirsutum* lines. The initial decline in root growth and subsequent reduction in germination with increasing PEG induced stress, has been reported in different crops (Bibi *et al.*, 2009; Nautiyal, 2009). The average germination in *G. hirsutum* which ranged between 15% to 82% under 15% PEG still lowered under 20% PEG especially for lines, VAR 2516 and JBWR-GISV-61 (Figs. 1a & b). The lines, JBWR-9, Oil-1167, YG-496 and BW-CNH-1025 revealed more sensitivity towards PEG stress under both 15% and 20% PEG treatments. Apparently, JBWR-9 was the most affected line as the seeds did not germinate even in 15% PEG. However in *G. arboreum*, the difference in response was not much and all lines maintained a higher germination percentage (above 80%) in both 15% and 20% PEG solutions except two lines viz., AC-53 and AC-622 wherein germination under 20% PEG significantly reduced from 90% to 55% in former and from 85% to 40% in later (Figs. 2a & b). The difference in response between species might be due to slow mobilization of proteins in the sensitive species compared to the relatively tolerant species as observed in soybean (Samarah and Mullan, 2006). In cotton, it has been reported that developmentally-regulated heat shock proteins HSP 101 and HSP 17.6 appeared in the cotyledons of water-stressed cotton seedlings under PEG induced water deficit stress which were absent in cotyledons from well watered seedlings (Burke and Mahony, 2001). *G. arboreum* genotypes commonly called as *desi* cotton of Indian origin, are known to emerge earlier and to be more drought- tolerant than *G. hirsutum* (upland cotton). An earlier study on *G. hirsutum* and *G. arboreum* cultivars also revealed low/non-sensitivity of latter towards germination stress induced by methanol (Santhy and Deshmukh, 2008). Genotypic variation was observed for response to the simulated stress in both *G. hirsutum* and *G. arboreum*

Table 1. List of Germplasm lines with their IC numbers, seed index and initial germination%

Germplasm Line	IC No.	Seed index	Mean germination %
<i>G. arboreum</i>			
A21	412026	6.2	85
A27	412027	6.1	84
AC-7	412040	5.5	85
AC-11	412043	6.1	85
BLL-AC-48	412078	6	78
AC-53	412081	5.7	78
AC-63	412085	5.0	88
AC-545	412102	6.1	84
AC616	412107	6.7	78
MNL-AC617	412108	6.0	80
AC622	412114	6.5	80
AC-45	412074	5.8	82
<i>G. hirsutum</i>			
JBWR-9	M-7-CC	10.2	76
Oil-1167	357682	9.8	82
YG-496	357011	7.6	88
BW-CNH-1025	357540	8.6	80
BBR-210	356725	6.3	75
VAR-2516	359031	7.9	85
JBWR-GISV-61	GISV-61	6.8	88
MHL-12	356527	7.5	94
YG-2852	EC-138570	7.6	88
BW-496	357011	9.4	86

**(a) Under 15% PEG osmoticum****(b) Under 20% PEG osmoticum****Fig. 1. Variation in response to polyethylene glycol-simulated drought stress during germination in *G. hirsutum* germplasm lines****(a) Under 15% PEG osmoticum****(b) Under 20% PEG osmoticum****Fig. 2. Variation in response to polyethylene glycol-simulated drought stress during germination in *G. arboreum* germplasm lines**

lines and it was high under 20% PEG concentration. The speed of germination observed by the total number of seeds germinated during the initial days also revealed the maximum germination percentage attained by 3rd to 5th

day under both 15% and 20% PEG in all *G. arboreum* lines revealing them to be having high seed vigor and better speed of germination (Fig. 2). However, *G. hirsutum* lines showed a gradual germination distributed over

the seven days indicating a lower speed of germination (Fig. 1). The early emergence of *G. arboreum* and escape from drought stress due to higher reserve utilization efficiency has already been reported (Santhy *et al.*, 2009). The better PEG stress tolerance of *G. arboreum* and few lines of *G. hirsutum* may thus be a reliable indication as regards their ease of germination under comparatively adverse soil/water conditions which needs to be further ascertained.

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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of ICAR in its XXth meeting held on September 15, 2009 at the National Bureau of Plant Genetic Resources, New Delhi, approved the registration of following 62 germplasm lines out of 146 proposals considered. The information on registered germplasm is published with the purpose

to disseminate the information to respective breeders for utilization of these genetic stocks in their crop improvement programmes. Upon request, the developer(s)/author(s) is/are obliged to distribute the material for crop improvement programs of National Agricultural Research System.

1. RPBio-189 (IET19045) (IC569676; INGR09070), a Paddy (*Oryza sativa*) Germplasm with High Bacterial Blight Resistance, Yield and Fine-grain type

RM Sundaram¹, MR Vishnupriya², N Shobha Rani¹, GS Laha¹, BC Viraktamath¹, SM Balachandran¹, NP Sarma¹, B Mishra¹, G Ashok Reddy¹ and RV Sonti²

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Samba Mahsuri (BPT5204), released by Acharya NG Ranga Agricultural University (ANGRAU), A.P., in 1986, is a well known quality rice variety which gets high price on account of its high consumer preference and is now considered as a “Mega Variety”. It has spread too many Indian states and occupies ~3.3% of the rice area in the country but lacks resistance/tolerance to major pests and diseases. Through a collaborative research project funded by National Agricultural Technology Project (NATP) and executed by the Directorate of Rice Research (DRR), Hyderabad and Centre for Cellular and Molecular Biology (CCMB), Hyderabad. Three bacterial blight (BB) resistance genes- *Xa21*, *xa13* and *xa5* have been introgressed into the genetic background of Samba Mahsuri from a donor line SS1113 through marker-assisted backcross breeding. At each backcross generation, PCR-based molecular markers linked to the three resistance (R) genes were used to identify plants possessing the R genes.

After identification of resistant plants, parental polymorphic rice microsatellite markers were used to identify the resistant backcross plant possessing maximum introgression from the recurrent parent genome (i.e. Samba Mahsuri genome). At BC₄F₁ generation, the best resistant backcross plant selected based on marker analysis

Important agro-morphological characteristics of RPBio-189 (IET19045)

Characteristics	Description
Plant height (cm)	89
Plant type	Semi-dwarf
No. of tillers/plant	15-18
No. of panicle per square meter	325
Days to 50% flowering	110 days
Panicle type	Compact
Panicle exertion	Completely exerted
Awning	Awnless
Apiculus colour	Absent
1000-grain weight (g)	22
Kernel length (mm)	4.82
L/B ratio	2.83
Elongation ratio	2.03
Kernel appearance	Medium slender
Hulling recovery (%)	70.8
Head rice recovery (%)	65.0
Alkali value	5.0
Amylose content (%)	24.30
Gel consistency (mm)	39
Water uptake (ml) during cooking	122 ml
Resistance to bacterial blight	Resistant

was selfed to obtain BC₄F₂ plants. Through marker analysis, five BC₄F₂ plants possessing the three R genes in homozygous condition were identified and progenies of these homozygous lines were later evaluated in limited field trial for yield and agronomic parameters at the experimental farm of DRR. The analysis showed that the homozygous lines resemble the recurrent parent (Samba Mahsuri) in yield, duration and other agro-

*Compiled and edited by: Anjali Kak and RK Tyagi, Division of Germplasm Conservation, National Bureau of Plant Genetic Resources, New Delhi-110 012

morphological parameters. Analysis of grain quality revealed that the gene-pyramid lines resemble the recurrent parents closely. Finally, when the plants were exposed to a virulent isolate of the BB pathogen (named DX066), all the three-gene pyramid lines showed complete resistance to the pathogen with lesion lengths less than 3 cm. Four of the promising three-gene pyramid lines derived from BC₄F₅ generation lines (viz. RPBio-170, RPBio-189, RPBio-197 and RPBio-226) were nominated for field evaluation along with parental materials for trait verification in All India Coordinated Rice Improvement

Programs during Kharif 2005 and Kharif 2006. One of the three gene pyramid lines, RPBio-189 (IET19045) exhibited high level of bacterial blight resistance and higher grain yield as compared to Samba Mahsuri. Further, the culture was equivalent to all grain and cooking quality parameters except that of water uptake during cooking, wherein RPBio-189 (IET19045) exhibited a unique feature of very low water uptake of only 122 ml. Thus, RPBio-189 is unique and different from Samba Mahsuri in terms of higher yield, bacterial blight resistance and low water uptake during cooking.

2. Culture No: IET 9691 (IC569481; INGR09071), a Paddy (*Oryza sativa*) Germplasm with Resistance to Bacterial Blight (BB) Resistance and Excellent Grain and Cooking Quality

GS Varaprasad, G Padmavathi, N Shobha Rani, P Krishna Murthy, SP Singh and BC Viraktamath

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Soil phosphorus (P) deficiency limits rice yields on a variety of soils that are typically found in the tropics. Hence development of germplasm adopted to such conditions requires in-built mechanisms of high nutrient use-efficiency. Developing genetically enhanced plants with better P use efficiency (PUE) through efficient P absorption, transportation and internal utilization are of paramount importance.

IET 9691 designated as RP2235-48-54-6 and derived from the cross, IR 50/ Phalguna was developed through pedigree method during 1981 at the Directorate of Rice Research, Hyderabad. It is a mid-early duration culture tolerant to phosphorus deficient soils with higher root volume and root weight and has high yielding ability in phosphorus deficient and normal soils.

IET 9691 is a semi-dwarf with plant height of 95 cm, compact and non-lodging plant type. It possesses intermediate and well exerted panicles. With flowering duration of 88 days and maturity duration of 118 days, IET 9691 records about 400 panicles per square meter. With long slender quality grains, IET 9691 possesses 55% head rice recovery, intermediate amylose content, intermediate alkali spreading value and soft gel consistency. This culture is resistant to gall midge, moderately resistant to stem borer, bacterial leaf blight and brown spot. IET 9691 evaluated under AICRIP during 1985-1987 in

variety trials was identified as a promising entry for irrigated areas of Andhra Pradesh, Karnataka and Orissa against released varieties Vikas and Ratna (Draft proceedings, XXIV Annual Rice Workshop, 1989).

IET 9691 exhibited P use efficiency with higher grain yield response to applied P even at higher P levels of 40, 50 and 60 kg P₂O₅ / ha. Grown in p deficient soils, the sensitive check entry IET 17025 recorded low grain yield of 0.02, 1.62, 2.48, 2.65, 2.79, 3.12, 3.32 t/ha while IET 9691 recorded high grain yield of 1.64, 3.54, 4.13, 4.69, 4.94, 5.28, 6.70 t/ha at P0, P10, P20, P30, P40, P50 and P60 kg/ha respectively demonstrating the superiority in p deficit soils. IET 9691 has higher root activity resulting in the higher phosphorous use efficiency (Krishnamurthy *et al.*, 2004). Utilisation of IET 9691 in the development of varieties for p deficit soils would enhance the production and accrue high net returns to farmers.

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morphological parameters. Analysis of grain quality revealed that the gene-pyramid lines resemble the recurrent parents closely. Finally, when the plants were exposed to a virulent isolate of the BB pathogen (named DX066), all the three-gene pyramid lines showed complete resistance to the pathogen with lesion lengths less than 3 cm. Four of the promising three-gene pyramid lines derived from BC₄F₅ generation lines (viz. RPBio-170, RPBio-189, RPBio-197 and RPBio-226) were nominated for field evaluation along with parental materials for trait verification in All India Coordinated Rice Improvement

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3. RP4518-2-6(RPMRE-1) (IC569649; INGR09072), a Paddy (*Oryza sativa*) Germplasm with Resistance to Gall Midge and Brown Plant Hopper

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The breeding line RPMRE-1 (Rice Project Multiple Resistance Entomology – RP4518-2-6) was developed at DRR by making a cross between MR 1523 x Abhaya and subsequently following Pedigree selection method. RPMRE-1 showed resistance to gall midge, brown plant hopper and white backed plant hopper consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trials (Ref: DRR, Progress Report 2006 & 2007). The morpho-agronomic characters are given in the table.

Character	Details
Time of heading	104 days (Medium duration)
Basal leaf colour	Green
Stem Length	57 cms (Very short)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain aroma	Absent
Resistance genes ¹	Gm4 + Gm11
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	Resistance to DRR

4. RP4621-1842(RPMRE-2) (IC569650; INGR09073), a Paddy (*Oryza sativa*) Germplasm with Multiple Resistances to Gall Midge, Brown Plant Hopper, White Backed Plant Hopper and Green Leaf Hopper

The breeding line RPMRE-2 (Rice Project Multiple Resistance Entomology – RP4621-1842) was developed at DRR by making a cross between Aganni x Bhumansan and subsequently following Pedigree selection method. RPMRE-2 showed resistance to rice gall midge, brown plant hopper, white backed plant hopper and green leaf hopper consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trials (Ref: DRR, Progress Report 2006 & 2007). The morpho-agronomic characters are given in the table.

Character	Details
Time of heading	106 days (Medium duration)
Basal leaf sheath colour	Green
Stem Length	111 cm (Medium)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain aroma	Absent
Resistance genes ¹	Unknown
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	At DRR
Resistance to white backed plant hopper (WBPH) ^{2,3}	At DRR
Resistance to green leaf hopper ^{2,3}	At Coimbatore

5. RP4621-1845(RPMRE-3) (IC569651; INGR09074), a Paddy (*Oryza sativa*) Germplasm with Multiple Resistance to Gall Midge, Brown Plant Hopper White Backed Plant Hopper and Green Leaf Hopper

The breeding line RPMRE-3 (Rice Project Multiple Resistance Entomology – RP4621-1845) was developed at DRR by making a cross between Aganni x Bhumansan and subsequently following Pedigree selection method. RPMRE-3 showed resistance to rice gall midge, brown plant hopper, white backed plant hopper and green leaf hopper consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trials (Ref: DRR, Progress Report 2006 & 2007). The morpho-agronomic characters are given in the table.

Character	Details
Time of heading	106 days (Medium duration)
Basal leaf sheath colour	Green
Stem Length	112 cm (Medium)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain Aroma	Absent
Resistance genes ¹	Unknown
Resistance to Gall Midge Biotypes ^{2,3}	Resistance to biotypes 1,2,4 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	At Coimbatore and DRR
Resistance to white backed plant hopper (WBPH) ^{2,3}	At DRR
Resistance to green leaf hopper ^{2,3}	At Coimbatore

3. RP4518-2-6(RPMRE-1) (IC569649; INGR09072), a Paddy (*Oryza sativa*) Germplasm with Resistance to Gall Midge and Brown Plant Hopper

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Character	Details
Time of heading	104 days (Medium duration)
Basal leaf colour	Green
Stem Length	57 cms (Very short)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain aroma	Absent
Resistance genes ¹	Gm4 + Gm11
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	Resistance to DRR

4. RP4621-1842(RPMRE-2) (IC569650; INGR09073), a Paddy (*Oryza sativa*) Germplasm with Multiple Resistances to Gall Midge, Brown Plant Hopper, White Backed Plant Hopper and Green Leaf Hopper

The breeding line RPMRE-2 (Rice Project Multiple Resistance Entomology – RP4621-1842) was developed at DRR by making a cross between Aganni x Bhumansan and subsequently following Pedigree selection method. RPMRE-2 showed resistance to rice gall midge, brown plant hopper, white backed plant hopper and green leaf hopper consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trials (Ref: DRR, Progress Report 2006 & 2007). The morpho-agronomic characters are given in the table.

Character	Details
Time of heading	106 days (Medium duration)
Basal leaf sheath colour	Green
Stem Length	111 cm (Medium)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain aroma	Absent
Resistance genes ¹	Unknown
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	At DRR
Resistance to white backed plant hopper (WBPH) ^{2,3}	At DRR
Resistance to green leaf hopper ^{2,3}	At Coimbatore

5. RP4621-1845(RPMRE-3) (IC569651; INGR09074), a Paddy (*Oryza sativa*) Germplasm with Multiple Resistance to Gall Midge, Brown Plant Hopper White Backed Plant Hopper and Green Leaf Hopper

The breeding line RPMRE-3 (Rice Project Multiple Resistance Entomology – RP4621-1845) was developed at DRR by making a cross between Aganni x Bhumansan and subsequently following Pedigree selection method. RPMRE-3 showed resistance to rice gall midge, brown plant hopper, white backed plant hopper and green leaf hopper consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trials (Ref: DRR, Progress Report 2006 & 2007). The morpho-agronomic characters are given in the table.

Character	Details
Time of heading	106 days (Medium duration)
Basal leaf sheath colour	Green
Stem Length	112 cm (Medium)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain Aroma	Absent
Resistance genes ¹	Unknown
Resistance to Gall Midge Biotypes ^{2,3}	Resistance to biotypes 1,2,4 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	At Coimbatore and DRR
Resistance to white backed plant hopper (WBPH) ^{2,3}	At DRR
Resistance to green leaf hopper ^{2,3}	At Coimbatore

3. RP4518-2-6(RPMRE-1) (IC569649; INGR09072), a Paddy (*Oryza sativa*) Germplasm with Resistance to Gall Midge and Brown Plant Hopper

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Character	Details
Time of heading	104 days (Medium duration)
Basal leaf colour	Green
Stem Length	57 cms (Very short)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain aroma	Absent
Resistance genes ¹	Gm4 + Gm11
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	Resistance to DRR

4. RP4621-1842(RPMRE-2) (IC569650; INGR09073), a Paddy (*Oryza sativa*) Germplasm with Multiple Resistances to Gall Midge, Brown Plant Hopper, White Backed Plant Hopper and Green Leaf Hopper

The breeding line RPMRE-2 (Rice Project Multiple Resistance Entomology – RP4621-1842) was developed at DRR by making a cross between Aganni x Bhumansan and subsequently following Pedigree selection method. RPMRE-2 showed resistance to rice gall midge, brown plant hopper, white backed plant hopper and green leaf hopper consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trials (Ref: DRR, Progress Report 2006 & 2007). The morpho-agronomic characters are given in the table.

Character	Details
Time of heading	106 days (Medium duration)
Basal leaf sheath colour	Green
Stem Length	111 cm (Medium)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain aroma	Absent
Resistance genes ¹	Unknown
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	At DRR
Resistance to white backed plant hopper (WBPH) ^{2,3}	At DRR
Resistance to green leaf hopper ^{2,3}	At Coimbatore

5. RP4621-1845(RPMRE-3) (IC569651; INGR09074), a Paddy (*Oryza sativa*) Germplasm with Multiple Resistance to Gall Midge, Brown Plant Hopper White Backed Plant Hopper and Green Leaf Hopper

The breeding line RPMRE-3 (Rice Project Multiple Resistance Entomology – RP4621-1845) was developed at DRR by making a cross between Aganni x Bhumansan and subsequently following Pedigree selection method. RPMRE-3 showed resistance to rice gall midge, brown plant hopper, white backed plant hopper and green leaf hopper consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trials (Ref: DRR, Progress Report 2006 & 2007). The morpho-agronomic characters are given in the table.

Character	Details
Time of heading	106 days (Medium duration)
Basal leaf sheath colour	Green
Stem Length	112 cm (Medium)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain Aroma	Absent
Resistance genes ¹	Unknown
Resistance to Gall Midge Biotypes ^{2,3}	Resistance to biotypes 1,2,4 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	At Coimbatore and DRR
Resistance to white backed plant hopper (WBPH) ^{2,3}	At DRR
Resistance to green leaf hopper ^{2,3}	At Coimbatore

6. RP4639-110(RPMRE-4) (IC569652; INGR09075), a Paddy (*Oryza sativa*) Germplasm with Broad Spectrum Gall Midge Resistance

The breeding line RPMRE-4 (Rice Project Multiple Resistance Entomology – RP4639-110) was developed at DRR by making a cross between TN1 1523 x Abhaya and subsequently following Pedigree selection method. RPMRE-4 showed resistance to rice Gall midge consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trails (Ref: DRR, Progress Report 2006 & 2007). The morpho-agronomic characters are given in the table.

Character	Details
Time of heading	97 days (Medium duration)
Basal leaf colour	Green
Stem Length	78 cm (Very short)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain aroma	Absent
Resistance genes ¹	<i>Gm4</i>
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4, 4M & 6

7. RP4642-669(RPMRE-5) (IC569653; INGR09076), a Paddy (*Oryza sativa*) Germplasm with Multiple Resistance to Gall Midge, Brown Plant Hopper White Backed Plant Hopper and Green Leaf Hopper

The breeding line RPMRE-5 (Rice Project Multiple Resistance Entomology – RP4642-669) was developed at DRR by making a cross between ARC 15831 x W 1263 and subsequently following pedigree selection method. RPMRE-5 showed resistance to rice gall midge, brown plant hopper, white backed plant hopper and green leaf hopper consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trials (Ref: DRR, Progress Report 2006 & 2007). The morpho agronomic characters are given in Table 1.

Table 1. Details of morpho-agronomic traits

Character	Details
Time of heading	94 days (Medium duration)
Basal leaf sheath colour	Green
Stem Length	91 cm (Short)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain Aroma	Absent
Resistance genes ¹	Unknown + <i>GM1</i> Gene
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4,6 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	Resistant at Coimbatore and DRR
Resistance to white backed plant hopper (WBPH) ^{2,3}	Resistant at DRR and Coimbatore
Resistance to green leaf hopper ^{2,3}	Resistant at Coimbatore

Insect pests cause significant yield loss in rice. Development and cultivation of resistant varieties form an important component of IPM (Bentur, 2007). However, sources of resistance against different pests being diverse and different, it becomes tedious to develop multiple pest resistant varieties. Addressing this problem we made crosses between different donor parents, screening the early generations against gall midge biotypes 1,4 and 4M and selecting few promising lines. These lines were tested under AICRIP against major insect pests of rice during 2006 and 2007. As a result we have identified five cultures that posses multiple insect pest resistance (Table 2). These improved germplasm, now registered

Table 2. New improved rice germplasm with multiple insect resistance

Designation	Cross	Resistance
RPMRE1(RP4518-2-6)	MR1523 × Abhaya	GM biotypes 1,2,4&4M + BPH
RPMRE2(RP4621-1842)	Aganni × Bhumansan	GM biotypes 1,2,4 & 4M + BPH + WBPH+GLH
RPMRE3(RP4621-1845)	Aganni × Bhumansan	GM biotypes 1,2,4 & 4M +BPH+WBPH+GLH
RPMRE4(RP4639-110)	TN1 × Abhaya	GM biotypes 1,2,4,4M & 6
RPMRE5(RP4642-669)	ARC15831 × W1263	GM biotypes 1,2,4,4M & 6

with NBPGR and seed multiplied at DRR, are available for the breeders upon request.

Broad spectrum of gall midge resistance in RPMRE1 is contributed by the combination of *Gm4* and *Gm11* genes whereas in RPMRE5 *Gm1* and *Gm8* are the likely genes. In RPMRE2 and RPMRE3 gall midge resistance from *Gm8* gene in Aganni is likely to be complemented from an unknown gene of Bhumansan. In RPMRE4, only *Gm4* from Abhaya is the known resistance gene against gall midge. Genetics of plant hopper resistance

6. RP4639-110(RPMRE-4) (IC569652; INGR09075), a Paddy (*Oryza sativa*) Germplasm with Broad Spectrum Gall Midge Resistance

The breeding line RPMRE-4 (Rice Project Multiple Resistance Entomology – RP4639-110) was developed at DRR by making a cross between TN1 1523 x Abhaya and subsequently following Pedigree selection method. RPMRE-4 showed resistance to rice Gall midge consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trails (Ref: DRR, Progress Report 2006 & 2007). The morpho-agronomic characters are given in the table.

Character	Details
Time of heading	97 days (Medium duration)
Basal leaf colour	Green
Stem Length	78 cm (Very short)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain aroma	Absent
Resistance genes ¹	<i>Gm4</i>
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4, 4M & 6

7. RP4642-669(RPMRE-5) (IC569653; INGR09076), a Paddy (*Oryza sativa*) Germplasm with Multiple Resistance to Gall Midge, Brown Plant Hopper White Backed Plant Hopper and Green Leaf Hopper

The breeding line RPMRE-5 (Rice Project Multiple Resistance Entomology – RP4642-669) was developed at DRR by making a cross between ARC 15831 x W 1263 and subsequently following pedigree selection method. RPMRE-5 showed resistance to rice gall midge, brown plant hopper, white backed plant hopper and green leaf hopper consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trials (Ref: DRR, Progress Report 2006 & 2007). The morpho agronomic characters are given in Table 1.

Table 1. Details of morpho-agronomic traits

Character	Details
Time of heading	94 days (Medium duration)
Basal leaf sheath colour	Green
Stem Length	91 cm (Short)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain Aroma	Absent
Resistance genes ¹	Unknown + <i>GM1</i> Gene
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4,6 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	Resistant at Coimbatore and DRR
Resistance to white backed plant hopper (WBPH) ^{2,3}	Resistant at DRR and Coimbatore
Resistance to green leaf hopper ^{2,3}	Resistant at Coimbatore

Insect pests cause significant yield loss in rice. Development and cultivation of resistant varieties form an important component of IPM (Bentur, 2007). However, sources of resistance against different pests being diverse and different, it becomes tedious to develop multiple pest resistant varieties. Addressing this problem we made crosses between different donor parents, screening the early generations against gall midge biotypes 1,4 and 4M and selecting few promising lines. These lines were tested under AICRIP against major insect pests of rice during 2006 and 2007. As a result we have identified five cultures that posses multiple insect pest resistance (Table 2). These improved germplasm, now registered

Table 2. New improved rice germplasm with multiple insect resistance

Designation	Cross	Resistance
RPMRE1(RP4518-2-6)	MR1523 × Abhaya	GM biotypes 1,2,4&4M + BPH
RPMRE2(RP4621-1842)	Aganni × Bhumansan	GM biotypes 1,2,4 & 4M + BPH + WBPH+GLH
RPMRE3(RP4621-1845)	Aganni × Bhumansan	GM biotypes 1,2,4 & 4M +BPH+WBPH+GLH
RPMRE4(RP4639-110)	TN1 × Abhaya	GM biotypes 1,2,4,4M & 6
RPMRE5(RP4642-669)	ARC15831 × W1263	GM biotypes 1,2,4,4M & 6

with NBPGR and seed multiplied at DRR, are available for the breeders upon request.

Broad spectrum of gall midge resistance in RPMRE1 is contributed by the combination of *Gm4* and *Gm11* genes whereas in RPMRE5 *Gm1* and *Gm8* are the likely genes. In RPMRE2 and RPMRE3 gall midge resistance from *Gm8* gene in Aganni is likely to be complemented from an unknown gene of Bhumansan. In RPMRE4, only *Gm4* from Abhaya is the known resistance gene against gall midge. Genetics of plant hopper resistance

in RPMRE1, RPMRE2 and RPMRE3 is not known.

Reference

Bentur JS (2007) Host-plant resistance to insects as a core of rice IPM. In: PK Aggarwal, JK Ladha, RK Singh, C Devakumar,

B Hardy, (eds) Science, Technology, and Trade for Peace. Manila (Philippines): International Rice Research Institute, New Delhi (India): Indian Council of Agricultural Research and New Delhi (India): National Academy of Agricultural Sciences, pp 419-435.

8. DRR 4A & 4B (IC569482 & IC569483; INGR09077), a Paddy (*Oryza sativa*) Germplasm with Cytoplasmic Male Sterility with Higher Rate of Stigma Exsertion, MS Grain Type and High Head Rice Recovery, Semi Dwarf Stature

MS Ramesha, BC Virakatamath and M Ilyas Ahmed

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(E-mail: mugalodimsr@yahoo.com)

Higher rate of stigma exsertion on A-line (>84%). Higher rate of out crossing (>62%). Purple coloured basal leaf sheath, apiculus and stigma.

Table1. Salient botanical/morphological traits of DRR-4A and 4B

Character	DRR 4A	DRR 4B
Plant height (cm)	55 cm	60 cm
Plant type	Semi-dwarf	Semi-dwarf
Number of tillers/plant	12-15	14-16
Days of 50% flowering	92-97	89-94
Panicle type	Compact	Compact
Panicle exertion (%)	82	99
Awning	Absent	Absent
Apiculus colour	Purple	Purple
Husk colour	Brown	Brown
1000 grain weight (gm)	23g	23g
Basal leaf sheath	Purple	Purple
Stigma colour	Purple	Purple
Anther colour	Straw	Yellow
Anther type	Shriveled	Plumpy
Grain type	Medium	Medium
	slender	slender
Spikelet (colour of tip of lemma)	Purple	Purple
Spikelet (density of pubescence of lemma)	Strong	Strong
Male sterility	100%	Nil
Lemma and Palea colour	Brown furrows	Brown furrows
	on straw	on straw
Sterile lemma colour	Straw	Straw
Head Rice Recovery (%)	—	66.0
LB ratio	—	2.54
Grain chalkiness	—	VOC
Alkali spreading value	—	5.0
Amylose content (%)	—	22.77
Gel consistency (mm)	—	44
Water uptake (ml)	—	190

DRR by making a cross between Aganni x Bhumansan and subsequently following Pedigree selection method. RPMRE-2 showed resistance to rice gall midge, brown plant hopper, white backed plant hopper and green leaf hopper consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trials (Ref: DRR, Progress Report 2006 & 2007). The morpho-agronomic characters are given in Table 2.

Table 2. Details of morpho-agronomic traits

Character	Details
Time of heading	106 days (Medium duration)
Basal leaf sheath colour	Green
Stem Length	111 cm (Medium)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain aroma	Absent
Resistance genes ¹	Unknown
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	At DRR
Resistance to white backed plant hopper (WBPH) ^{2,3}	At DRR
Resistance to green leaf hopper ^{2,3}	At Coimbatore

in RPMRE1, RPMRE2 and RPMRE3 is not known.

Reference

Bentur JS (2007) Host-plant resistance to insects as a core of rice IPM. In: PK Aggarwal, JK Ladha, RK Singh, C Devakumar,

B Hardy, (eds) Science, Technology, and Trade for Peace. Manila (Philippines): International Rice Research Institute, New Delhi (India): Indian Council of Agricultural Research and New Delhi (India): National Academy of Agricultural Sciences, pp 419-435.

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Table1. Salient botanical/morphological traits of DRR-4A and 4B

Character	DRR 4A	DRR 4B
Plant height (cm)	55 cm	60 cm
Plant type	Semi-dwarf	Semi-dwarf
Number of tillers/plant	12-15	14-16
Days of 50% flowering	92-97	89-94
Panicle type	Compact	Compact
Panicle exertion (%)	82	99
Awning	Absent	Absent
Apiculus colour	Purple	Purple
Husk colour	Brown	Brown
1000 grain weight (gm)	23g	23g
Basal leaf sheath	Purple	Purple
Stigma colour	Purple	Purple
Anther colour	Straw	Yellow
Anther type	Shriveled	Plumpy
Grain type	Medium	Medium
	slender	slender
Spikelet (colour of tip of lemma)	Purple	Purple
Spikelet (density of pubescence of lemma)	Strong	Strong
Male sterility	100%	Nil
Lemma and Palea colour	Brown furrows	Brown furrows
	on straw	on straw
Sterile lemma colour	Straw	Straw
Head Rice Recovery (%)	—	66.0
LB ratio	—	2.54
Grain chalkiness	—	VOC
Alkali spreading value	—	5.0
Amylose content (%)	—	22.77
Gel consistency (mm)	—	44
Water uptake (ml)	—	190

DRR by making a cross between Aganni x Bhumansan and subsequently following Pedigree selection method. RPMRE-2 showed resistance to rice gall midge, brown plant hopper, white backed plant hopper and green leaf hopper consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trials (Ref: DRR, Progress Report 2006 & 2007). The morpho-agronomic characters are given in Table 2.

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Character	Details
Time of heading	106 days (Medium duration)
Basal leaf sheath colour	Green
Stem Length	111 cm (Medium)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain aroma	Absent
Resistance genes ¹	Unknown
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	At DRR
Resistance to white backed plant hopper (WBPH) ^{2,3}	At DRR
Resistance to green leaf hopper ^{2,3}	At Coimbatore

5. RP4621-1845(RPMRE-3) (IC569651; INGR09074), a Paddy (*Oryza sativa*) Germplasm with Multiple Resistance to Gall Midge, Brown Plant Hopper White Backed Plant Hopper and Green Leaf Hopper

JS Bentur and GSV Prasad

Directorate of Rice Research, Rajendranagar, Hyderabad-500 030, Andhra Pradesh

(E-mail: gsvprasad@drircar.org)

The breeding line RPMRE-3 (Rice Project Multiple Resistance Entomology – RP4621-1845) was developed at DRR by making a cross between Aganni x Bhumansan and subsequently following Pedigree selection method. RPMRE-3 showed resistance to rice gall midge, brown plant hopper, white backed plant hopper and green leaf hopper consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trials (Ref: DRR, Progress Report 2006 & 2007). The morpho agronomic characters are given in the Table.

Character	Details
Time of heading	106 days (Medium duration)
Basal leaf sheath colour	Green
Stem Length	112 cm (Medium)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain Aroma	Absent
Resistance genes ¹	Unknown
Resistance to Gall Midge Biotypes ^{2,3}	Resistance to bio types 1,2,4 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	At Coimbatore and DRR
Resistance to white backed plant hopper (WBPH) ^{2,3}	At DRR
Resistance to green leaf hopper ^{2,3}	At Coimbatore

6. RP4639-110(RPMRE-4) (IC569652; INGR09075), a Paddy (*Oryza sativa*) Germplasm with Broad Spectrum Gall Midge Resistance

JS Bentur and GSV Prasad

Directorate of Rice Research, Rajendranagar, Hyderabad-500 030, Andhra Pradesh

(E-mail: gsvprasad@drircar.org)

The breeding line RPMRE-4 (Rice Project Multiple Resistance Entomology – RP4639-110) was developed at DRR by making a cross between TN1 1523 x Abhaya and subsequently following Pedigree selection method. RPMRE-4 showed resistance to rice Gall midge consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trails (Ref: DRR, Progress Report 2006 & 2007). The morpho agronomic characters are given in the table.

Character	Details
Time of heading	97 days (Medium duration)
Basal leaf colour	Green
Stem Length	78 cm (Very short)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain aroma	Absent
Resistance genes ¹	Gm4
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4, 4M & 6

5. RP4621-1845(RPMRE-3) (IC569651; INGR09074), a Paddy (*Oryza sativa*) Germplasm with Multiple Resistance to Gall Midge, Brown Plant Hopper White Backed Plant Hopper and Green Leaf Hopper

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Character	Details
Time of heading	106 days (Medium duration)
Basal leaf sheath colour	Green
Stem Length	112 cm (Medium)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain Aroma	Absent
Resistance genes ¹	Unknown
Resistance to Gall Midge Biotypes ^{2,3}	Resistance to bio types 1,2,4 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	At Coimbatore and DRR
Resistance to white backed plant hopper (WBPH) ^{2,3}	At DRR
Resistance to green leaf hopper ^{2,3}	At Coimbatore

6. RP4639-110(RPMRE-4) (IC569652; INGR09075), a Paddy (*Oryza sativa*) Germplasm with Broad Spectrum Gall Midge Resistance

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Character	Details
Time of heading	97 days (Medium duration)
Basal leaf colour	Green
Stem Length	78 cm (Very short)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain aroma	Absent
Resistance genes ¹	Gm4
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4, 4M & 6

7. RP4642-669(RPMRE-5) (IC569653; INGR09076), a Paddy (*Oryza sativa*) Germplasm with Multiple Resistance to Gall Midge, Brown Plant Hopper White Backed Plant Hopper and Green Leaf Hopper

JS Bentur and GSV Prasad

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(E-mail: gsvprasad@drircar.org)

The breeding line RPMRE-5 (Rice Project Multiple Resistance Entomology – RP4642-669) was developed at DRR by making a cross between ARC 15831 x W 1263 and subsequently following pedigree selection method. RPMRE-5 showed resistance to rice gall midge, brown plant hopper, white backed plant hopper and green leaf hopper consistently for the last 2 years in All India Coordinated Rice Improvement Programme (AICRP) trials (Ref: DRR, Progress Report 2006 & 2007). The morpho-agronomic characters are given in Table 1.

Table 1. Details of morpho-agronomic traits

Character	Details
Time of heading	94 days (Medium duration)
Basal leaf sheath colour	Green
Stem Length	91 cm (Short)
Decorticated grain type	Short bold
Decorticated grain colour	Light brown
Decorticated grain Aroma	Absent
Resistance genes ¹	Unknown + <i>Gm1</i> Gene
Resistance to gall midge biotypes ^{2,3}	Resistance to biotypes 1,2,4,6 & 4M
Resistance to brown plant hopper (BPH) ^{2,3}	Resistant at Coimbatore and DRR
Resistance to white backed plant hopper (WBPH) ^{2,3}	Resistant at DRR and Coimbatore
Resistance to green leaf hopper ^{2,3}	Resistant at Coimbatore

Insect pests cause significant yield loss in rice. Development and cultivation of resistant varieties form an important component of IPM (Bentur, 2007). However, sources of resistance against different pests being diverse and different, it becomes tedious to develop multiple pest resistant varieties. Addressing this problem we made crosses between different donor parents, screening the early generations against gall midge biotypes 1,4 and 4M and selecting few promising lines. These lines were tested under AICRIP against major insect pests of rice

during 2006 and 2007. As a result we have identified five cultures that possess multiple insect pest resistance (Table 2). These improved germplasm, now registered with NBPGR and seed multiplied at DRR, are available for the breeders upon request.

Table 2. New improved rice germplasm with multiple insect resistance

Designation	Cross	Resistance
RPMRE1(RP4518-2-6)	MR1523×Abhaya	GM biotypes 1,2,4&4M + BPH
RPMRE2(RP4621-1842)	Aganni×Bhumansan	GM biotypes 1,2,4 & 4M + BPH + WBPH+GLH
RPMRE3(RP4621-1845)	Aganni×Bhumansan	GM biotypes 1,2,4 & 4M +BPH+ WBPH+GLH
RPMRE4(RP4639-110)	TN1×Abhaya	GM biotypes 1,2,4, 4M & 6
RPMRE5(RP4642-669)	ARC15831×W1263	GM biotypes 1,2,4, 4M & 6

Broad spectrum of gall midge resistance in RPMRE1 is contributed by the combination of *Gm4* and *Gm11* genes whereas in RPMRE5 *Gm1* and *Gm8* are the likely genes. In RPMRE2 and RPMRE3 gall midge resistance from *Gm8* gene in Aganni is likely to be complemented from an unknown gene of Bhumansan. In RPMRE4, only *Gm4* from Abhaya is the known resistance gene against gall midge. Genetics of plant hopper resistance in RPMRE1, RPMRE2 and RPMRE3 is not known.

Reference

- Bentur JS (2007) Host-plant resistance to insects as a core of rice IPM. In: PK Aggarwal, JK Ladha, RK Singh, C Devakumar, B Hardy, (eds) Science, Technology, and Trade for Peace. Manila (Philippines): International Rice Research Institute, New Delhi (India): Indian Council of Agricultural Research and New Delhi (India): National Academy of Agricultural Sciences, pp 419-435.

8. DRR 4A & 4B (IC569482 & IC569483; INGR09077), a Paddy (*Oryza sativa*) Germplasm with Cytoplasmic Male Sterility with Higher Rate of Stigma Exsertion, MS Grain Type and High Head Rice Recovery, Semi Dwarf Stature

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Higher rate of stigma exsertion on A-line (>84%). Higher rate of out crossing (>62%). Purple coloured basal leaf sheath, apiculus and stigma.

Table1. Salient botanical/morphological traits of DRR-4A and 4B

Character	DRR 4A	DRR 4B
Plant height (cm)	55 cm	60 cm
Plant type	Semi-dwarf	Semi-dwarf
Number of tillers/plant	12-15	14-16
Days of 50% flowering	92-97	89-94
Panicle type	Compact	Compact
Panicle exertion (%)	82	99
Awning	Absent	Absent
Apiculus colour	Purple	Purple
Husk colour	Brown	Brown
1000 grain weight (gm)	23g	23g
Basal leaf sheath	Purple	Purple
Stigma colour	Purple	Purple
Anther colour	Straw	Yellow
Anther type	Shriveled	Plumpy
Grain type	Medium slender	Medium slender
Spikelet (colour of tip of lemma)	Purple	Purple
Spikelet: density of pubescence of lemma	Strong	
Male sterility	100%	Nil
Lemma and Palea colour on straw	Brown furrows on straw	Brown furrows
Sterile lemma colour	Straw	Straw
Head Rice Recovery (%)	—	66.0
LB ratio	—	2.54
Grain chalkiness	—	VOC
Alkali spreading value	—	5.0
Amylose content (%)	—	22.77
Gel consistency (mm)	—	44
Water uptake (ml)	—	190
Decorticated grain aroma	—	Absent

9. DRR 5A & 5B (IC569484 & IC569485; INGR09078), a Paddy (*Oryza sativa*) Germplasm with Cytoplasmic Male Sterility, Medium Maturity, High Rate of Stigma Exsertion in A & B lines, Medium Slender Grain, High Head Rice Recovery, Higher Rate of out Crossing in A line and Good Tillering Capacity

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Higher rate of stigma exsertion on A and B lines. Higher rate of out crossing and semi dwarf stature. Medium maturity group and good tillering capacity.

Table1. Salient botanical/morphological traits of DRR-5A and 5B

Character	DRR 5A	DRR 5B
Plant height (cm)	60 cm	63 cm
Plant type	Semi-dwarf	Semi-dwarf
Number of tillers/plant	12-15	13-16
Days of 50% flowering	101-104	98-102
Panicle type	Compact	Compact
Panicle exertion (%)	80	98
Awning	Absent	Absent
Apiculus colour	Yellowish	Yellowish
Husk colour	Brown	Brown
1000 grain weight (gm)	24g	24g
Basal leaf sheath	Green	Green
Stigma colour	Light green	Light green
Anther colour	White/Straw	Yellow
Anther type	Shriveled	Plumpy
Grain type	Medium slender	Medium slender
Spikelet (colour of tip of lemma)	Straw	Straw
Spikelet: density of pubescence of lemma	Strong	Strong
Male sterility	100%	Nil
Lemma and Palea colour on straw	Brown furrows on straw	Brown furrows on straw
Sterile lemma colour	Straw	Straw
Head Rice Recovery (%)	—	62.90
LB ratio	—	2.57
Grain chalkiness	—	Absent
Alkali spreading value	—	5.0
Amylose content (%)	—	21.26
Gel consistency (mm)	—	66
Water uptake (ml)	—	285
Decorticated grain aroma	—	Absent

8. DRR 4A & 4B (IC569482 & IC569483; INGR09077), a Paddy (*Oryza sativa*) Germplasm with Cytoplasmic Male Sterility with Higher Rate of Stigma Exsertion, MS Grain Type and High Head Rice Recovery, Semi Dwarf Stature

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Panicle type	Compact	Compact
Panicle exertion (%)	82	99
Awning	Absent	Absent
Apiculus colour	Purple	Purple
Husk colour	Brown	Brown
1000 grain weight (gm)	23g	23g
Basal leaf sheath	Purple	Purple
Stigma colour	Purple	Purple
Anther colour	Straw	Yellow
Anther type	Shriveled	Plumpy
Grain type	Medium slender	Medium slender
Spikelet (colour of tip of lemma)	Purple	Purple
Spikelet: density of pubescence of lemma	Strong	
Male sterility	100%	Nil
Lemma and Palea colour on straw	Brown furrows on straw	Brown furrows
Sterile lemma colour	Straw	Straw
Head Rice Recovery (%)	—	66.0
LB ratio	—	2.54
Grain chalkiness	—	VOC
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Plant type	Semi-dwarf	Semi-dwarf
Number of tillers/plant	12-15	13-16
Days of 50% flowering	101-104	98-102
Panicle type	Compact	Compact
Panicle exertion (%)	80	98
Awning	Absent	Absent
Apiculus colour	Yellowish	Yellowish
Husk colour	Brown	Brown
1000 grain weight (gm)	24g	24g
Basal leaf sheath	Green	Green
Stigma colour	Light green	Light green
Anther colour	White/Straw	Yellow
Anther type	Shriveled	Plumpy
Grain type	Medium slender	Medium slender
Spikelet (colour of tip of lemma)	Straw	Straw
Spikelet: density of pubescence of lemma	Strong	Strong
Male sterility	100%	Nil
Lemma and Palea colour on straw	Brown furrows on straw	Brown furrows on straw
Sterile lemma colour	Straw	Straw
Head Rice Recovery (%)	—	62.90
LB ratio	—	2.57
Grain chalkiness	—	Absent
Alkali spreading value	—	5.0
Amylose content (%)	—	21.26
Gel consistency (mm)	—	66
Water uptake (ml)	—	285
Decorticated grain aroma	—	Absent

10. DRR 9A & 9B (IC569486 & IC569487; INGR09079), a Paddy (*Oryza sativa*) Germplasm with Cytoplasmic Male Sterile line Medium Maturity Group and Higher Rate of Stigma Exsertion, Higher Rate of out Crossing in A line Plants with Semi Dwarf Stature, High Head Rice Recovery and Intermediate Amylose Content

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Higher rate of stigma exsertion on A and B lines. Higher rate of out crossing and semi dwarf stature. Medium maturity group and good tillering capacity.

Table 1. Salient botanical/morphological traits of DRR-9A and 9B

Character	DRR 9A	DRR 9B
Plant height (cm)	65 cm	68 cm
Plant type	Semi-dwarf	Semi-dwarf
Number of tillers/plant	14-16	15-18
Days of 50% flowering	101-106	99-103
Panicle type	Compact	Compact
Panicle exertion (%)	83	98
Awning	Absent	Absent
Apiculus colour	Yellowish	Yellowish
Husk colour	Brownish	Brownish
1000 grain weight (gm)	23g	23g
Basal leaf sheath	Green	Green
Stigma colour	Light green	Light green
Anther colour	Straw	Yellow
Anther type	Shriveled	Plumpy
Grain type	Short bold	Short bold
Spikelet (colour of tip of lemma)	Yellowish	Yellowish
Spikelet: density of pubescence of lemma	Strong	Strong
Male sterility	100%	Nil
Lemma and Palea colour	Brownish	Brownish
Sterile lemma colour	Straw	Straw
Head Rice Recovery (%)	—	61.5
LB ratio	—	2.42
Grain chalkiness	—	VOC
Alkali spreading value	—	4.0
Amylose content (%)	—	23.13
Gel consistency (mm)	—	65
Water uptake (ml)	—	310
Decorticated grain aroma	—	Absent

11. DRR 10 A & 10B (IC569488 & IC569489; INGR09080), a Paddy (*Oryza sativa*) Germplasm with Cytoplasmic Male Sterile line with Higher Rate of Stigma Exsertion, Higher out Crossing Ability of A line, Medium Maturity Group with Semi Dwarf Plant Type, Medium Slender Grain Type with Good Tillering Ability

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CMS line with stable complete male sterility. Higher rate of stigma exsertion and out crossing. Medium maturity group.

Table1. Salient botanical/morphological traits of DRR-10A and 10B

Character	DRR 10A	DRR 10B
Plant height (cm)		58 cm 61 cm
Plant type	Semi-dwarf	Semi-dwarf
Number of tillers/plant	12-16	13-18
Days of 50% flowering	104	100-102
Panicle type	Compact	Compact
Panicle exertion (%)	84	98
Awning	Absent	Absent
Apiculus colour	Yellow	Yellow
Husk colour	Brownish	Brownish
1000 grain weight (gm)	24g	24g
Basal leaf sheath	Green	Green
Stigma colour	Light green	Light green
Anther colour	Straw/white	Yellow
Anther type	Shriveled	Plumpy
Grain type	Medium selender	Medium selender
Spikelet (colour of tip of lemma)	Yellow	Yellow
Spikelet: density of pubescence of lemma	Strong	Strong
Male sterility	100%	Nil
Lemma and Palea colour	Dark Brown	Dark Brown
Sterile lemma colour	Straw	Straw
Head Rice Recovery (%)	—	62.3
LB ratio	—	2.51
Grain chalkiness	—	VOC
Alkali spreading value	—	4.0
Amylose content (%)	—	20.99
Gel consistency (mm)	—	69
Water uptake (ml)	—	295
Decorticated grain aroma	—	Absent

12. RPHR-2 (IC569490; INGR09081), a Paddy (*Oryza sativa*) Germplasm, Japonica Plant Type with Long and Heavy Panicles and Dark Green Thick Leaves, Strong and Broad Spectrum of Fertility Restoration with Medium Slender Grain Type and High Head Rice Recovery. High Pollen Load and 36-45 days of Grain Filling Period

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13. RPHR-12 (IC569491; INGR09082), a Paddy (*Oryza sativa*) Germplasm with Strong and Broad Spectrum of Restoration, Tropical Japonica Plant Type with Sturdy Clum, Dark Green and Thick Leaves with Late Senescence, High Pollen Load, Long and Heavy Panicles and Prolonged Grain Filling Period

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Table1. Salient botanical/morphological traits of restorer line (RPHR-2)

Character	Description
Plant height (cm)	90-95 cm
Plant type	Japonica type
Number of tillers/plant	15-18
Days of 50% flowering	108-112
Panicle type	Compact and very long
Panicle exertion (%)	Just exerted (100%)
Awning	Occasionally present
Apiculus colour	Yellowish
Husk colour	Golden
1000 grain weight (gm)	22
Basal leaf sheath	Green
Leaf: Ligule shape	Split
Leaf: Ligule colour	White
Leaf: Anthocyanin coloration of Auricles	Colourless
Stigma colour	White
Anther colour	Yellow
Anther type	Plumpy
Grain type	Medium slender
Spikelet (colour of tip of lemma)	Yellowish
Spikelet: density of pubescence of lemma	Medium
Sterile lemma colour	Straw
Lemma and Palea colour	Golden
Leaf senescence	Late
Flag leaf: attitude of blade	Erect
Leaf: width of blade	Broad
Decorticated grain aroma	Absent
Culm: attitude	Erect
Head Rice Recovery (%)	65.7
LB ratio	2.56
Grain chalkiness	VOC
Alkali spreading value	5.0
Amylose content (%)	24.77
Gel consistency (mm)	70
Water uptake (ml)	275

Table 1. Salient botanical/morphological traits of restorer line (RPHR-12)

Character	Description
Plant height (cm)	90-95 cm
Plant stature	Semi tall (Japonica)
Number of tillers/plant	10-12
Days of 50% flowering	106-110
Panicle type	Compact and long
Panicle exertion (%)	Just exerted (99%)
Awning	Nil
Leaf: width of blade	Broad
Husk colour	Golden brown
1000 grain weight (gm)	23
Basal leaf sheath colour	Green
Ligule shape	Acute
Ligule colour	Light purple
Leaf: Anthocyanin coloration of Auricles	Colourless
Stigma colour	White
Anther colour	Yellow
Anther type	Plumpy
Grain type	Medium bold
Spikelet (colour of tip of lemma)	Purple
Spikelet: density of pubescence of lemma	Strong
Sterile lemma colour	Straw
Lemma and Palea colour	Golden brown
Flag leaf: attitude of blade	Erect
Leaf senescence	Late
Decorticated grain aroma	Absent
Culm: attitude	Erect
Stem: Anthocyanine colouration of node	Absent

12. RPHR-2 (IC569490; INGR09081), a Paddy (*Oryza sativa*) Germplasm, Japonica Plant Type with Long and Heavy Panicles and Dark Green Thick Leaves, Strong and Broad Spectrum of Fertility Restoration with Medium Slender Grain Type and High Head Rice Recovery. High Pollen Load and 36-45 days of Grain Filling Period

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13. RPHR-12 (IC569491; INGR09082), a Paddy (*Oryza sativa*) Germplasm with Strong and Broad Spectrum of Restoration, Tropical Japonica Plant Type with Sturdy Clum, Dark Green and Thick Leaves with Late Senescence, High Pollen Load, Long and Heavy Panicles and Prolonged Grain Filling Period

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Table1. Salient botanical/morphological traits of restorer line (RPHR-2)

Character	Description
Plant height (cm)	90-95 cm
Plant type	Japonica type
Number of tillers/plant	15-18
Days of 50% flowering	108-112
Panicle type	Compact and very long
Panicle exertion (%)	Just exerted (100%)
Awning	Occasionally present
Apiculus colour	Yellowish
Husk colour	Golden
1000 grain weight (gm)	22
Basal leaf sheath	Green
Leaf: Ligule shape	Split
Leaf: Ligule colour	White
Leaf: Anthocyanin coloration of Auricles	Colourless
Stigma colour	White
Anther colour	Yellow
Anther type	Plumpy
Grain type	Medium slender
Spikelet (colour of tip of lemma)	Yellowish
Spikelet: density of pubescence of lemma	Medium
Sterile lemma colour	Straw
Lemma and Palea colour	Golden
Leaf senescence	Late
Flag leaf: attitude of blade	Erect
Leaf: width of blade	Broad
Decorticated grain aroma	Absent
Culm: attitude	Erect
Head Rice Recovery (%)	65.7
LB ratio	2.56
Grain chalkiness	VOC
Alkali spreading value	5.0
Amylose content (%)	24.77
Gel consistency (mm)	70
Water uptake (ml)	275

Table 1. Salient botanical/morphological traits of restorer line (RPHR-12)

Character	Description
Plant height (cm)	90-95 cm
Plant stature	Semi tall (Japonica)
Number of tillers/plant	10-12
Days of 50% flowering	106-110
Panicle type	Compact and long
Panicle exertion (%)	Just exerted (99%)
Awning	Nil
Leaf: width of blade	Broad
Husk colour	Golden brown
1000 grain weight (gm)	23
Basal leaf sheath colour	Green
Ligule shape	Acute
Ligule colour	Light purple
Leaf: Anthocyanin coloration of Auricles	Colourless
Stigma colour	White
Anther colour	Yellow
Anther type	Plumpy
Grain type	Medium bold
Spikelet (colour of tip of lemma)	Purple
Spikelet: density of pubescence of lemma	Strong
Sterile lemma colour	Straw
Lemma and Palea colour	Golden brown
Flag leaf: attitude of blade	Erect
Leaf senescence	Late
Decorticated grain aroma	Absent
Culm: attitude	Erect
Stem: Anthocyanine colouration of node	Absent

14. RPHR-517 (IC569492; INGR09083), a Paddy (*Oryza sativa*) Germplasm with Broad Spectrum of Fertility Restoration and with Good Plant Type, High Rate of Pollen Production with Medium Slender Grain Type, Tall Stature with High Heterotic Potential and Late Maturity Duration

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Table 1. Salient botanical/morphological traits of restorer line (RPHR-517)

Character	Description
Plant height (cm)	105-110 cm
Plant type	Tall
Number of tillers/plant	12-15
Flowering duration (days)	116-118
Panicle type	Compact and long
Panicle exertion (%)	99%
Awning Absent	
Apiculus colour	Yellow
Husk colour	Straw
1000 grain weight (gm)	19
Basal leaf sheath colour	Green
Leaf: Ligule shape	Split
Leaf: Ligule colour	White
Leaf: Anthocyanin coloration of Auricles	Colourless
Stigma colour	White
Anther colour	Yellow
Anther type	Plumpy
Grain type	Medium slender
Spikelet (colour of tip of lemma)	Yellow
Spikelet: density of pubescence of lemma	Medium
Sterile lemma colour	Straw
Lemma and Palea colour	Straw
Flag leaf: attitude of blade	Erect
Leaf senescence	Late
Decorticated grain aroma	Absent
Culm: attitude	Erect
Leaf: width of blade	Medium

15. RPHR-619 (IC569493; INGR09084), a Paddy (*Oryza sativa*) Germplasm with Strong and Broad Spectrum of Fertility Restoration. Tall Stature, Intermediate Plant Type with Synchronous Tillering, High Pollen Load and Slow Leaf Senescence with Medium Maturity

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Table1. Salient botanical/morphological traits of restorer line (RPHR-619)

Character	Description
Plant height (cm)	102-105 cm
Plant stature	Tall (Intermediate type)
Number of tillers/plant	15-18
Flowering duration (days)	105-108
Panicle type	Compact
Panicle exertion (%)	Just exerted (100%)
Awning	Absent
Apiculus colour	Yellowish
Husk colour	Golden brown
1000 grain weight (gm)	22
Basal leaf sheath colour	Green
Leaf: Ligule shape	Split
Leaf: Ligule colour	White
Leaf: Anthocyanin coloration of Auricles	Colourless
Stigma colour	White
Anther colour	Yellow
Anther type	Plumpy
Grain type	Medium bold
Spikelet (colour of tip of lemma)	Yellowish
Spikelet: density of pubescence of lemma	Medium
Sterile lemma colour	Straw
Flag leaf: attitude of blade	Semi-Erect
Leaf senescence	Late
Decorticated grain aroma	Absent
Culm: attitude	Erect
Leaf: width of blade	Medium

14. RPHR-517 (IC569492; INGR09083), a Paddy (*Oryza sativa*) Germplasm with Broad Spectrum of Fertility Restoration and with Good Plant Type, High Rate of Pollen Production with Medium Slender Grain Type, Tall Stature with High Heterotic Potential and Late Maturity Duration

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Table 1. Salient botanical/morphological traits of restorer line (RPHR-517)

Character	Description
Plant height (cm)	105-110 cm
Plant type	Tall
Number of tillers/plant	12-15
Flowering duration (days)	116-118
Panicle type	Compact and long
Panicle exertion (%)	99%
Awning Absent	
Apiculus colour	Yellow
Husk colour	Straw
1000 grain weight (gm)	19
Basal leaf sheath colour	Green
Leaf: Ligule shape	Split
Leaf: Ligule colour	White
Leaf: Anthocyanin coloration of Auricles	Colourless
Stigma colour	White
Anther colour	Yellow
Anther type	Plumpy
Grain type	Medium slender
Spikelet (colour of tip of lemma)	Yellow
Spikelet: density of pubescence of lemma	Medium
Sterile lemma colour	Straw
Lemma and Palea colour	Straw
Flag leaf: attitude of blade	Erect
Leaf senescence	Late
Decorticated grain aroma	Absent
Culm: attitude	Erect
Leaf: width of blade	Medium

15. RPHR-619 (IC569493; INGR09084), a Paddy (*Oryza sativa*) Germplasm with Strong and Broad Spectrum of Fertility Restoration. Tall Stature, Intermediate Plant Type with Synchronous Tillering, High Pollen Load and Slow Leaf Senescence with Medium Maturity

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Table1. Salient botanical/morphological traits of restorer line (RPHR-619)

Character	Description
Plant height (cm)	102-105 cm
Plant stature	Tall (Intermediate type)
Number of tillers/plant	15-18
Flowering duration (days)	105-108
Panicle type	Compact
Panicle exertion (%)	Just exerted (100%)
Awning	Absent
Apiculus colour	Yellowish
Husk colour	Golden brown
1000 grain weight (gm)	22
Basal leaf sheath colour	Green
Leaf: Ligule shape	Split
Leaf: Ligule colour	White
Leaf: Anthocyanin coloration of Auricles	Colourless
Stigma colour	White
Anther colour	Yellow
Anther type	Plumpy
Grain type	Medium bold
Spikelet (colour of tip of lemma)	Yellowish
Spikelet: density of pubescence of lemma	Medium
Sterile lemma colour	Straw
Flag leaf: attitude of blade	Semi-Erect
Leaf senescence	Late
Decorticated grain aroma	Absent
Culm: attitude	Erect
Leaf: width of blade	Medium

16. RPHR-1005 (IC569494; INGR09085), a Paddy (*Oryza sativa*) Germplasm with Broad Spectrum of Fertility Restoration and with Good Plant Type, High Rate of Pollen Production and Good Combining Ability. BPT5204 Derivative with Short Slender Grain, Lower Panicle Position and Prominent Top Leaves

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Table1. Salient botanical/morphological traits of restorer line (RPHR-1005)

Character	Description
Plant height (cm)	86-95 cm
Plant type	Semi-dwarf
Number of tillers/plant	15-18
Days of 50% flowering	104-108
Panicle type	Compact and long
Panicle exertion (%)	Just exerted (99%)
Awning	No
Spikelet (colour of tip of lemma)	Yellowish
Husk colour	Straw
1000 grain weight (gm)	17
Basal leaf sheath	Green
Leaf: Ligule shape	Split
Leaf: Ligule colour	White
Leaf: Anthocyanin coloration of Auricles	Colourless
Stigma colour	White
Anther colour	Yellow
Anther type	Plumpy
Grain type	Medium slender
Sterile lemma colour	Straw
Spikelet: density of pubescence of lemma	Medium
Flag leaf: attitude of blade	Erect
Leaf senescence	Late
Culm: attitude	Erect
Decorticated grain aroma	Absent
Stem: anthocyanin colouration of node	Absent
Head Rice Recovery (%)	54.2
LB ratio	2.64
Grain chalkiness	VOC
Alkali spreading value	4.0
Amylose content (%)	24.66
Gel consistency (mm)	68
Water uptake (ml)	305

17. RPHR-1096 (IC569495; INGR09086), a Paddy (*Oryza sativa*) Germplasm with Broad Spectrum of Fertility Restoration and Easily Observable Morphological Marker Purple Basal Leaf Sheath and Purple Apiculus, High Rate of Pollen Production, Slow Leaf Senescence and High Head Rice Recovery, Tall Stature and Intermediate Plant Type with Late Maturity

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Table 1. Salient botanical/morphological traits of restorer line (RPHR-2)

Character	Description
Plant height (cm)	100-105 cm
Plant stature	Tall
Number of tillers/plant	15-20
Days of 50% flowering	112-115
Panicle type	Compact and very long
Panicle exertion (%)	Well exerted
Awning	Absent
Apiculus colour	Purple
Husk colour	Straw
1000 grain weight (gm)	24
Basal leaf sheath colour	Purple
Leaf: Ligule shape	Split
Leaf: Ligule colour	Purple
Leaf: Anthocyanin coloration of Auricles	Purple
Stigma colour	Purple
Anther colour	Yellow
Anther type	Plumpy
Grain type	Short bold
Spikelet (colour of tip of lemma)	Purple
Spikelet: density of pubescence of lemma	Medium
Sterile lemma colour	Straw
Leaf senescence	Late
Flag leaf: attitude of blade	Erect
Leaf: width of blade	Broad
Decorticated grain aroma	Absent
Culm: attitude	Erect
Stem: anthocyanin colouration of nodes	Absent
Head Rice Recovery (%)	63.5
LB ratio	2.14
Grain chalkiness	VOC
Alkali spreading value	4.0
Amylose content (%)	20.48
Gel consistency (mm)	52
Water uptake (ml)	260

16. RPHR-1005 (IC569494; INGR09085), a Paddy (*Oryza sativa*) Germplasm with Broad Spectrum of Fertility Restoration and with Good Plant Type, High Rate of Pollen Production and Good Combining Ability. BPT5204 Derivative with Short Slender Grain, Lower Panicle Position and Prominent Top Leaves

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Table 1. Salient botanical/morphological traits of restorer line (RPHR-1005)

Character	Description
Plant height (cm)	86-95 cm
Plant type	Semi-dwarf
Number of tillers/plant	15-18
Days of 50% flowering	104-108
Panicle type	Compact and long
Panicle exertion (%)	Just exerted (99%)
Awning	No
Spikelet (colour of tip of lemma)	Yellowish
Husk colour	Straw
1000 grain weight (gm)	17
Basal leaf sheath	Green
Leaf: Ligule shape	Split
Leaf: Ligule colour	White
Leaf: Anthocyanin coloration of Auricles	Colourless
Stigma colour	White
Anther colour	Yellow
Anther type	Plumpy
Grain type	Medium slender
Sterile lemma colour	Straw
Spikelet: density of pubescence of lemma	Medium
Flag leaf: attitude of blade	Erect
Leaf senescence	Late
Culm: attitude	Erect
Decorticated grain aroma	Absent
Stem: anthocyanin colouration of node	Absent
Head Rice Recovery (%)	54.2
LB ratio	2.64
Grain chalkiness	VOC
Alkali spreading value	4.0
Amylose content (%)	24.66
Gel consistency (mm)	68
Water uptake (ml)	305

17. RPHR-1096 (IC569495; INGR09086), a Paddy (*Oryza sativa*) Germplasm with Broad Spectrum of Fertility Restoration and Easily Observable Morphological Marker Purple Basal Leaf Sheath and Purple Apiculus, High Rate of Pollen Production, Slow Leaf Senescence and High Head Rice Recovery, Tall Stature and Intermediate Plant Type with Late Maturity

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Table 1. Salient botanical/morphological traits of restorer line (RPHR-2)

Character	Description
Plant height (cm)	100-105 cm
Plant stature	Tall
Number of tillers/plant	15-20
Days of 50% flowering	112-115
Panicle type	Compact and very long
Panicle exertion (%)	Well exerted
Awning	Absent
Apiculus colour	Purple
Husk colour	Straw
1000 grain weight (gm)	24
Basal leaf sheath colour	Purple
Leaf: Ligule shape	Split
Leaf: Ligule colour	Purple
Leaf: Anthocyanin coloration of Auricles	Purple
Stigma colour	Purple
Anther colour	Yellow
Anther type	Plumpy
Grain type	Short bold
Spikelet (colour of tip of lemma)	Purple
Spikelet: density of pubescence of lemma	Medium
Sterile lemma colour	Straw
Leaf senescence	Late
Flag leaf: attitude of blade	Erect
Leaf: width of blade	Broad
Decorticated grain aroma	Absent
Culm: attitude	Erect
Stem: anthocyanin colouration of nodes	Absent
Head Rice Recovery (%)	63.5
LB ratio	2.14
Grain chalkiness	VOC
Alkali spreading value	4.0
Amylose content (%)	20.48
Gel consistency (mm)	52
Water uptake (ml)	260

18. KRL 3-4 (IC408331; INGR09087), a Wheat (*Triticum aestivum*) Germplasm with Salt Tolerance, Water Logging Tolerance, Red Grain, Low Sodium Uptake under Salinity

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KRL 3-4 is a salt and water-logging tolerant genotype developed at CSSRI, Karnal, through recombination breeding involving the parentage HD 1982/Kharchia 65. The genotype is unique with respect to red grain colour and very high level of tolerance to salinity, sodicity and water-logging stresses.

Morpho-agronomic Characteristics

The genotype has light green foliage with erect growth habit. The plants are very long with non waxy blade and ear. Ears are parallel and white in colour with spreading awns. The grains are red and elliptical with medium size. KRL 3-4 is being used as a tolerant check for All India Salinity/Alkalinity Tolerance screening Nursery and has out yielded Kharchia 65 (this has the reputation of the most salt tolerant genotype) from 2004-05 to 2008-09 crop seasons in different salt affected locations (Karnal, Hisar, Bawal, Faizabad, Kanpur, Lucknow, Bhilwara and Bharuch).

Associated Characters and Cultivated Practices

The genotype KRL 3-4 is much improved from Kharchia 65 (red grains) on account of high yielding ability along with high level of salinity, sodicity and water logging

tolerance. The genotype is characterized by low sodium uptake under salinity. The sodium uptake of KRL 3-4 ($300 \pm 12 \mu\text{mol/g}$) has been found to be lower than Kharchia 65 ($525 \pm 55 \mu\text{mol/g}$) in saline soils (Kulshreshtha, 2008). The salt tolerance of KRL 3-4 along with low sodium uptake makes it highly useful for incorporating salt tolerance trait. In addition to having better regulation over the uptake of Na and K in sodicity and Na and Cl in salinity, KRL 3-4 possesses higher tissue tolerance for Al, B and Fe. These regulatory mechanisms are maintained even when sodic or saline stress situations are accompanied by waterlogging stress.

KRL 3-4 gives its best expression in sodic/reclaimed sodic soils. However under high sodic conditions (pH more than 9.3), the genotype can provide much better yield than the prevalent variety PBW 343. Standard agronomical cultural practices are required to raise the crop.

Reference

Kulshreshtha N (2008) Breeding wheat varieties for salt tolerance in India: Present status and future prospects. In: NPS Yaduvanshi, RK Yadav, DS Bundela, N Kulshreshtha and G Singh (eds) Chemical Changes and Nutrient Transformation in Sodic/poor Quality Water Irrigated Soils, pp 269-274.

19. NRCSFR-06-1 (IC569675; INGR09088), a Sorghum (*Sorghum bicolor*) Germplasm with Source of Shoot Fly Tolerance with Multiple Resistances to Leaf Diseases and also Agronomic Superiority and Yield

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NRCSFR 06-1 (SPV 1518 X IS 2122) is the outcome of breeding for shoot fly resistance. The line possesses shoot fly resistance compared to resistant check, IS 2312

as tested across location during 2006, 2007 and 2008 under AICSIP. It was found to have better plant type with tan back ground compared to the resistant sources.

18. KRL 3-4 (IC408331; INGR09087), a Wheat (*Triticum aestivum*) Germplasm with Salt Tolerance, Water Logging Tolerance, Red Grain, Low Sodium Uptake under Salinity

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KRL 3-4 is a salt and water-logging tolerant genotype developed at CSSRI, Karnal, through recombination breeding involving the parentage HD 1982/Kharchia 65. The genotype is unique with respect to red grain colour and very high level of tolerance to salinity, sodicity and water-logging stresses.

Morpho-agronomic Characteristics

The genotype has light green foliage with erect growth habit. The plants are very long with non waxy blade and ear. Ears are parallel and white in colour with spreading awns. The grains are red and elliptical with medium size. KRL 3-4 is being used as a tolerant check for All India Salinity/Alkalinity Tolerance screening Nursery and has out yielded Kharchia 65 (this has the reputation of the most salt tolerant genotype) from 2004-05 to 2008-09 crop seasons in different salt affected locations (Karnal, Hisar, Bawal, Faizabad, Kanpur, Lucknow, Bhilwara and Bharuch).

Associated Characters and Cultivated Practices

The genotype KRL 3-4 is much improved from Kharchia 65 (red grains) on account of high yielding ability along with high level of salinity, sodicity and water logging

tolerance. The genotype is characterized by low sodium uptake under salinity. The sodium uptake of KRL 3-4 ($300 \pm 12 \mu\text{mol/g}$) has been found to be lower than Kharchia 65 ($525 \pm 55 \mu\text{mol/g}$) in saline soils (Kulshreshtha, 2008). The salt tolerance of KRL 3-4 along with low sodium uptake makes it highly useful for incorporating salt tolerance trait. In addition to having better regulation over the uptake of Na and K in sodicity and Na and Cl in salinity, KRL 3-4 possesses higher tissue tolerance for Al, B and Fe. These regulatory mechanisms are maintained even when sodic or saline stress situations are accompanied by waterlogging stress.

KRL 3-4 gives its best expression in sodic/reclaimed sodic soils. However under high sodic conditions (pH more than 9.3), the genotype can provide much better yield than the prevalent variety PBW 343. Standard agronomical cultural practices are required to raise the crop.

Reference

Kulshreshtha N (2008) Breeding wheat varieties for salt tolerance in India: Present status and future prospects. In: NPS Yaduvanshi, RK Yadav, DS Bundela, N Kulshreshtha and G Singh (eds) Chemical Changes and Nutrient Transformation in Sodic/poor Quality Water Irrigated Soils, pp 269-274.

19. NRCSFR-06-1 (IC569675; INGR09088), a Sorghum (*Sorghum bicolor*) Germplasm with Source of Shoot Fly Tolerance with Multiple Resistances to Leaf Diseases and also Agronomic Superiority and Yield

C Aruna, PG Padmaja, Vittal Sharma, T Hussain, VR Bhagwat, S Audilakshmi and N Seetharama

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NRCSFR 06-1 (SPV 1518 X IS 2122) is the outcome of breeding for shoot fly resistance. The line possesses shoot fly resistance compared to resistant check, IS 2312

as tested across location during 2006, 2007 and 2008 under AICSIP. It was found to have better plant type with tan back ground compared to the resistant sources.

20. PEC 17 (IC392140; INGR09089), a Sorghum (*Sorghum bicolor*) Germplasm, Source of High Grain Yield and High Biomass under Rabi Conditions and Shallow Soil

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Sorghum germplasm PEC 17 (IC 392140) with high grain yield and high biomass was identified at Directorate of Sorghum Research (DSR), Hyderabad. The germplasm was collected from Bidar district of Karnataka. The germplasm was screened for *rabi* adaptation at Parbhani, Bijapur, Solapur and Rahuri during *rabi* 2006-07 & 2007-08 with the objective to characterize plant traits for improving productivity and stress tolerance. Sixty *rabi* landraces along with the temperate stay-green types were evaluated. The germplasm PEC 17 was superior for chlorophyll stability index (CSI). It is promising for higher biomass and grain yield with stress tolerance traits in comparison with the national check Maulee. This germplasm has higher grain yield with 57 g grain yield per plant. It is late flowering (178 days) with

medium plant height (200 cm), small stem diameter (1.7 cm) and higher grain weight (39 g/100 grains)

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22. MS 3042 A &B (IC572930; INGR09098), a Sorghum (*Sorghum bicolor*) Germplasm with Dwarf MS line with High Crude Protein
 MS 3151A &B (IC572931; INGR09099), a Sorghum (*Sorghum bicolor*) Germplasm with New Medium Early Duration Male Sterile line with High Stalk Protein
 MS 3062A &B (C572932; INGR09100), a Sorghum (*Sorghum bicolor*) Germplasm with Medium Tall Male Sterile line with Good Quality of Stalk
 MS 3009A &B (IC572933; INGR09101), a Sorghum (*Sorghum bicolor*) Germplasm with Medium Duration Sorghum MS line with Superior Stover Quality
 MS 3182A &B (IC572934; INGR09102), a Sorghum (*Sorghum bicolor*) Germplasm with New Medium Dwarf MS line with High ash% in Stalk

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23. EC-1 (IC345703; INGR09103), a Sorghum (*Sorghum bicolor*) germplasm with Source of Resistance to Multiple Foliar Diseases
 EC-31 (IC345733; INGR09104), a Sorghum (*Sorghum bicolor*) Germplasm with Source of Resistance to Multiple Foliar Diseases
 EC-32 (IC345734; INGR09105), a Sorghum (*Sorghum bicolor*) Germplasm with Source of Resistance to Multiple Foliar Diseases
 SEVS-6 (IC345772; INGR09106), a Sorghum (*Sorghum bicolor*) Germplasm with Source of Resistance to Multiple Foliar Diseases

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The sorghum germplasm EC 1 (IC 345703), EC 31 (IC 345733), EC 32 (IC 345734), and SEVS 6 (IC 345772) are potential source for multiple leaf disease resistant. This germplasm was screened for leaf disease resistance during *kharif* (2006) at the National Research Centre for Sorghum (NRCS), Hyderabad. Twenty yellow sorghum (*pachcha jonna*) collected from Andhra Pradesh were evaluated for their disease adoption at NRCS in randomized block design with three replications. Severe incidence of leaf blight (mean incidence score of 3.7), zonate leaf spot (2.8) and anthracnose (3.7) were observed. Four germplasm lines (EC 1, EC 31, EC 32 and SEVS 6) recorded the lowest average foliar disease index of <2

compared to other entries and showed multiple foliar disease resistance.

As *Pachcha jonna* is very popular in the Andhra Pradesh. It is grown during the *kharif* and *maghi* (late *kharif*) seasons in the state. The fodder quality of the variety is depending on the leaf disease resistant. These entries with multiple leaf diseases will definitely improve the returns to the farmers of the *kharif* and *maghi* sorghum growing areas in the semi-arid tropics of the country.

Reference

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24. ICU-7 (IC573438; INGR09107), a Blackgram (*Vigna mungo*) Germplasm with Exceptionally Large Seed Size. 100-Seed Weight 4.65 g (35.2% Higher than Pant Urd-19)

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(E-mail: dhanpalsingh@indiatimes.com)

25. PG 063 (IC573446; INGR09108), a Chickpea (*Cicer arietinum*) Germplasm with High Yield (24.9 g/Plant) and Dwarf and Bushy Plant Type

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The germplasm line PG 063 has been derived from a wide cross (PG 92-97 × *C. reticulatum*) between cultivated and wild species. The line PG 063 is high yielding with dwarf and bushy plant type.

26. PM 06-34 (IC573449; INGR09109), a Mung bean (*Vigna radiata*) Germplasm with High Iron (9.18 mg/100 g) Content and High Pods (48.7)/Plant and High Resistance to MYMV

DP Singh, RK Khulbe and CS Kar

GB Pant University of Agriculture and Technology, Pantnagar-263 145, Uttarakhand

(E-mail: dhanpalsingh@indiatimes.com)

The germplasm line PM 06-34 has been derived from a wide cross (BDYR-1 × DPU 88-31) between mung bean and black gram. Iron content and pod per plant of this line are 16.5 and 52.2% higher, respectively, than the check Pant M-4. The line is also highly resistant to mung bean yellow mosaic virus disease.

27. PM 06-36 (IC573450; INGR09110), a Mung Bean (*Vigna radiata*) Germplasm with High Iron (11.70 mg/100 g) Content, with High Resistant to MYMV

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GB Pant University of Agriculture and Technology, Pantnagar-263 145, Uttarakhand

(E-mail: dhanpalsingh@indiatimes.com)

The germplasm line PM 06-36 has been derived from a wide cross (BDYR-1 × DPU 88-31) between mung bean and black gram. Iron content of this line is 48.5% higher, respectively, than the check Pant M-4. The line is also highly resistant to mung bean yellow mosaic virus disease.

28. PM 06-37 (IC573451; INGR09111), a Mung bean (*Vigna radiata*) Germplasm with High Iron (11.18 mg/100 g) Content with High Resistance to MYMV

DP Singh, RK Khulbe and CS Kar

GB Pant University of Agriculture and Technology, Pantnagar-263 145, Uttarakhand
(E-mail: dhanpalsingh@indiatimes.com)

The germplasm line PM 06-37 has been derived from a wide cross (BDYR-1 × DPU 88-31) between mung bean and black gram. Iron content of this line is 41.9%

higher, respectively, than the check Pant M-4. The line is also highly resistant to mung bean yellow mosaic virus disease.

29. PM 06-40 (IC573453; INGR09112), a Mung bean (*Vigna radiata*) Germplasm with High Zinc (3.56 mg/100 g) Content with High Pods (47.0)/Plant, Early Maturity (24.7 days of Initial Flowering) and High Resistance to MYMV

DP Singh, RK Khulbe and CS Kar

GB Pant University of Agriculture and Technology, Pantnagar-263 145, Uttarakhand
(E-mail: dhanpalsingh@indiatimes.com)

The germplasm line PM 06-40 has been derived from a wide cross (BDYR-1 × DPU 88-31) between mung bean and black gram. Zinc content and pod per plant of this line are 7.2 and 46.9% higher than the check

Pant M-4. Besides, the line is 25.2% early than the check for days to initial flowering. The line is also highly resistant to mung bean yellow mosaic virus disease.

30. PM 06-43 (IC573454; INGR09113), a Mung bean (*Vigna radiata*) Germplasm with High Iron (10.59 mg/100 g) Content, Higher Pods (4.7)/Cluster with High Resistance to MYMV

DP Singh, RK Khulbe and CS Kar

GB Pant University of Agriculture and Technology, Pantnagar-263 145, Uttarakhand
(E-mail: dhanpalsingh@indiatimes.com)

The germplasm line PM 06-43 has been derived from a wide cross (BDYR-1 × DPU 88-31) between mung bean and black gram. Iron content and pod per plant

of this line are 34.4 and 42.2% higher than the check Pant M-4. The line is also highly resistant to Mung bean yellow mosaic virus disease.

31. PM 06-44 (IC573455; INGR09114), a Mung bean (*Vigna radiata*) Germplasm with High Iron (Fe) (11.35 mg/100 g) Content and High Resistance to MYMV

DP Singh, RK Khulbe and CS Kar

GB Pant University of Agriculture and Technology, Pantnagar-263 145, Uttarakhand
(E-mail: dhanpalsingh@indiatimes.com)

The germplasm line PM 06-44 has been derived from a wide cross (BDYR-1 × DPU 88-31) between mung bean and black gram. Iron content of this line is 44.1

higher than the check Pant M-4. The line is also highly resistant to mung bean yellow mosaic virus disease.

32. PM 06-50 (IC573456; INGR09115), a Mung bean (*Vigna radiata*) Germplasm with High Iron (8.29 mg/100 g), Zinc (4.19 mg/100 g) and Protein (25.8%) Content and High Resistance to MYMV

DP Singh, RK Khulbe and CS Kar

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(E-mail: dhanpalsingh@indiatimes.com)

The germplasm line PM 06-50 has been derived from a wide cross (BDYR-1 × DPU 88-31) between mungbean and blackgram. Iron, Zinc and protein content of this line are 5.2, 26.2 and 8.6.9% higher, respectively, than

the check Pant M-4. Besides, the line is 25.2% early than the check for days to initial flowering. The line is also highly resistant to Mungbean yellow mosaic virus disease.

33. AKS/S 41 (IC570613; INGR 09116), a Safflower (*Carthamus tinctorius*) Germplasm with Dwarf Plant Type and Basal Branching Starting at Elongation

SN Deshmukh and MM Wakode

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(E-mail: srsoilseedspdkv@rediffmail.com)

Safflower is one of the most important oilseed crops of *rabi* season having high quality oil. The dwarf genotype with good yield is rare in safflower. The registered genotype AKS/S 41 is having dwarf stature plant along with the branching very close to the ground giving bushy appearance. The average height of this genotype is 66 cm. The genotype AKS/S 41 is developed at Crop Research Unit (Oilseeds), Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (MS) by selection in safflower variety PBNS 12.

Morpho-agronomic Characters

Though the genotype AKS/S 41 is a dwarf with basal branching starting at elongation it is not early maturing. It took 86 days to 50% flowering, 133 days to mature.

It produces 15 q/ha seed yield with oil content 27 %, hull content 48%, test weight of 5.5 g (Table 1) and having spiny nature (Anonymous, 2008). The flowers are yellow and turn to orange and remain orange after fading.

Associate Characters and Cultivated Practices

AKS/S 41 showed drought tolerant nature with high drought tolerant efficiency (88%). The reaction to *Alternaria* and wilt diseases is comparable to the nationally released safflower varieties. For aphid the genotype showed tolerant to moderately tolerant grade which is comparable to the national varieties.

The required cultivation practices as usual, sowing time, from Last week of September to first week of

31. PM 06-44 (IC573455; INGR09114), a Mung bean (*Vigna radiata*) Germplasm with High Iron (Fe) (11.35 mg/100 g) Content and High Resistance to MYMV

DP Singh, RK Khulbe and CS Kar

GB Pant University of Agriculture and Technology, Pantnagar-263 145, Uttarakhand
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The germplasm line PM 06-44 has been derived from a wide cross (BDYR-1 × DPU 88-31) between mung bean and black gram. Iron content of this line is 44.1

higher than the check Pant M-4. The line is also highly resistant to mung bean yellow mosaic virus disease.

32. PM 06-50 (IC573456; INGR09115), a Mung bean (*Vigna radiata*) Germplasm with High Iron (8.29 mg/100 g), Zinc (4.19 mg/100 g) and Protein (25.8%) Content and High Resistance to MYMV

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The germplasm line PM 06-50 has been derived from a wide cross (BDYR-1 × DPU 88-31) between mungbean and blackgram. Iron, Zinc and protein content of this line are 5.2, 26.2 and 8.6.9% higher, respectively, than

the check Pant M-4. Besides, the line is 25.2% early than the check for days to initial flowering. The line is also highly resistant to Mungbean yellow mosaic virus disease.

33. AKS/S 41 (IC570613; INGR 09116), a Safflower (*Carthamus tinctorius*) Germplasm with Dwarf Plant Type and Basal Branching Starting at Elongation

SN Deshmukh and MM Wakode

Oilseeds Research Unit, Dr Panjabrao Deshmukh Krishi Vidyapeeth, Akola-444 104, Maharashtra
(E-mail: srsoilseedspdkv@rediffmail.com)

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Associate Characters and Cultivated Practices

AKS/S 41 showed drought tolerant nature with high drought tolerant efficiency (88%). The reaction to *Alternaria* and wilt diseases is comparable to the nationally released safflower varieties. For aphid the genotype showed tolerant to moderately tolerant grade which is comparable to the national varieties.

The required cultivation practices as usual, sowing time, from Last week of September to first week of

Table 1. Morpho-agronomic description of AKS/S 41

Characters	Mean of Eleven AICRP Centers			CD (P=0.05)	CV (%)
	AKS/S 41	A-1 (National Check)	PBNS-40 (National Check)		
Seed yield (Kg/ha)	1521	1620	1562	72	12.7
Oil content (%)	27	27	27		
Oil yield (Kg/ha)	415	439	432		
Hull content (%)	48.5	49.6	48.9		
Days to 50% flowering	86	86	85		
Days to maturity	133	132	132		
No. of effective capitula/plant	24.9	24.0	23.6		
No. of seeds/capitulum	24	25	23		
100 seed weight (g)	5.5	6.2	58		
Volume weight (g/l)	638	649	674		
Harvest index	31	31	29		
Biological yield (Kg/ha)	4917	5732	5586		
Plant height (cm)	66	82	115		

October. The seed rate required is 10-12 kg/ha, with spacing of 45 x 20 cm row to row and plant to plant respectively. The recommended dose of fertilizer is 25:25:0 kg NPK/ha for rain fed conditions of Vidarbha region of Maharashtra state.

References

Anonymous (2008) Annual Report Safflower 2007-08. Directorate of Oilseeds Research, Rajendranagar, Hyderabad, India.

34. “30814” (IC439707; INGR09117), a Cotton (*Gossypium arboreum*) Germplasm with Immunity to Grey Mildew (*Ramularia areola*)
- “30826” (IC439721; INGR09118), a Cotton (*Gossypium arboreum*) Germplasm with Immunity to Grey Mildew (*Ramularia areola*)
- “30856” (IC439749; INGR09119), a Cotton (*Gossypium arboreum*) Germplasm with Immunity to Grey Mildew (*Ramularia areola*)

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Gossypium arboreum L. germplasm lines are immune to *Ramularia areola* Atk. the Grey mildew areolate

disease of cotton. The immune lines can be used in resistance breeding programme.

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Gossypium arboreum L. germplasm lines are immune to *Ramularia areola* Atk. the Grey mildew areolate

disease of cotton. The immune lines can be used in resistance breeding programme.

35. SS 2040 (EC460686; INGR09120), a Potato (*Solanum tuberosum* ssp. *andigena*-cultivated species) clone with Frost Tolerance of Cultivated Tetraploid Potato Species *Solanum tuberosum* ssp. *andigena*

SK Luthra¹, J Gopal², P Manivel², Vinod Kumar³, BP Singh¹ and SK Pandey²

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²Central Potato Research Institute, Shimla-171 001, Himachal Pradesh

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(E-mail: skluthra@hotmail.com)

SS 2040 an elite potato genetic stock with frost tolerance has been registered as unique germplasm by the Plant Germplasm Registration Committee of the Indian Council of Agricultural Research vide Registration No INGR 09121. SS 2040 is a clonal selection from the segregating progeny of the accession SS 2040 (EC460686) of cultivated tetraploid potato species *Solanum tuberosum* ssp. *andigena*

In India, 85-90% of potatoes are grown during short winter days from October to February in sub-tropical plains. In north-western and west-central plains, the crop is prone to frost during December and January, and losses vary from year to year depending upon the intensity of the frost. The development of frost tolerant varieties may be helpful for sustainable production of potatoes. A severe incidence of frost was observed during January 7-9, 2006 in northern plains of India and potato crop was damaged significantly. This natural opportunity was effectively utilized to screen 30 clones of cultivated species *Solanum tuberosum* ssp. *andigena* for frost tolerance at CPRI Campus, Modipuram, Meerut. The genotype SS 2040 a clone of cultivated tetraploid potato

species *Solanum tuberosum* ssp. *andigena* was found highly tolerant (only 10% foliage injury due to frost) to frost during the severe spell of frost (Luthra *et al.*, 2007). The clone SS 2040 has good tuberization with acceptable tuber characters.

The plant of SS 2040 is tall, open canopy structure, open leaf structure, leaflets are ovate lanceolate with medium waviness and flower is red purple. The clone SS 2040 is late maturing and possesses small sized tubers with yellow skin, round shape, medium-deep eyes and yellow flesh. The genotypes having yellow flesh are known to be nutritionally superior. The clone SS 2040 can be used for diversifying the source of tolerance to frost in cultivated potatoes since it is easily and directly crossable with the other predominant cultivated group *Tuberosum*.

References

Luthra SK, J Gopal, P Manivel, Vinod Kumar, BP Singh and SK Pandey (2007) Screening of wild and cultivated species of potato for frost tolerance in north-central plains of India. *Potato J.* **34**: 45-46.

36. SS 1725-22 (EC412923; INGR 09121), a Potato (*Solanum spegazzinii* - Diploid wild species) Germplasm with Frost Tolerance of Wild Potato Diploid Species *Solanum spegazzinii*

SK Luthra¹, J Gopal², P Manivel², Vinod Kumar³, BP Singh¹ and SK Pandey²

¹CPRI Campus, Modipuram, Meerut-250 110, Uttar Pradesh

²Central Potato Research Institute, Shimla-171 001, Himachal Pradesh

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(E-mail: skluthra@hotmail.com)

SS 1725-22 – an elite potato genetic stock with frost tolerance has been registered as unique germplasm by the Plant Germplasm Registration Committee of the

Indian Council of Agricultural Research vide Registration No. INGR 09121. SS 1725-22 is a clonal selection from the segregating progeny of the accession SS 1725

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In India, 85-90% of potatoes are grown during short winter days from October to February in sub-tropical plains. In north-western and west-central plains, the crop is prone to frost during December and January, and losses vary from year to year depending upon the intensity of the frost. The development of frost tolerant varieties may be helpful for sustainable production of potatoes. A severe incidence of frost was observed during January 7-9, 2006 in northern plains of India and potato crop was damaged significantly. This natural opportunity was effectively utilized to screen 30 clones of cultivated species *Solanum tuberosum* ssp. *andigena* for frost tolerance at CPRI Campus, Modipuram, Meerut. The genotype SS 2040 a clone of cultivated tetraploid potato

species *Solanum tuberosum* ssp. *andigena* was found highly tolerant (only 10% foliage injury due to frost) to frost during the severe spell of frost (Luthra *et al.*, 2007). The clone SS 2040 has good tuberization with acceptable tuber characters.

The plant of SS 2040 is tall, open canopy structure, open leaf structure, leaflets are ovate lanceolate with medium waviness and flower is red purple. The clone SS 2040 is late maturing and possesses small sized tubers with yellow skin, round shape, medium-deep eyes and yellow flesh. The genotypes having yellow flesh are known to be nutritionally superior. The clone SS 2040 can be used for diversifying the source of tolerance to frost in cultivated potatoes since it is easily and directly crossable with the other predominant cultivated group Tuberosum.

References

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36. SS 1725-22 (EC412923; INGR 09121), a Potato (*Solanum spegazzinii* - Diploid wild species) Germplasm with Frost Tolerance of Wild Potato Diploid Species *Solanum spegazzinii*

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SS 1725-22 – an elite potato genetic stock with frost tolerance has been registered as unique germplasm by the Plant Germplasm Registration Committee of the

Indian Council of Agricultural Research vide Registration No. INGR 09121. SS 1725-22 is a clonal selection from the segregating progeny of the accession SS 1725

(EC412923) of diploid potato wild species *Solanum spegazzinii*.

The potato crop grown in north-western and west-central plains is prone to frost during December and January, and losses vary from year to year depending upon the intensity of the frost. The development of frost tolerant varieties may be helpful for sustainable production of potatoes. A severe incidence of frost was observed during January 7-9, 2006 in northern plains of India and potato crop was damaged significantly. This natural opportunity was effectively utilized to screen 86 accessions of 21 tuber bearing wild *Solanum* species for frost tolerance at CPRI Campus, Modipuram, Meerut. The genotype SS 1725-22 a clone of wild diploid species *Solanum spegazzinii* was found highly tolerant (only 10% foliage injury due to frost) to frost during the severe spell of frost (Luthra *et al.*, 2007). Hijmans *et al.* (2003) also reported a high extent (38 out of 40 clones) of frost tolerance in *S. spagazzinii*. The clone SS 1725-22 has the good tuberization with acceptable tuber

characters.

The plant of SS 1725-22 is short, semi-compact canopy structure, open leaf structure, leaflets are narrow lanceolate with weak waviness and flower is blue violet. The clone SS1725-22 is late maturing and possesses attractive small sized tubers with white cream skin, ovoid, tapering, shallow eyes and white cream flesh. The wild diploid clone SS 1725-22 can be used for diversifying the source of tolerance to frost in cultivated potatoes by crossing it cultivated types following ploidy manipulation.

References

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37. P-61 (IC249349; INGR09122), a Brinjal (*Solanum melongena*) Germplasm with Resistance to Bacterial Wilt

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In India, brinjal is one of the important vegetable crops and known for its different shape and colour and this has distinct preference in cultivation is restricted due to bacterial wilt attack. The disease completely damages the crop in 2-3 days after attack. This disease is prevalent in hot and high rainfall areas. Therefore, identification of disease resistant genotypes will enhance its scope

of cultivation in hot and humid areas. The brinjal germplasm was evaluated at Kerala Agricultural University (KAU), Vellanikkara, as a part of multilocation evaluation of germplasm under AICRP (Vegetable crops) in March 2005. The evaluation site *i.e.* KAU, Vellanikkara, is a known bacterial wilt sick plot area and the above line has shown resistance to the bacterial wilt disease.

(EC412923) of diploid potato wild species *Solanum spegazzinii*.

The potato crop grown in north-western and west-central plains is prone to frost during December and January, and losses vary from year to year depending upon the intensity of the frost. The development of frost tolerant varieties may be helpful for sustainable production of potatoes. A severe incidence of frost was observed during January 7-9, 2006 in northern plains of India and potato crop was damaged significantly. This natural opportunity was effectively utilized to screen 86 accessions of 21 tuber bearing wild *Solanum* species for frost tolerance at CPRI Campus, Modipuram, Meerut. The genotype SS 1725-22 a clone of wild diploid species *Solanum spegazzinii* was found highly tolerant (only 10% foliage injury due to frost) to frost during the severe spell of frost (Luthra *et al.*, 2007). Hijmans *et al.* (2003) also reported a high extent (38 out of 40 clones) of frost tolerance in *S. spagazzinii*. The clone SS 1725-22 has the good tuberization with acceptable tuber

characters.

The plant of SS 1725-22 is short, semi-compact canopy structure, open leaf structure, leaflets are narrow lanceolate with weak waviness and flower is blue violet. The clone SS1725-22 is late maturing and possesses attractive small sized tubers with white cream skin, ovoid, tapering, shallow eyes and white cream flesh. The wild diploid clone SS 1725-22 can be used for diversifying the source of tolerance to frost in cultivated potatoes by crossing it cultivated types following ploidy manipulation.

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37. P-61 (IC249349; INGR09122), a Brinjal (*Solanum melongena*) Germplasm with Resistance to Bacterial Wilt

KK Gangopadhyay, P Sadhan Kumar, SK Mishra, Gunjeet Kumar, SK Yadav, Chitra Pandey, BL Meena, RK Mahajan, Mathura Rai, SK Sharma, DS Yadav and Manoj Singh

National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012

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In India, brinjal is one of the important vegetable crops and known for its different shape and colour and this has distinct preference in cultivation is restricted due to bacterial wilt attack. The disease completely damages the crop in 2-3 days after attack. This disease is prevalent in hot and high rainfall areas. Therefore, identification of disease resistant genotypes will enhance its scope

of cultivation in hot and humid areas. The brinjal germplasm was evaluated at Kerala Agricultural University (KAU), Vellanikkara, as a part of multilocation evaluation of germplasm under AICRP (Vegetable crops) in March 2005. The evaluation site *i.e.* KAU, Vellanikkara, is a known bacterial wilt sick plot area and the above line has shown resistance to the bacterial wilt disease.

38. Dholi-5 (IC090982; INGR09123), a Brinjal (*Solanum melongena*) Germplasm with Source of Resistance to Bacterial Wilt in Different Genetic Background

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39. Terminal flower mutant phenotype (IC565527; INGR09124), a Palak (*Beta palonga*) Germplasm with Terminal Flower, Thick Leaf, Big Seed Mutant of Palak

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Determinacy/indeterminacy of the inflorescence are usually a stable character and are often used in species identification. In several species, occasional conversions of an indeterminate into determinate ones have been reported. There has been a marked advance in the understanding of floral initiation and inflorescence development from studies of mutant plants displaying altered inflorescence development. Terminal flowers, are found in the *Arabidopsis* terminal flower1 (*TFL1*) mutant (Shannon and Meeks-Wagner 1991,1993; Alvarez *et al.*,1992; Ohshima *et al.*, 1997; Bradley *et al.*,1997) and in the *Antirrhinum centroradialis* (*CEN*) mutants (Bradley *et al.*,1996). The inflorescence of *Beta palonga* is indeterminate. In an earlier attempt the terminal flower mutant of *Beta palonga* was isolated (Mukherjee and Basu, 1985).

Morpho-agronomic Characters

Beta palonga (palak in Hindi, *palong* in Bengali) (Basu and Mukherjee, 1975) consumed as a leafy vegetable, is cultivated during the winter under tropical climatic condition throughout India. The lifecycle of *Beta palonga* has four distinct phases, juvenile phase (JV), adult

vegetative (AV), early reproductive phase (ER) and late reproductive phase, (LR). During transition to flowering (ER), a primary inflorescence is produced (Bolting). Late inflorescence (LR) primordia exclusively give rise to flowers. During flowering, apical dominance decreases allowing the secondary inflorescences (from the meristems in the axils of the rosette leaves) to develop. After maturation of the seeds, depending upon the temperature mature plants gradually dries up.

B. palonga is a long day plant and completes its lifecycle within 120 to 140 days. The mutant of *Beta* flowers early and completes its lifecycle comparatively in short time span (90 to 110 days). The data of day length and temperature of last five year (2000-2005) shows that there is a relationship among day length, temperature and bolting of the normal plant (Datta *et al.*, 2008). In *B. palonga*, bolting occurs during the end of December to first week of January under this agro climatic condition (in between 70 to 80 days), when the day length and temperature gradually increased day by day. But in case of mutant, it bolts early (in between 50 to 55 days). In a stagger plantation experiment (three

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different plots were sown at 10 days interval) of the mutant showed that it bolts in between 50 to 55 days irrespective of date of sowing, day length and temperature.

Associated Characters

To understand the conversion of indeterminate growth of inflorescence into a determinate type of inflorescence, the control of floral development of the mutant phenotype and to investigate the regulation of meristem identity and control of flower development of the mutant phenotype, degenerated primers were designed from the highly conserved region of floral identity gene *TFL1/CEN*. This resulted to 238 base pair specific amplified cDNA product by RT-PCR, named as PTC-1. Sequence analysis followed by BLAST showed high homology of the PTC with *TFL1/CEN* like gene indicating presence of *TFL1/CEN* homologue in *B. palonga*. Southern analysis indicates alteration of the genomic sequence of the mutant of *B. palonga*.

Importance of Terminal Flower Mutant

The terminal flower mutant of *B. palonga* passes through its life cycle very rapidly but produces relatively small amount of seed. In contrast normal *B. palonga* grows much longer and eventually produces much large quantity of seed. It remains to be seen whether up or down regulation of *TFL1* like gene expression through transgenic technologies could induce or reduce the vegetative phase of diverse crop plants. It, will therefore, be interesting to assess how *TFL1/CEN* like genes function in diverse plant species; the present investigation paved the way in this direction.

The production of terminal flower is thought to be an ancestral state from which the indeterminate condition evolved (Stebbins, 1974). By accelerating progression through phases, the terminal flower mutant, in effect, recapitulates the ancestral form. The evolution of an indeterminate inflorescence from an ancestor with a determinate inflorescence might be regarded as an example of neoteny (De Beer, 1940), a process in which juvenile traits persists into later periods of the life cycle. According to this view, the indeterminate growth of the wild-type apex may have arisen from *TFL1/CEN* or its' homologue activity, retarding its progression and ensuring that it

never reaches the mature determinate floral phase, exhibited by the ancestor (Ratcliffe *et al.*, 1998). *TFL1/CEN* and its' homologues are closely related and belong to a small gene family (*CETS*) that encodes ~23 kDa proteins (Pnueli *et al.*, 2001). Thus the genomic information of *TFL1/CEN* homologue from different plant species plays a major role in construction of phylogenetic relationship among diverse flowering plants.

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40. BS 35 (IC565533; INGR09125), an Okra (*Abelmoschus esculentus*) Germplasm with Thin (0.9 cm) and Long Fruit (26 cm)

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41. CHIG-15 (IC553244; INGR09126), a Ivy gourd (*Coccinia grandis*) Germplasm with Fruit Length (8.5-9 cm) and Uniform Cylindrical Shape

LK Bharathi, Vishalnath, G Naik, Sudhamoy Mondal and HS Singh

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CHIG-15 (IC553244) was identified from a collection of twenty ivy gourd genotypes for its culinary quality and yield. This is an early fruiting variety which starts fruit production 40 days after transplanting. The variety produces light green, long slender cylindrical fruits of 7.5-8.5 cm length with soft texture and has attractive stripes in skin. The variety has sequential fruiting habit

and fruits develop by means of vegetative parthenocarpy hence, there is no need of male plant for pollination and more number of female plants can be accommodated/unit areas. A single plant of CHIG-15 produces a yield of 20 kg fruits in a year. On the basis of superior performance, it has been sent for multi-location testing in Orissa.

42. NRCG09-1 (IC567685; INGR09127), a Ground nut (*Arachis hypogaea*) Germplasm with Multiple Phenotypic Marker Stock with Crinkle Leaf and White Testa Color. Near- Isogenic Line of Crinkle Leaf with Rose Testa Mutant NRCG09-2 (IC567686; INGR09128), a Ground nut (*Arachis hypogaea*) Germplasm with Multiple Phenotypic Marker Stock with Crinkle Leaf and Red Testa Color, Near-Isogenic Line of Crinkle Leaf with Rose Testa Mutant

SK Bera, T Radhakrishnan, AL Rathnakumar and P Paria

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‘Crinkle leaf-white testa’ mutant (INGR09127; IC567685) of groundnut was developed from the cross involving ‘crinkle leaf-rose testa’ mutants × ‘normal leaf-white testa’ germplasm. Similarly, ‘crinkle leaf-red testa’ mutant (INGR09128; IC567886) of groundnut was developed from the cross involving ‘crinkle leaf-rose testa’ mutant × ‘normal leaf-red testa’ germplasm. F₁ progeny was ‘crinkle leaf and rose testa’ in both the crosses indicating that rose testa colour is dominant over both white and red testa colour and crinkle leaf is dominant over normal leaf in these two crosses. ‘Crinkle leaf and testa colour

segregated into 9:3:3:1 in the F₂ populations of these two crosses indicating that crinkle leaf and testa colour (rose, red and white) are controlled by two different loci and segregate independently. These newly developed two mutants were evaluated for both qualitative and quantitative traits and were found to be agronomically similar to their female parent except testa colour. Such near-isogenic lines (NILs) with both recessive and dominant traits are important genetic stocks (multiple phenotypic markers) for investigating the function and regulation of genes.

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43. PANDAV (IC569194; INGR09129), a Chilli (*Capsicum annuum*) Germplasm with Erect Cluster Bearing De-stalking Nature of Fruits, Low Pungency and Bright Colour

K Ramesh

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The Chilli (*Capsicum annuum* L.) germplasm accession “PANDAV” assume importance in view of combination of a number of desirable morphological and agronomic traits. The most unique and distinguishing morphological traits are erect and clustered habit and de-stalking nature of fruits. The other advantage of this particular entry are uniformity and reduce time for drying of fruits as the fruits get dried on the plant itself as they are erect and exposed to direct sun light. Another advantage is the ease of harvesting of fruits without their pedicels

as this genotype bears erect fruits with de-stalking nature which reduce the labour cost to a great extent with almost zero aflatoxins. The significant biochemical traits like capsaicin and capsanthin are at desirable level with 0.5% and 150 ASTA units analyzed by the Spice Board making this genotype suitable for export market. This particular accession has generated lot of interest and is in great demand among the farming community around Tarulawada.

44. Co 0120 (IC565020; INGR09130), a Sugarcane (*Saccharum* spp. Hybrid) Germplasm with High Juice Quality Early in the Season (in 240 days) and High Sugar Recovery

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Co 0120 was derived from a general cross Co 89003 GC at Sugarcane Breeding Institute, Regional Centre, Karnal. The parent (Co 89003) is known for its high juice quality at 300 days, which is in cultivation in Punjab and Haryana states. The genotype flowers late during flowering season (November second fortnight) and is used as a female parent (pollen fertility below 20 %) as a source for juice quality. The clone has medium field habit. It has thin greenish yellow canes with cylindrical internodes, erect leaves and small dentoid auricle. Bud groove prominent extending to at least 3/4th of internode. The clone is free from spines, splits, pith and bud cushion. It was better for CCS% (240 days), CCS% (300 days) and sucrose 5 (300 days) than CoJ 64 and CoPant 84211 (early standards in North Western Zone) in Initial Varietal Trials in the zone. Co 0120 was tested during last 2001–02 to 2005–06

years at SBI, Regional Centre, Karnal for its juice quality in comparison to the best early standard CoJ 64 in the North-Western Zone (Table 1). Improvement in Co 0120 over CoJ 64 with respect to Pol% in juice was 18.66% during October, which reduced to 6.51% during March. These results indicated that Co 0120 is a potential donor for better juice quality especially for earliness. There is more or less linear sugar accumulation in Co 0120 from November to March. Pol% in Co 0120 on 3rd November was 18.20, 18.21 and 17.40 in autumn (12th October), spring (13th March) and summer (15th April) planted canes, respectively. It showed that there was very little effect of planting dates on pol% juice of Co 0120. Its potential was also evaluated at different sugar mills like Modinagar and Ajbapur in UP, and Dasua and Fazilka in Punjab which confirmed the superiority of Co 0120 over CoJ 64 and other early varieties.

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Co 0120 was derived from a general cross Co 89003 GC at Sugarcane Breeding Institute, Regional Centre, Karnal. The parent (Co 89003) is known for its high juice quality at 300 days, which is in cultivation in Punjab and Haryana states. The genotype flowers late during flowering season (November second fortnight) and is used as a female parent (pollen fertility below 20 %) as a source for juice quality. The clone has medium field habit. It has thin greenish yellow canes with cylindrical internodes, erect leaves and small dentoid auricle. Bud groove prominent extending to at least 3/4th of internode. The clone is free from spines, splits, pith and bud cushion. It was better for CCS% (240 days), CCS% (300 days) and sucrose 5 (300 days) than CoJ 64 and CoPant 84211 (early standards in North Western Zone) in Initial Varietal Trials in the zone. Co 0120 was tested during last 2001–02 to 2005–06

years at SBI, Regional Centre, Karnal for its juice quality in comparison to the best early standard CoJ 64 in the North-Western Zone (Table 1). Improvement in Co 0120 over CoJ 64 with respect to Pol% in juice was 18.66% during October, which reduced to 6.51% during March. These results indicated that Co 0120 is a potential donor for better juice quality especially for earliness. There is more or less linear sugar accumulation in Co 0120 from November to March. Pol% in Co 0120 on 3rd November was 18.20, 18.21 and 17.40 in autumn (12th October), spring (13th March) and summer (15th April) planted canes, respectively. It showed that there was very little effect of planting dates on pol% juice of Co 0120. Its potential was also evaluated at different sugar mills like Modinagar and Ajbapur in UP, and Dasua and Fazilka in Punjab which confirmed the superiority of Co 0120 over CoJ 64 and other early varieties.

Table 1. Pol % in juice in Co 0120 in comparison to CoJ 64 during 2001–2002 to 2005–2006 season at Sugarcane Breeding Institute, Regional Centre, Karnal

Variety	Year	October	November	December	January	February	March
Co 0120	2001-2002	—	18.21	—	19.02	20.13	19.98
	2002-2003	16.09	17.95	19.21	19.77	20.04	20.27
	2003-2004	16.67	17.96	18.54	19.37	19.46	20.04
	2004-2005	14.21	17.08	19.09	20.96	20.98	21.73
	2005-2006	17.62	18.86	19.24	19.42	20.35	21.86
	Mean	16.15	18.01	19.02	19.71	20.19	20.78
% Improvement over CoJ 64	18.66	10.63	9.25	8.54	7.00	6.51	
CoJ 64	2001-2002	—	15.06	—	17.91	18.81	19.30
	2002-2003	12.94	15.07	15.84	16.80	17.57	18.21
	2003-2004	16.12	16.76	18.13	18.50	18.80	19.36
	2004-2005	10.74	16.48	17.58	19.23	19.74	19.84
	2005-2006	14.63	18.02	18.08	18.35	19.44	20.82
	Mean	13.61	16.28	17.41	18.16	18.87	19.51

45. Co 91002 (IC565021; INGR09131), a Sugarcane (*Saccharum* spp. Hybrid) Germplasm with Good Sugar Accumulation (300 days of age, AVT) for Both Peninsular and East Coast Regions and Resistance to Smut and Drought

KV Bhagyalakshmi, R Nagarajan, G Hemaprabha, P Govindaraj, S Alarmelu, RM Shanthi, KG Somarajan, M Sanjiva Reddy, M Madhusudhana Rao and N Vijayan Nair

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Co 91002 was evaluated during 1996-1998 in AICRP(S) trails of both Peninsular and East Coast zones of India. Based on the mean of two plant crops Co 91002 was among top three in 8 trails for CCS% and in 6 trails for Sucrose% expressing its advantage for juice quality. This clone has the potential for early high sugar accumulation (at 300 days of crop age) with an improvement of 9.29% over Co 85004 and 5.57% over CcC 671 in three centers of peninsular zone (Coimbatore, Pune and Pravaranagar).

The clone also performed well in Mandya (Karnataka) and in the high recovery regions of Maharashtra. In addition, the clone also performed well in three centers of East Coast Zone viz., Anakapalle, Chiplima and Cuddalore for early high sugar (300 days) with an overall

improvement of 14.46% compared over Co 6907 and 4.95% over Co 7508.

Due to moderate yield levels, this clone could not be considered for release as a variety for the zone, hence proposed as a genetic stock for early high sugar. The clone possess resistant to smut and drought. The genotype has field habits like tall, medium thick canes without spines or splits. The genotype flowers during mid season (during November) under Coimbatore conditions. The clone is used as a female parent as a source for juice quality, smut resistant and drought resistant by the breeders of the Institute and its use in breeding programmes is expected to produce early high quality genotypes in sugarcane.

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