

Intellectual Property Rights and Agro-biodiversity

Umesh Srivastava

Indian Council of Agricultural Research, Krishi Anusandhan Bhawan-II, Pusa, New Delhi-110 012

Agrobiodiversity is the backbone of a nation's food security and the basis of economic development as a whole. The Intellectual Property Rights (IPR) regime is encouraging commercialization of seed development, monoculture, protection of new plant varieties, microorganisms, and genetically modified organisms. As a consequence, our rich biological diversity is being eroded irreversibly. This paper seeks to analyze the impacts of the international legal framework for the promotion of intellectual property rights on India's legal regime concerning the control over biological resources and inventions derived from biological resources. The paper analyses these enactments in the context of the move towards the control of biological resources and derived products through property rights. It also focuses on the issue of control over biological resources and derived products and seeks to provide a broader analysis of the changing international legal framework and its impacts on national law and policy-making concerning the management of biological resources. There was strong support for CBD and the fair and equitable sharing of the benefits arising from such use. TRIPS agreement of WTO vs CBD and gender implication of TRIPS was discussed. In addition, contribution of traditional knowledge and practices of local and indigenous communities for conservation was also emphasized for the effective maintenance of such knowledge systems.

Key words: Agrobiodiversity, IPR, Trade Related Intellectual Property Rights Agreement, World Trade Organization, Genetic resources

The last decade witnessed intensive debates on the issues of agro-biodiversity and intellectual property rights (IPRs). The two international treaties around which such debate has been revolving with significant consequences for public policy relating to intellectual property rights, biodiversity and associated knowledge systems, are the Convention on Biological Diversity (CBD) and the Trade Related Intellectual Property Rights (TRIPS) agreement of the World Trade Organisation (WTO). The CBD mandates countries to safeguard biodiversity and the traditions and knowledge of indigenous and other local communities associated with this biodiversity, and lays down the basic elements for access to that biodiversity and the associated knowledge systems. The TRIPS obliges party countries to modify their national IPR regimes to meet much-enhanced international standards, which would have significant implications for biodiversity and the associated knowledge systems. In addition, the World Intellectual Property Organisation (WIPO) and other international institutions are increasingly becoming active on the subject.

The essential principles of the CBD most relevant to the debate of IPRs over biological resources can be summarized as:

- the state has sovereign control over the biological resources within the limits of their national jurisdiction and shall ensure conservation and sustainable use of the same;

- while states shall have the authority to determine access to their biological resources, they shall endeavour to create conditions to facilitate such access;
- such access shall be granted on mutually agreed terms and subject to the prior informed consent of the party providing such access;
- the benefits of the commercial or other utilization of the genetic resources shall be shared in a fair and equitable way with the party providing such access; and
- the wider application of the knowledge, innovations and practices of indigenous and other local communities shall be done with the approval and involvement of the holders of such knowledge.

The aspects of the TRIPS agreement with implications for the above principles of the CBD are:

- it mandates developing countries to amend their existing regimes for the protection of intellectual property and adopt ones similar to those prevailing in the industrialised countries;
- it proposes an almost all-encompassing coverage under the patent system, and mandates that patents shall be available for inventions, whether products or processes, in all fields of technology. The coverage so defined is aimed at extending the fields of activity under patents to cover selected forms of life which were hitherto not considered patentable by most countries;

- As regards plant varieties, the TRIPS Agreement provides that protection has to be provided? either by patents or by an effective *sui generis* system or by any combination thereof?

In response to the debate at the international level, at the national levels there is considerable activity. Several countries (India, Mexico, Peru, Philippines, Costa Rica, Eritrea and Fiji) have come up with legislation, or coming up with other measures, which respond to the above treaties or in other ways deal with the relationship between IPRs and biodiversity. Of particular interest to many countries, especially in the 'developing' world, are the attempts to respond to the CBD-TRIPs debate through legislative and administrative measures in order to achieve the following:

- Protecting indigenous knowledge (traditional and modern) from being 'pirated' and used in IPR claims by industrial/commercial interests;
- Regulating access to biological resources so that historical 'theft' of these resources by the more powerful sections of the global society can be stopped, and communities/countries are able to gain control and benefits from their use.

All countries are now required to respond to this issue, especially given the following specific decisions taken at international forums:

- Decisions at successive Conferences of the Parties (CoPs) to the CBD, asking for more in-depth understanding, case studies, and other follow-up on the relationship between IPRs and biodiversity in general, and TRIPs and CBD in particular; and to work towards the protection of indigenous and local community knowledge, if need be through alternative IPR regimes.
- Decision arrived at the fourth meeting of the Subsidiary Body on Scientific, Technical and Technological Advice (SBSTTA) that recommend Parties not to approve field-testing of such technologies until appropriate scientific information can justify such testing, citing the precautionary approach and lack of reliable data. SBSTTA also invited the FAO, UNESCO, UNEP and other competent organizations to further study the potential impacts of such technologies.

IPRs Related to Agro-biodiversity

Intellectual Property Rights (IPRs), as the term suggests, are meant to be rights to ideas and information, which

are used in new inventions or processes. These rights enable the holder to exclude imitators from marketing such inventions or processes for a specified time; in exchange, the holder is required to disclose the formula or idea behind the product/process. The effect of IPRs is therefore monopoly over commercial exploitation of the idea/information, for a limited period. The stated purpose of IPRs is to stimulate innovation, by offering higher monetary returns than the market otherwise might provide.

While IPRs such as copyrights, patents and trademarks are centuries old, the extension of IPRs to living beings and knowledge/technologies related to them is relatively recent. In 1930, the U.S. Plant Patent Act was passed which gave IPRs to asexually reproduced plant varieties. Several other countries subsequently extended such or other forms of protection to plant varieties, until in 1961, an International Convention for the Protection of New Varieties of Plants was signed. Most signatories were industrialized countries, who had also formed a Union for the Protection of New Varieties of Plants (UPOV). This treaty came into force in 1968.

The types of IPR Agreement covers following, distinct types of (intangible) property, for which Intellectual Property (IP) is coined, namely:

- Copyright (and related rights): the rights of performers, producers of sound recordings and broadcasting organizations.
- Trademarks (including Service marks).
- Geographical Indications (including appellation of origin), Geographical Indications (GIs) cover place names used to identify products, which have a particular quality or other characteristics because they come from that place. Under the Agreement, GIs are protected, as Agreement provides "indications which identify a good as originating in the territory of a Member, or a region or locality in that territory, where a given quality, reputation or other characteristics of the good is essentially attributable to its GIs" (Article 22).
- Obligations (under TRIPS) only relate to GIs that are protected in their country of origin.
- Industrial designs.
- Patents (including the Protection of new Varieties of Plants (PVP)).
- Patent gives a monopoly right [to patentee] to exploit the invention for a period of 17-20 years. Once a

patent is granted that patentee may give license [for the technology] to other individuals/companies.

- The Layout- designs (topographies) of Integrated Circuits and
- Undisclosed Information (including trade secrets and test data).
- Accordingly, depending upon the type of IP, the protection can be provided e.g. books, paintings and films come under copyrights; inventions can be patented and product(s) logos can be registered as trademarks; and so on.
- Inventions covered, under the Agreement, for purpose of protection must qualify following criteria:
 - they must be new, must involve inventive step(s), and are capable of industrial application.
 - In regard to the minimum standards, under the Agreement, each of the main element is defined namely: subject matter to be protected, the right(s) to be conferred, permissible exception(s) to those right(s), and the minimum duration of protection.

Plant varieties or breeders' rights (PVRs/PBRs) give the right-holder limited regulatory powers over the marketing of 'their' varieties. Till recently, most countries allowed farmers and other breeders to be exempted from the provisions of such rights, as long as they did not indulge in branded commercial transactions of the varieties. Now, however, after an amendment in 1991, UPOV itself has tightened the monopolistic nature of PVRs/PBRs, and some countries have substantially removed the exemptions to farmers and breeders.

Historically, plant varieties had been exempted from the international patent regime in deference to farmers' traditional practices of saving and exchanging seeds. Industrialized countries, however, have been debating on the issue of PBRs as a form of monopoly to encourage plant breeding activity. This culminated in the conclusion of the International Convention for the Protection of New Varieties of Plants (UPOV Convention) in 1978, which was amended in 1991, further strengthening the monopolistic hold of plant breeders. The parties to the UPOV Convention, included, until recently, mainly Organization for Economic Co-operation and Development (OECD) countries. The TRIPS Agreement now extends the requirement to protect plant varieties to all World Trade Organization (WTO) Member States.

In addition, in many countries, patents with full monopolistic restrictions are now applicable to plant

varieties, microorganisms, and genetically modified organisms. In 1972, the U.S. Supreme Court ruled that microbiologist Ananda Chakrabarty's patent claim for a genetically engineered bacterial strain, was permissible. This legitimized the view that anything made by humans and not found in nature was patentable. Finally, several patent claims have been made, and some granted, on human genetic material, including on material that has hardly been altered from its natural state?

Till very recently, these trends were restricted to some countries, which could not impose them on others. However, with the signing of the TRIPs agreement, this has changed. TRIPs requires that all signatory countries accept some 'effective' form of IPRs on plant varieties, either patents or some *sui generis* (new) version. TRIPs allows countries to exclude animals and plants *per se* from patentability. However, the provisions above have serious enough implications, for no longer are countries allowed to exclude patenting of life forms altogether (micro-organisms have to be open for patenting). Nor is there likely to be a great amount of flexibility in evolving *sui generis* systems of plant variety protection, for the term 'effective' may well be interpreted by industrial countries to mean a UPOV-like model.

The history of IPRs shows that the monopolistic hold of governments, corporations and some individuals over biological resources and related knowledge is continuously increasing. As the examples noted in the Introduction show, a substantial amount of this monopolization is built upon, and through the appropriation of, the resources conserved and knowledge generated by indigenous and other local communities.

The Intellectual Property Right in India

Under article 70.8 and 70.9 of the TRIPS agreement, India is obliged to amend its Patent Act to provide legal coverage to global inventions on pharmaceuticals and agro-chemicals in the form of product patents starting January 1, 2005. While the debate continues as to how best protect indigenous knowledge and provide for biosafety under TRIPs, foreign multinationals were pressuring India to adopt Exclusive Marketing Rights (EMRs) in the interim. India received an adverse judgment delivered by the Dispute Settlement Body (DSB) of the WTO on a case relating to pharmaceutical and agro-chemical products filed by the US and earlier by the EU. Now India has to amend its patent law before April 19, 1999 to comply with the DSB judgment. This has created an atmosphere of desperation in the government as law

makers hurry to adhere to the WTO deadline. In accordance with the TRIPs agreements, countries that do not provide for product patents before 2005 are required to provide a mailbox facility for receiving applications and grant EMRs to companies with patented products and marketing approval in any WTO signatory country prior to January 1, 2005.

The Rajya Sabha (Upper House of the Indian Parliament) passed the Patent (Amendment) Bill 1998 on 23 November, 1998, which provides for EMR's. The President of India promulgated the Patent (Amendment) Ordinance, 1999 (No. 3 of 1999) on January 8 that also provides for EMR's on pharmaceuticals and agri-chemicals. Ordinances immediately become law for the duration of 6 months. Thus, the Patent Ordinance has been approved in order to by-pass the patent system and grant EMRs as a statutory right to pharmaceuticals and agri-chemicals. The Patent Bill, however, which, if approved, would become an Act, is to come up for approval during the current Budget Session of the Lok Sabha (Lower House). EMRs essentially guarantee a monopoly market to "claimants" without means for review and rejection of biohazardous or biopirated products. Indeed, EMRs are a claim to marketing as a right, not an approved privilege. EMRs are granted to foreign companies merely on the basis of foreign patents, even if these foreign patents are based on the piracy of Indian indigenous knowledge, and can be used to establish market monopolies in India, thus destroying the socio-economic basis of survival a large number of India people. On the basis of biopiracy patents and patents granted in any other country after 1995, a corporation can claim exclusive marketing monopoly on formulations based on ginger, pepper, harrar, amla, etc. with only minor modifications in methods of extraction and processing. Further, since many of the plants we use for medicine are also used for food, EMRs on formulations based on indigenous knowledge will create monopolies on food items, raise prices, and thus undermine food rights and food security.

The Indian government has been supporting EMRs under the myth that they will promote scientific research in India. Since the EMR ordinance is for exclusive marketing rights in India on the basis of foreign patents and it by-passes the patent system, Indian Research and Development (R&D) will not be protected or enhanced. In fact Indian R & D budget will shrink as exclusive monopolies destroy the economy. The safeguards measure

as given under the Patent (Amendment) Bill 1999 or the Patent Ordinance 1999 is very vague and diluted. India has introduced a compulsory licensing provision to curb unduly price increases by MNC drug manufacturers. This gives the government the right to grant a license to produce drug to any company even if another company is given an EMR. However, compulsory licensing, as stands in the Bill and the Ordinance offers no safeguard since compulsory licensing applies to manufacturers, while EMR's are rights to sell. Compulsory licensing is therefore a fictitious safeguard. Interestingly, the US has already filed a complaint to the WTO against this illusionary provision of compulsory licensing.

Price control mechanisms on medicines or an India food item sold as medicinal formulations (e.g. ginger, haldi, pepper, etc.) will also not work, since EMR's will be granted as statutory rights in which government intervention will be treated as illegitimate. Once EMRs are granted, foreign corporations can not be forced to sell medicines and agricultural chemicals at cheaper prices. In fact, the whole point of EMRs is to be able to bypass the price regulation system already in place in the country, which ensures that the essential commodities of food and medicine are accessible to the people of the country, especially the poor. Therefore the claim of the government on the various aspects of safeguards are totally misleading and there are absolutely no safeguards available to protect the national interest in the EMRs system. Rather than adopt the EMR route, India should draft a new patent law that addresses the challenges of the age of biology. Strengthening the patent system allows for examination of foreign applications on the grounds of patentability and protection of environmental, human, and animal health and moral order. While EMRs will provide no protection from the introduction of biohazardous material and the perpetuation of biopiracy, a strict and strong patent law has the potential to guard the basic right of the Indian people to food and health from the pharmaceutical and agri-chemical MNCs.

IPRs vs. Biodiversity

The CBD has two interesting provisions relating to IPRs. One, Article 16.5 states that Contracting Parties shall cooperate to ensure that IPRs are 'supportive of and do not run counter to its (the CBD's) objectives'. However, this is 'subject to national legislation and international law'. Another, Article 22 states that the CBD's provisions will not affect rights and obligations of countries to other 'existing international agreements, except where the

exercise of those rights and obligations would cause a serious damage or threat to biological diversity'. Read together and in the spirit of the CBD, many people have said there is a basis for countering the runaway march of the IPR regimes described above. But in order for this argument to hold, the actual impacts of IPRs on biodiversity need to be examined. This is a difficult subject, for direct impacts are hard to perceive. However, the following aspects must be considered:

- Current IPR regimes have allowed industrial and commercial interests to appropriate the resources and knowledge of resource-rich but economically poor countries and communities, further 'impoverishing' them or excluding them from technological improvements.
- IPRs are likely to greatly intensify the trend to homogenize agricultural production and medicinal plant use systems. In agriculture, for instance, any corporation which has spent enormous amounts of money obtaining an IPR, would want to push its varieties in as large an area as possible. The result would be serious displacement of local diversity of crops (though of course IPRs would not be the only factor in this).
- Increasingly species-wide IPRs (such as those on transgenic cotton and soybean) could stifle even public sector and small-scale private sector crop variety development.
- Having to pay substantial royalties to industrial countries and corporations could greatly increase the debt burdens of many countries. This could further intensify the environmental and social disruption that is caused when debt repayment measures are taken up, such as the export of natural products.
- Farmers who innovate on seeds through re-use, exchange with other farmers, and other means, would be increasingly discouraged from doing so if the tighter regimes that UPOV 1991 sanctifies are imposed on their countries; these regimes would also increase the economic burden on farmers, further discouraging innovation.
- The ethical aspects of IPRs are serious, and to many communities and people the most important reasons for opposing current IPR regimes: the patenting of life forms (abhorrent to many traditional societies and modern conservationists because of its assumption that nature exists apart from, and solely for the use of, humans); the privatization of knowledge

(repugnant to many societies which held knowledge to largely, though by no means only, in the public domain); and others.

TRIPs vs. CBD

The TRIPs agreement is only likely to greatly intensify the impacts outlined above. In particular, its attempt to homogenize IPR regimes militates against a country's or community's freedom to choose the way in which it wants to deal with the use and protection of knowledge. Equally important, it contains no provision for the protection of indigenous and local community knowledge. Such knowledge, because of its nature, may not be amenable to protection under current IPR regimes. Finally, it has no recognition of the need to equitably share in the benefits of knowledge related to biodiversity. Indeed, it legitimizes the conventional inequities that have characterized the interactions between the industrial-commercial use of biodiversity-related knowledge, and the community/citizen use of such knowledge.

The negative impacts of TRIPs on the three objectives of the CBD are already beginning to be felt, or threatened, in some countries. There is an urgent need to explore whatever spaces are available within existing regimes, to counter these threats, and to examine alternative regimes which have conservation, sustainable use, and equitable benefit-sharing built into them.

TRIPs vs. CBD in India

India is currently considering two laws to follow up TRIPs and CBD: the Plant Varieties and Farmers' Rights (PPV&FR) and the Biological Diversity Act (BDA), respectively. The PVPFR is supposed to be India's *sui generis* plant variety protection regime (as per Article 27(3)b of TRIPs). The Biodiversity Act (BDA) on the other hand, is being conceived as a law to implement the CBD provisions in relation to access to genetic resource and sharing of benefits from use of such resources. However, in several ways these proposed laws are not in harmony:

- The Biological Diversity Act (BDA) provides for the protection of local community rights in a broad sense, and recognizes that members of the local community, acting through the Biodiversity Management Committees at the local level, shall be consulted before biological resources and the knowledge and information of the community pertaining to the same is accessed. The PVPFR, however, contains only a narrow definition of farmers'

rights (the right to reuse, exchange, and sell except as branded product) protected plant varieties; it does not provide for the protection of farmers' own varieties (which are unlikely to pass the stringent tests of novelty, distinctiveness, etc.) but rather focuses on benefiting formal sector plant breeders.

- Whereas the Biological Diversity Act (BDA) explicitly provides for benefit-sharing measures with local communities, the PVPFR has no such provision.
- The BDA also puts in place a mechanism for Prior Informed Consent (PIC) of the concerned authorities, and in consultation with the affected local PVPFR however does not contain any provision mandating PIC when varieties developed by farmers are accessed for research and commercial purposes. Its provision enabling claims by farmers and communities to claim compensation upon proving they had made a 'significant contribution' to the variety granted protection under the Act, represents an unfair deal for farmers. In effect, it puts in place the grounds for an unfair legal battle between a large breeding corporation with economic and legal resources, and a farmer/farming community who is at a distinct economic disadvantage?
- The BDA attempts to include local community representatives at various levels of decision-making and has provisions to the effect that the decision making authorities at the state and national levels shall consist of representatives of local communities. The PVPFR, however envisages a bureaucratic management structure with no representation from local farming communities or NGOs;
- Whereas the BDA requires impact assessments of proposed projects that are likely to have adverse impact on biological diversity to ensure that they are in harmony with biodiversity conservation and sustainable use, the PVPFR does not require any such assessments for plant variety protection applications.

Though essentially favouring the further expansion of current IPR regimes, there are some provisions in TRIPs that can be exploited by communities and countries interested in protecting their interests against those of dominant industrial-commercial forces:

- Article 8 allows for legal measures to protect public health/nutrition, and public interest; though environmental protection is not explicitly built into this, it could be justified as being in 'public interest'.

Unfortunately, this clause is subject to 'the provisions of TRIPs', which leaves wide open the interpretation of its applicability.

- Article 22 allows for the protection of products which are geographically defined through "geographical indications". This could help protect some products which are known by the specific locations in which they have originated. It is debatable whether, for instance, Basmati rice could have been protected in this manner (the name does not derive from any location, but the variety is known to come from a particular geographical area). Countries like India already has domestic legislation on this.
- Article 27(2) allows for exclusion, from patentability, inventions whose commercial use needs to be prevented to safeguard against 'serious prejudice' to the environment. This is somewhat convoluted, because a country will first need to determine such serious prejudice, justify the prevention of commercial use, and then only be able to justify non-granting of patents.
- Article 27(3) allows countries to exclude plants and animals from patentability, and also plant varieties, so long as there is some other 'effective' form of IPR to such varieties. As mentioned above, what is 'effective' is likely to be determined by powerful countries, in which case the almost patent-like regime being advocated by UPOV could well be pushed. However, an exceptionally bold country could well experiment with completely different *sui generis* systems, and face up to any charges that are brought against it at WTO.

As mentioned above, both Article 16(5) and Article 22 provide countries with some maneuverability with regard to IPRs. If indeed a country can establish that IPRs run counter to conservation, sustainable use, and/or equitable benefit-sharing, it should be justified in excluding such IPRs. However, the caveat 'subject to national legislation and international law' may well make this difficult, since TRIPs is also 'international law'. Between TRIPs and the CBD, which holds legal priority? Legal opinion would perhaps be that TRIPs, being the later treaty, would supercede CBD in case of a conflict. However, given that CBD deals much more with the protection of public interest and morality, which TRIPs acknowledges as valid grounds for any measures that countries want to take, it could be argued that CBD's provisions should supercede those of TRIPs. This interface has not yet been

tested in any active case in the international arena; only when it does, will we know what interpretation is likely to hold. The CBD, unfortunately, is at a serious disadvantage as it does not yet have a dispute resolution mechanism of its own, unlike the WTO.

Perhaps the most crucial provision within CBD may be Article 8j, which requires countries to respect and protect indigenous and local community knowledge, ensure that such communities are asked before using their knowledge for wider society, and further ensure the equitable sharing of benefits arising from such use. Built into this provision are the seeds of a radically different vision of protecting knowledge and generating and sharing benefits from it. Discussions within the CBD forums, including at successive Conferences of Parties (CoPs), have demonstrated this potential, especially since a wide range of indigenous and local community groups have used the forums to push their case.

Under the changing IPR Regimes, a combination of the relevant clauses in TRIPs and the CBD, can be used to argue for modifications in existing IPR regimes which can help to safeguard public interest. Many people have argued, for instance, that apart from the usual criteria of novelty, etc. that are required of an IPR applicant, the following should also be sought as part of the application:

- Source (country/community/person) of the material or information that has gone into the produce/process for which an IPR is claimed;
- Proof of prior informed consent from the country and community of origin;
- Details of the benefit-sharing arrangements entered into with the community of origin, wherever applicable.

Countries like India have also suggested that all IPR applications, which are related to biodiversity and biodiversity-related knowledge, should be posted on the Clearing House Mechanism (set up under the CBD), giving concerned countries and communities/persons an opportunity to object if they feel that their rights have been violated. These suggestions have, of course, not yet been accepted at an international level, but are being built into some domestic legislation.

A number of NGOs and individuals have advocated various forms of intellectual rights regimes which recognize the essentially community-based nature of a lot of biodiversity-related knowledge. At an international level, for instance, an alternative to UPOV has been

suggested by Indian NGOs Gene Campaign which focuses equally on farmers' and breeders' rights. There have also been suggestions for recognition of concepts such as Traditional Resource Rights, which encompass not just intellectual but also physical resource and cultural rights. Countries like the Philippines are attempting to try such regimes, though the experience is far too short to make any judgments of their efficacy. In addition, WIPO and other international agencies are also studying the possibilities of protecting indigenous and local community knowledge through alternative regimes.

The power invested under TRIPs in the 'Dispute Settlement Body' and the 'TRIPs Council' over-ride the jurisdiction and mandates of CBD and Biosafety Protocol (BP), as also the Convention on International Trade in Endangered Species (CITES), ILO Conventions (1957/107; 1989/169) dealing with the protection of the rights of indigenous people and local communities, the Declaration of the UN's Economic and Social Council (ECOSOC) on the rights of indigenous peoples (especially resolutions 1990/27 and 1991/31) and FAO's international undertaking on plant genetic resources. This power can nullify concepts and principles which are essential for sustainable development and environmental quality, and which were achieved after several rounds of international deliberations: The concept of sovereignty, the 'precautionary', 'internalising' and 'polluter-pays' principles, and equitable benefit-sharing of genetic resources. Several agreements within WTO, particularly TRIPs (Article 27(3)b), directly or indirectly, affect biodiversity conservation.

With respect to intellectual property, TRIPs (Articles 3 and 4) requires member-states to observe the principles of 'national treatment' and 'most-favoured nation'. Of seven forms of intellectual property protection (copyright, patenting, plant variety protection, industrial design, geographical indications, lay-out design of integrated circuits, and trade secrets) the three most important for biodiversity and biosafety are patents, Plant Variety Protection (PVP) and geographical indications. Article 27 of TRIPs sets the framework of the patent regime while Article 31 provides for compulsory licensing. Indian Parliament has already passed the 'Protection of Plant Varieties and Farmers' Rights Act 2001', following the provisions of UPOV. Since the emergence of the WTO regime, three Articles of CBD have assumed greater relevance: Article 8(J) which relates to the preservation and maintenance of traditional knowledge systems of

local communities, through equitable sharing of benefits; Article 16 covering the whole issue of access to and transfer of technology including biotechnology; and Article 15.1 pertaining to the rights over genetic resources.

Indigenous and Local Community Rights

Article 8 (J) imposes a major responsibility on nations to establish a critical balance between biodiversity conservation and the protection of the rights of the indigenous and local communities. The debate on Intellectual Property Rights (IPRs) and on Article 8(J) took an interesting turn at the fifth meeting of the Conference of Parties (nations), at Nairobi in May 2000, with the Working Group II recommending the continuous involvement of indigenous people while the intellectual regime was being implemented. It also called for, *inter alia*, the full and direct participation of indigenous and local communities including women; recognition of the collective dimension of indigenous knowledge and the issues related to Mutually Agreed Terms (MAT)/Prior Informed Consent (PIC); and direct involvement of indigenous technical experts. The report recommended that parties support the development of traditional knowledge registers, recognized that the maintenance of such knowledge requires maintenance of cultural identities and the material base, and emphasised the need for indigenous and local communities to control and determine MAT/PIC arrangements so as to make informed decisions. The Working Group set out a two-phase approach for implementation. The first phase includes tasks that address participatory mechanisms, strategies and trends, benefit-sharing, exchange and dissemination of information, and other legal elements. The second phase would include participatory processes for conservation and systematic use, and other monitoring elements.

Access to and Transfer of Biotechnology

Article 16 covering 'Access to and transfer of technology' particularly emphasizes that transfer of technology should be provided and/or facilitated under fair and most favourable terms. In the case of patents and other property rights, such access and transfer are to be provided only after honouring IPRs. It further stipulates that measures be taken at the policy level to ensure that the private sector facilitates access to joint development and transfer of technology, subject to national and international laws.

Access to Genetic Resources

Article 15 on access to genetic resources provides a framework for establishing that States have sovereign

right over their natural resources. It says that access to genetic resources shall be subject to the PIC of the Contracting Parties providing such resources. PIC is an important mechanism as it ensures community participation in decision-making. The royalty-sharing experiment between the Kani tribe and the Tropical Botanical Garden and Research Institute (TBGRI), Thiruvananthapuram (Kerala), is an example of this.

Points of Conflict

The points of conflict are:

- a) Recognition of national sovereignty under the CBD implies that countries have the right to prohibit IPRs on life forms (biological resources). TRIPS overlooks this right by requiring the provision of IPRs on micro-organisms, non-biological and microbiological process, as well patents and/or *sui generis* protection on plant varieties.
- b) The CBD gives nations a legal basis to demand equitable benefit sharing arising from the use of biological resources and associated traditional knowledge, practices and innovations. TRIPS negates the broad historical contributions made by the communities in the IPRs regime and establishes the monopolistic control of the patent holder. Thus, there will be no legal synergies between these two sets of rights, and
- c) The CBD gives Parties legal authority to provide access based on PIC and MAT to biological resources. TRIPS ignores this authority. d) The CBD places public interest and common good over private property and vested interest. TRIPS does the opposite. To deal with this conflicting situation, CBD must be fully developed as an effective international instrument if it is to promote the sustainable use and conservation of biodiversity, based on community control of resources.

For example, since the WTO has an effective dispute redressal system, there is an urgent need for the establishment of a similar system under the CBD in the light of Article 22 (1) that states that the provisions of CBD 'shall not affect the rights and obligations of any party deriving from any existing international agreement except where the exercise of those rights and obligations would cause a serious damage or threat to biological diversity. This would bring the CBD at par with the WTO Agreements *vis-à-vis* biodiversity conservation and the sustainable use of biological resources.

Taking into account the precautionary approach, the objective of the Biosafety Protocol, under the CBD, is 'to contribute to ensuring an adequate level of protection in the field of the safe transfer, handling and use of Living Modified Organisms (LMOs) resulting from modern biotechnology that may have adverse effects on the conservation and sustainable use of biological diversity, taking also into account risks to human health, and specifically focusing on trans-boundary movements' (Article 1). Surprisingly, the definition of LMO (Article 3) does not include 'product thereof' and as such these would be internationally unregulated. However, 'the protocol shall apply to the trans-boundary movement, transit, handling and use of all LMOs that may have adverse effects... 'in accordance with its objectives (Article 4), and exclude LMOs which are pharmaceuticals (LMO-P) for human uses and are covered by other international agreements or organizations (Article 5). LMOs intended for direct use as food, feed or for processing have also been excluded from the regular Advanced Informed Agreement and risk assessment (Article 7.2), but alternative procedures have been set.

GATT

Three major provisions of the WTO, if narrowly interpreted, may have serious implications for the implementation of Biosafety Protocol (BP). GATT provides justification for trade barriers that are necessary to protect animal and plant life and health, and relate to the conservation of exhaustible natural resources. Using these provisions, Trade Related Environmental Measures (under GATT) may be invoked as per the requirement of BP. However, the existing GATT panel has not taken measures comparable with the biosafety measures involving questions of scientific uncertainty, ethical and socio-economic considerations, and the diverse levels of risk-awareness in different WTO Parties.

Sanitary and Phytosanitary Measures

The Agreement on Sanitary and Phytosanitary Measures (SPS) under WTO has refined the rights and obligations of the Parties while adopting measures to protect human, animal and plant life, and health risks arising from the introduction of food, disease-carrying or disease-causing organisms, including the entry and establishment of pests. It is to be noted that Article 2 (2) of the SPS requires parties to base their SPS measures on scientific principles and not to maintain these without sufficient scientific evidence. This means that the importing countries might

not accept the safety measures which are adopted by exporting countries in the absence of scientific certainty. Besides, the LMO labelling scheme could still be defended by the importing countries as it would not create 'arbitrary or unjustifiable discrimination', or represent a 'misguided restriction' on international trade.

Technical Barriers to Trade

The Agreement on Technical Barriers to Trade (TBT) aims to ensure that parties do not use domestic regulations, standards, testing and certification procedures to create unnecessary obstacles to trade.

- It has been designed to prevent arbitrary standards from being used to protect industries from foreign competitors. It encourages international standards that producers must comply with to gain access to different markets.
- The TBT agreement includes obligations relating to the preparation, adoption and application of technical regulations and standards, and the procedures for assessing whether the products conform to these regulations and standards. The agreement also imposes requirements for labelling of products.
- It is to be seen how countries not party to the CBD and the BP use these WTO agreements from the perspective of biosafety concerns. The preamble of the Biosafety Protocol reflects the compromise reached at Cartagena in May 2000.
- As the preamble is weaker than the text agreed upon earlier in Miami, the substantive articles are also rendered vulnerable to misuse due to the specific provisions in the protocol that refer to other international obligations.

Apart from the specific points of conflict between the CBD and the WTO, there are broader issues of lack of compatibility between the various WTO agreements and the CBD, including the Biosafety Protocol. These include:

- The enhancement of global trade through implementing the WTO Agreements may aggravate the unsustainable use of biodiversity, which is contrary to the objectives of CBD.
- The increased transportation activity and infrastructure development to promote global trade may have an adverse impact on the functioning of ecosystems, which could result in biodiversity losses.
- The trans-boundary movement of biological products, including LMOs in trade may result in the accidental

introduction of alien species which may lead to destabilization of native species.

- The liberalization of trade and investment may intensify the direct and indirect adverse impacts on biodiversity and the supporting habitats.
- The WTO agreements may interfere with the international/ national subsidies as incentives to the industry, or with conservation laws and policies which seek control of traded goods.
- Moreover, built into the WTO agreements are various policy interventions for trade enhancement which may completely ignore the cost required for maintaining the environmental functions of the major habitats, thus, resulting in unsustainable production or trade in certain sectors.

Resolving the Conflicts

If the WTO Agreements and the CBD (inclusive of the Biosafety Protocol) are to be implemented in the interest of human survival and well-being, urgent measures are required to be taken to ensure that the objectives of CBD are not undermined by the narrow agenda of WTO Agreements, particularly of TRIPS. These measures would include: First, that nations recognize and affirm in law the primacy of the CBD over the TRIPS in the areas of biological resources and traditional knowledge systems. Second, the collective rights of indigenous and local communities to freely use, exchange and develop biodiversity should be recognized as a priori rights and be placed over and above private intellectual property rights. This has to be reflected in legislation and public policy at the national level. Third, the implementation of TRIPS in developing countries should be challenged so as to make these compatible with the provisions of the CBD. Fourthly, during the review of TRIPS, it should be ensured that there is an option to exclude all life forms and related knowledge from the IPR system.

If such measures are taken by the parties concerned, the Convention on Biological Diversity and the Biosafety Protocol could provide an innovative approach to the interface of trade and environmental concerns, and set a precedent for 'sustainable trade agreements' so that the potential value of biological resources can be optimised on an equitable basis for the welfare of human beings.

Gender Implications of TRIPS

Viewed from the point of women who are poor and are struggling with issues of sustainable livelihoods in farming

and other sectors of the economy, the fundamental issues in the intellectual property rights debate are fourfold:

- One basic challenge is access to affordable medicines – for HIV/AIDS, infectious diseases and reproductive health. HIV/AIDS and infectious diseases impact upon women on multiple levels. They ravage the body of the usually under nourished women (a problem linked to underlying customary practices regarding the distribution of food between boys and girls, men and women within families), with significant implications for women's morbidity and mortality. Furthermore, these diseases increase women's caretaking burden in the home and community.
- The second set of challenges that TRIPS poses for women is around access to seeds for food production, food security and adequate nutrition.
- The third set of challenges is access to, and control of, land; the use of natural and genetic resources; and access to technology and fertilizer for improving the chronically low productivity of women farmers.
- The fourth TRIPS-related issue is the level of the recognition of, and compensation for, traditional and local knowledge among women as compared to men.

A patented and more access restrictive IPR world is likely to exacerbate women's relatively restricted condition in subsistence farming and increase their poverty. Undeniably, women, more than men, experience barriers in accessing credit, land and technology. This, coupled with the trend in trade reform of removal of subsidies and the general deteriorating conditions for local agricultural production, is bound to worsen the plight of women in subsistence farming further. IPRs also pose other more direct threats:

- The patenting of seeds and micro-organisms, which is associated with a significant rise in the cost of farming inputs;
- The increasing privatization of genetic resources and agricultural knowledge, some of which is occurring via biopiracy and bio-prospecting;
- The trend towards the concentration of farming in the hands of wealthy farmers and multinational corporations (MNCs). This is a phenomenon that is partly due to the rise of industrial agriculture, but is likely to be exacerbated by TRIPS which can bring about the monopolization of knowledge and resources in the areas of agriculture, medicines and pharmaceuticals.

1) *Resource-Poor Farmers*

Patents on seed and microorganisms such as algae, bacteria and fungi increase the cost of seed and fertilizers. Increasingly, many of the inputs needed for farming must be obtained in the market. Patents and more expansive breeder rights encourage restrictions on the exchange, use or sale of seeds by farmers. This puts resource-poor farmers, many of whom are women, at a severe disadvantage. Given existing disparities between women and men's access to cash and credit, which are necessary to facilitate the purchase of fertilizer and seed, women farmers tend to have a higher risk of falling into chronic indebtedness. Male farmers, as a group, tend to have greater access to cash and credit. Men also tend to plant hybrids as a cash crop). Such crops not only require extensive and intensive land use, including the application of pesticides, but also are often very labour intensive. The impacts on women are twofold: in many cases, they lose access to fertile land for their own production, and their labour is also relied upon for weeding and other tasks. Not only is their workload increased, but they also suffer greater exposure to pesticides.

2) *Rising Expenses of Farming*

In the context of women's already weak or non-existent ownership and insecurity of land tenure, the rising expenses of farming are likely to severely compromise the livelihood of women farmers and increase their marginalization and impoverishment. Protection of plant varieties (PPV), which is urgently framed in terms of the rights of commercial breeders, will affect female and small farmers' access to germplasm as well as to scientific knowledge. Through its focus on monoculture, PPV will tend to retard diversity in plants and thus have an adverse impact on biodiversity with important consequences for local food security, including decreased nutrition. Biodiversity is also critical to the survival and future growth potential of women farmers who have little access to mechanized tools, equipment and chemicals to manage and manipulate the soil, create and divert streams of water, and improve crop yields. Biodiversity helps in the promotion of soil fertility, and soil conservation and management, as well as affecting the nutritional content of plants and agricultural output. Women have been critical in the maintenance and

preservation of biodiversity in many communities for centuries.

3) *Protecting Traditional Knowledge*

Central to this issue is the nature and kind of protection provided for traditional knowledge in terms of recognition of the contribution of female and male farmers, and the nature of provisions for benefit sharing and prior consent. To what extent do these take account of women's inventions and contribution to natural and genetic resource management? Who is consulted in establishing benefit sharing and prior consent agreements? What is the process for enhancing the traditional knowledge of men and women? This is a particularly difficult area. The wider issue of whose consent is asked for, and who gains or loses from the privatization of collective knowledge, is related to the role and contribution of women, as well as the structural and social limitations they face within the formal and informal agricultural sector. It is normally the case that women have a triple burden in undertaking the traditionally prescribed role of caring for children and the elderly, engaging in food production as well as household duties and carrying out the tasks of enhancing, developing and transmitting agricultural knowledge and know-how in the community. Yet this is often not recognized, acknowledged or compensated for in models for protecting traditional knowledge or in benefit-sharing agreements.

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Managing Rice Biodiversity by Smallholder Farmers: A Case Study in Barak Valley, Assam

Tapasi Das and Ashesh Kumar Das*

Department of Ecology and Environmental Science, Assam University, Silchar-788 011, Assam

The indigenous rice germplasm of North-East India represents a wealth of valuable genes, which is threatened with the introduction, and popularization of high yielding varieties. As such there is an urgent need to inventorise the indigenous rice varieties and examine the role of traditional farming systems in the on-farm conservation of agrobiodiversity. In this paper, an attempt was made to study the on-farm conservation strategy of rice diversity by smallholder farmers and the traditional farming practices in a village Dorgakona (24°4'N latitude and 92° 41'E longitude) in Barak Valley (South Assam), North-East India. An inventory of rice diversity was made and a total of 12 traditional cultivars were recorded from the study site. Since farmers on the basis of their local knowledge shape the crop diversity, an attempt was made to examine the role of farmers' traditional knowledge in the maintenance of rice diversity. The present study indicates that farmers in Barak Valley still cultivate traditional varieties and modern varieties have not been successful in completely replacing them. The study reveals that the farmers in more fragile ecosystems maintain more crop diversity to adapt to the heterogeneous environment. Also smallholder farmers are the main preservers and managers of agrobiodiversity, and the traditional ecological knowledge and the heterogeneous environment are the main factors determining the diversity and conservation of local paddy land races.

Key words: Rice diversity, Traditional knowledge, Farmers' seed bank, Conservation

India is very rich in its rice germplasm reserve and the existence of 50,000 accessions have been estimated so far and 17,000 rice cultivars have been assembled in Madhya Pradesh State alone (Richharia, 1979). However in recent decades, the green revolution of modern, high yielding varieties of crops has displaced the vast mosaic of traditional crop varieties (Maheswari, 1997). Rice is the principal crop for the people of North-East India. The indigenous germplasm of North-East India represents a wealth of valuable gene systems (Sharma *et al.*, 1971). The heterogeneity in the environmental, conditions and cultivation of crops in three rice growing seasons has resulted in a large diversity of crops in the region (Das and Ahmed, 1995). Traditional farming systems are still widely practiced in North-East India including Barak Valley of South Assam. Traditional farming systems are important *in situ* conservation sites of crop diversity. According to the United Nations Convention on Biological Diversity *in situ* conservation is "the conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural surroundings, and in the case of domesticated or cultivated species, in the surrounding where they have developed their distinctive properties". Traditional farming systems not only serve to preserve the diversity of local varieties but also the human knowledge and

behavioral practices that have shaped this diversity (Bellon, 1996). In accordance with the Convention of Biological Diversity Article 7,8 and 10(c) the inventorisation of such areas can help in the identification and conservation of biodiversity while assessing the sustainability of the system. Small scale farmers in such farming systems have been known to retain folk varieties also known as landraces and continue to grow them even as they experiment with and adopt modern high yielding varieties (Bellon, 1996). The need for systematic collection of rice landraces and its wild relatives from the unexplored areas in the North-East India (Hore and Sharma, 1991; NBPGR, 1999; Paroda and Malik, 1990) and the need for on-farm conservation were emphasized by Hore (1999) and Kothari (1997). The inventorisation and collection of rice germplasm in North-East India can serve to preserve the indigenous rice cultivars while assessing the impact green revolution had on the rice diversity of the region. In the present paper, attempt was made to inventorise the rice varieties cultivated with special importance given to local landraces and investigate the role traditional ecological knowledge of the small holder farmers, had in managing and conserving the agrobiodiversity of Barak Valley, Assam.

Material and Method

The study was carried out in a village Dorgakona (24°41'N latitude and 92° 41'E longitude) of Cachar

* Corresponding author's E-mail: asheshdas@sancharnet.in

district of Barak Valley, Assam, North-East India. The rice farmers in this area are basically tea labours and small holders. The valley has an undulating topography characterized by hills, hillocks (locally known as *tillah*) wide plains and low-lying waterlogged areas (locally called *beels*). The study area experiences a warm humid climate with a mean annual rainfall of 2660 mm, most of which is received from May to September. The temperature ranges from a minimum of 11°C (January) to a maximum of 32.6°C (August).

The management of agrobiodiversity through cultivation of paddy landraces was studied by primary interaction with 30 farmers through schedule method (Bellon *et al.* 1997; Chambers and Thrupp, 1989) and periodic visit to the farmers' field. Rice germplasm collected from the study area were sent to NBPGR Headquarters to obtain IC Number. Relative importance value of rice varieties was computed on the basis of percent land area occupied by each variety and percent farmers cultivating the variety (Bellon and Brush, 1994).

Results and Discussion

Traditional Farming Practices

Rice is traditionally grown in the study area in three well defined seasons- Sali (winter rice), Aus (autumn rice) and Boro (summer rice). The traditional cultivation methods of rice in the area include sowing, transplanting, harvesting and storage (Fig. 1). First stage in this system involves preparing the seed bed and raising rice seedlings in nurseries. In the second stage preparatory operation of land for transplantation is done, which involves flooding the land and then ploughing (*haal chaash*) with oxen or buffaloes using traditional implements (*haal/langol*) followed by leveling with ladder (*moi*).

Ploughing is repeated several times (4-5) in order to incorporate crop residues and bury weeds. Where the soil is deep and soft, and land preparation cannot be done by animals, preparatory operation is done manually by hoe (*kudaal*). In the third stage the seedlings are transplanted (*haali rua*) after 4-5 weeks into puddled field carrying 5-10 cm water. Transplantation involves thrusting the seedling of 3-6 into holes made by the hand and is usually done by female members of the family. Finally after 3-4 months, the harvesting (*dhaan kaata*) is done by sickles, and then the separation of grains or mounding (*maara*) is done by animals. Grains are winnowed by bamboo implements (*daala*) and stored as seed in traditional storage systems (*Ugaar/Dol/Machan*) or processed for consumption. The straw separated from grain is stored for fodder.

Farmers' Management of Rice Diversity

A total of 25 rice varieties cultivated in the three cropping seasons were recorded in the area. Of these, 20 were farmers' varieties and the rest were modern varieties. Farmers' varieties include crop populations, which farmers have identified and named as units (Lando and Mak, 1994). Farmers mostly grow traditional varieties in the three rice growing seasons. Of the 25 varieties recorded, 12 are traditional varieties covering an area of 15.47 ha, which is more than 50 per cent of the total area. This indicates the local availability of wide indigenous diversity to farmers. The large diversity of rice is managed by the farmers as an adaptive strategy to cope with heterogeneous and uncertain ecological and socioeconomic environments, including different soil types (Das and Das, 2004). Similar reports indicating the dominance of traditional varieties have been made by other workers (Table 1). Of the three cropping seasons,

Table 1. Farmers' management of rice diversity in asia

Country	Rice ecosystem	Sample size	Varieties			Average farm size(ha)
			Traditional	Modern	Average/farmer	
Cambodia						
Lando and Mak, 1994	Rainfed Lowland	17	9	2	1.7	1.1
Malaysia						
Lambert, 1985	Swamp	28	32	0	3.0	0.53
Thailand						
Dennis, 1987	Rainfed Lowland	20	2	1	1.3	0.86
Orissa						
Kshirsagar and Pandey, 1996	Rainfed Lowland	50	33	14	4.7	1.30
Barak Valley, South Assam, N.E. India.						
Paul 2003	Rainfed Lowland	30	31	7	5.07	2.37
Barak Valley, South Assam, N.E. India.						
Das and Das, 2004	Rainfed Lowland	50	25	7	3.4	0.91



Ploughing of paddy field



Transportation of rice seedlings for transplantation



Transplantation of rice seedlings



Harvesting of rice



Mounding of rice by bullocks



Manual separation of grain from straw after mounding



Winnowing of mounded grains



Drying of grains in field

Fig. 1: Traditional rice farming practice

Sali is the most important cropping season in the area and it coincides with the Harvest festival (*makar sankranti*). It is sown in July-August and harvested in November- December. Larger number of rice varieties is cultivated in this season (20), of which 10 are traditional varieties. The relative importance value for rice varieties in the Sali cropping season (Fig. 2) shows that the *Chhatoki* variety dominate the rice area. This variety occupies larger land area (17.05%) and is cultivated by larger number of farmers (50%). Of the other traditional varieties *Chhoeamara* occupies the second position. These two varieties are highly preferred because of their stress tolerant and eating quality. Farmers cultivating modern varieties were also found to cultivate a traditional variety to spread the risk of crop failure, which was reported by farmers to be often associated with the high yielding varieties.

The diversity of traditional varieties is still maintained by the farmers because of their agromorphological characteristics and traditional ecological knowledge base (Table 2). Traditional cultivars are still popular for their palatability and reliable yield performance even under low input conditions (Shiva et al., 1995). Traditional varieties such as *Chhatoki*, *Chhoeamara* and *Khoibaruah* have red kernel and are highly preferred because of their rich taste and high nutrition content. Varieties such

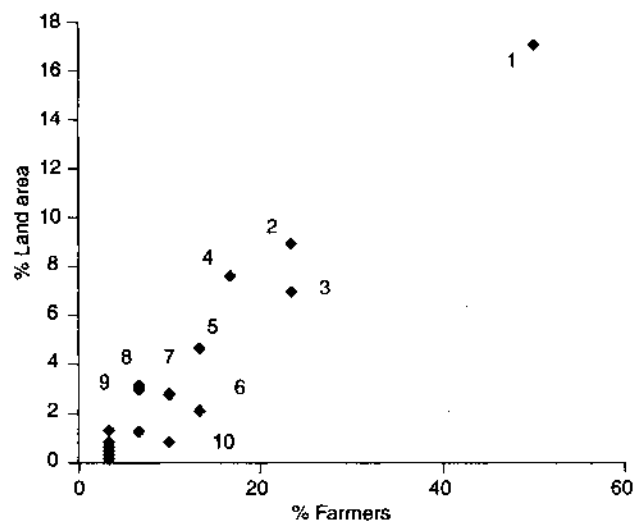


Fig. 2: Relative importance of rice varieties (1) *Chhatoki*, (2) *Nagrasail*, (3) *Chhoeamara*, (4) *Badaal*, (5) *Ranjit*, (6) *Latoi*, (7) *Terabali*, (8) *Ikorjali*, (9) *Irri*, (10) *Birain* Others: *Kartika*, *Pankaj*, *Moinahaal*, *Krishna*, *Baigon Bichi*, *Kualijira*, *Balam*, *Ranjit*, *Aizong*, *Pakhi Biroen*

as *Birain* and *Pakhi Birain* are used in the preparation of rice flakes, while *Chhoeamara* is used for preparation of puffed rice. Certain varieties such as *Bashphool* and *Kaalijira* are also preferred for their scented aromatic character. Many traditional varieties find use as indigenous medicine. Varieties such as *Baigon Bichi* are used to

Table 2. Characteristics of Important Rice Varieties

IC No.	Vernacular name	Important characteristics
IC-311452	Latoi	Fat rice, tasty, moderate yield, high fodder value, can grow in any type of soil.
IC-311453	Mayamati	Scented sweet rice, red kernel, medium fine rice, good yield. Less pest, can grow in any soil.
IC-311454	Chhatoki (lal)	Red kernel, fat rice, good yield, less Pest, tasty, high fodder value, can grow in any type of soil.
IC-311456	Chhoeamara	Red kernel, fat rice, sweet and tasty rice, less pest, yield moderate, shattering quality high, fodder value very high, can grow in any type of soil.
IC-311458	Lal Kartika	Medium fine rice, good yield, can grow in sandy soil.
IC-311459	Moinahaal	Medium fine rice, scented, tasty, less pest, good yield, can grow in moist fertile soil.
IC-311461	Terabali	Very fine rice, yield good, less pest, commercial value high, can grow in athali + batu soil.
IC-311462	Balam	Round fat rice, yield high, can grow in athali soil.
IC-311464	Kaalajira	Very small and fine scented rice, medicinal, yield good, very high commercial value, can grow in athali type soil that is less fertile.
IC-311466	Baigon Bichi	Very small fine rice, yield good, medicinal value, can grow in clayey soil
IC-311467	Berapua	Scented fine rice, cultivated for religious purpose, medicinal, high commercial value, pest resistant, can grow in moist blackish soil.
IC-311468	Kaala Birain	Red kernel, fat rice, used in festivities for pancakes and rice flakes, can grow in athali soil.
IC-311469	Lal Birain	Red kernel, tasty and fat rice, yield good, used in festivities for pancakes and rice flakes, can grow in athali soil.
IC-311470	Puthi Birain	Tasty fat rice, used for making traditional chungu pitha, pancakes and rice flakes, can grow in moist athali soil.
IC-311471	Pakhi Birain	Red kernel used in festivities, can grow in kaala type soil.
IC-408350	Khoibaruah	Presence of long awn in grain, difficult to mound because of awn, long grain, fine rice, red kernel, tasty, yield good, grown in poli/athali soil, old and popular boro variety.
IC-408354	Bashphool	Small blackish grain, fine rice, increases on cooking, yield good, cultivated in poti type soil.

revive sick people. The potent medicinal value of the variety and the resultant high commercial value is an important factor in farmers' decision to cultivate the variety. Also mentionable is the variety '*Berapua*' which is rare in the village and has high commercial and medicinal value besides being of religious importance. Another such instance of cultivation of medicinal rice with commercial value (*Navara*) has also been reported from Malabar, Kerala (John and Nizar, 1998). Traditional varieties such as *Kartika* have religious significance and are used as offerings during sacred ceremonies. Certain traditional varieties (*Terabali*, *Kaalajira*) are still retained by the farmers because of their high commercial value. Farming is predominantly subsistence based and farmers rarely sell rice but prefer to retain certain costly varieties to provide a source of cash in times of emergency.

Farmers reported that traditional varieties show superior performance in terms of pest resistance, flood resistance and show better adaptation to the variable production environment. Farmers' selection of traditional varieties is based on its performance in the field, its yield and its tolerance to stress. Farmers in the study area have a deep knowledge about the characteristics of the traditional varieties and its performance under different environmental stresses. Based on their knowledge and preferences they continue to match cultivars to different environmental conditions in the field while discarding varieties with inferior value for a particular set of qualities such as yield, adaptation to soil quality etc. In this context farmers reported two varieties *Chhatoki* and *Chhoeamara* to be the most stress tolerant. The fact that traditional farmers have a well documented knowledge of their crops and crop varieties has also been well documented by human ecologists, anthropologists and ethnobiologists (Bellon, 1991). Farmers informed that they often have fragmented land holdings with differing soil types and the soil in the village is predominantly of poor quality which favours the selection of traditional varieties in relation to their indigenous soil knowledge. Brush (1995) also observed that farmers keep local landraces in fields that are relatively marginal and characterized by poorer soils. The yield from traditional varieties are low but farmers still continue to cultivate them, even as they adopt newer varieties, because compared to modern varieties the yield from traditional varieties are reliable and prevents the risk of yield failure (Harwood, 1979). The traditional varieties can serve as important source of genes for

developing improved varieties. In this context it is mentioned that IR-72 a modern variety of rice was developed by cross breeding 22 landraces (Maheshwari, 1996). Certain traditional varieties (*Terabali*, *Kaalajira*, *Baigon Bichi*) were found to be on the verge of extinction due to the displacement and replacement of varieties by farmers.

Traditional Seed Flow and Farmers' Seed Bank

Farmers' selection and management of crop diversity shape the crop genetic diversity. An important aspect in the management of crop diversity is the seed flow and traditional seed storage systems (Fig. 3). Several studies have documented the flow of seed of different varieties among small farmers (Sperling and Loevinshon, 1993). According to Pratap and Sthapit (1998) traditional seed supply systems are vital to the sustainability of subsistence farming and to the conservation of seeds of a variety of native crops and landraces. Seed flow in the area especially for land races happens as farmers exchange seeds among themselves within the same village, purchase seed from market or collect it from other farmers or relatives while travelling. The farmers in the area have their own seed storage systems or traditional seed bank (Fig. 4). Farmers on the basis of performance and preference select the varieties to be stored for seed. Selection of seed is done after harvesting. The grains from the upper portion of the healthy plant are usually separated by hand, foot or by beating with a stick and then sun dried for a day and stored. Storage for each variety is done separately in order to facilitate their identification and allocation to specific field conditions. Storage is done in bamboo

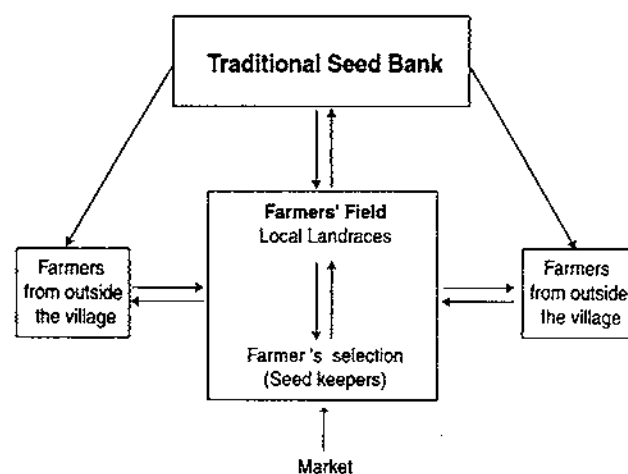


Fig. 3: Traditional seed flow



Fig 4: Farmers' seed bank and seed storage system

baskets (*dol/tukre*) or in godown (*Muchan/Ugaar*). The storage devices are made airtight by covering the mouth with straw and a mixture of cowdung and mud. The whole structure is also plastered with the mixture of cowdung and mud. Such storage systems remain pest free in majority of the cases and the viability of the seeds remain intact. These storage systems are the farmers' own seed bank. Swaminathan (1998) emphasized the urgent need to encourage and strengthen such *Field Gene Bank* already occurring at the village level for *in situ* on-farm conservation. In this context it is worth mentioning the setting up of a community seed bank in Tamil Nadu to revive the rapidly declining biodiversity of local varieties of paddy (Vijayalakshmi and Nambi, 1996), and an effort made by Virhi Beej Binimoy Kendra in Bankura district of West Bengal supported by Navdanya, New Delhi, to promote *in situ* conservation (Deb, 1999).

Conclusion

The study confirms that smallholder farmers of traditional farming systems are the main managers and preservers of agrobiodiversity. Such farmers continue to cultivate rice landraces even as they adopt newer varieties. Certain agromorphological characteristics, their adaptation to stressful environmental conditions and farmers' knowledge of the varieties favour the selection of traditional varieties. Such areas with stressful environmental conditions are hotspots of rice diversity and special importance to such areas and proper encouragement should be given to the smallholder farmers for on-farm conservation (e.g. developing market for landraces). Such on-farm conservation of traditional varieties is important as it may form a gene pool for future crop improvement programmes. In this context it is pertinent to mention the initiative of preparing a "People's Biodiversity

Register" (Gadgil and Rao, 1998) with the aim of i) helping people to access information on availability of seeds of various traditional crop cultivars in different regions, and special properties of these cultivars and ii) help in the continuation of traditional practices of conservation and sustainable use of biodiversity. The declaration of the International Year of Rice 2004 by United Nations General Assembly (UNGA) and to raise awareness of the importance of preserving benchmark traditional rice-based systems was a step towards conserving rice biodiversity (FAO, 2003).

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Diversity in Himalayan Hull-less Barley (*Hordeum vulgare* L.) Landraces Using AFLP and STMS Markers

K Venkatesan, IS Bisht* and KV Bhat

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

A total of 28 accessions naked barley landraces mainly from north-western Indian Himalaya comprising three main administrative regions, Jammu & Kashmir, Himachal Pradesh and Uttarakhand states together with five exotic accessions, four from Ethiopia and one from Nepal, were characterized using AFLP and STMS markers. The AFLP markers resolved inter-population diversity better particularly discriminating accessions from Uttarakhand Himalaya with specific adaptations. STMS markers used for studying population genetic parameters revealed that accessions from Jammu & Kashmir and Himachal Pradesh were more diverse than accessions from Uttarakhand and the exotic accessions. The group-wise F-statistics revealed that on average 68% of variation was apportioned among populations and 32% within populations. Understanding the population genetic parameters for *in situ* (on-farm) management of farmers' landraces and use of landraces representing locally common alleles for specific adaptations in crop improvement is suggested.

Key words: Naked barley, *Hordeum vulgare* L., Genetic diversity, North-western Himalaya, Molecular characterisation

Cultivated barley (*Hordeum vulgare* ssp. *vulgare*) can be classified into covered (hulled), and naked (hull-less) forms. Most barley varieties grown presently are of the hulled form, and they are mainly used for brewing malt and animal feed. By contrast, naked barley is produced on a small scale and used mainly as human food because of the ease in processing and edibility. Naked barley is attracting attention in recent years, as feed and as a healthy food because of the high feed value and abundance of dietary fibre, respectively (Liu *et al.*, 1996). According to a survey by Takahashi (1955), naked barley is distributed widely, but its frequency greatly differs among regions; naked barley accounts for more than 95% of the domesticated barley in the highlands of Nepal and Tibet, and almost 50% in China, Korea and Japan, but the frequency decreases toward the west, becoming low in Europe. In the regions where naked barley is grown at high frequencies, it is an important staple food.

The Himalayan barleys, particularly naked forms, are of great potential utility, which require research and marketing interventions. The Himalayas, Ethiopia, and Morocco have all been considered as centres of barley domestication (Åberg, 1938; Bekele, 1983; Molina-Cano *et al.*, 1987). The widespread distribution of naked barley makes the hulled or naked caryopsis character a key trait to follow the origin and domestication process of barley (Harlan, 1995; Salamini *et al.*, 2002). A recent study (Taketa *et al.*, 2004), however, indicates that naked barley has a monophyletic origin, probably in southwestern Iran,

and all naked barleys are likely to share a common ancestor.

In many areas in North-western Himalaya in proximity of Tibet, naked barley was widely cultivated till about 4 or 5 decades ago but its cultivation has gone down considerably in recent years. Naked barley landraces have gradually been replaced by wheat in these areas as a cereal of direct human consumption.

About 400 barley landraces including naked types have been collected recently from north-western Himalaya during 1999-2004 and are being maintained *ex situ* in National Genebank at the National Bureau of Plant Genetic Resources (NBPGR). These landraces are yet to be systematically characterized/evaluated. Limited information is, therefore, available on genetic diversity of existing naked barley landraces grown in north-western Himalayas. The extent of diversity between populations adapted to the high altitude region of north-western Himalayas would suggest need for their continuous collection and devising strategies for both *ex situ* and *in situ* (on-farm) conservation. It would also suggest possibility of utilizing the useful genetic variation in these landraces for improved yield and a better use of these products in agriculture and industry. Morphological diversity in naked barley landraces collected from north-western Himalaya was studied (Venkatesan *et al.* 2005). In the present paper, molecular diversity in selected barley populations from north-western Himalaya was studied using Amplified Fragment Length Polymorphism (AFLP) and Sequence Tagged Microsatellite Sites (STMS)

*Corresponding author: E-mail: bishtis@nbpgr.ernet.in

markers. While AFLP markers were used for inter-population diversity, the STMS markers were used mainly for study of population genetic parameters (intra-population variation).

Materials and Methods

The experimental material consisted of 28 naked barley populations assembled from different parts of north-western Himalayas and represented all agro-ecological conditions of the region. The material also included 5 naked barley landraces from exotic sources including 4 from Ethiopia and one from Nepal. The passport information on the origin of accessions is given in Table 1. Procedures involved in AFLP and STMS analyses are detailed below:

DNA Extraction

Extraction of total genomic DNA was carried out using method given by Saghai-Maroo *et al.* (1984) with minor modification. In each accession, healthy young leaves of same size were taken from 30 plants (6 weeks old) for bulk DNA extraction for AFLP characterization. For intra-population diversity analysis using STMS markers, DNA was extracted from 10 individual plants from each barley population.

Table 1. List of selected barley accessions for detailed diversity analysis

S.No.	Accession	Origin
1.	IC 260864	Uttarakhand
2.	IC 266944	Uttarakhand
3.	IC 355879	Uttarakhand
4.	IC 356114	Uttarakhand
5.	IC 356122	Uttarakhand
6.	IC 362237	Uttarakhand
7.	IC 362256	Uttarakhand
8.	IC 398291	Uttarakhand
9.	IC 406567	Uttarakhand
10.	IC 406568	Uttarakhand
11.	IC 406569	Uttarakhand
12.	IC 406570	Uttarakhand
13.	IC 406571	Uttarakhand
14.	IC 406572	Uttarakhand
15.	PI 176040	Uttarakhand
16.	KC/PS 37	Uttarakhand
17.	PI 429907	Jammu & Kashmir
18.	PI 429885	Jammu & Kashmir
19.	PI 429895	Jammu & Kashmir
20.	PI 429889	Jammu & Kashmir
21.	PI 429896	Jammu & Kashmir
22.	PI 429941	Himachal Pradesh
23.	PI 572605	Himachal Pradesh
24.	CHHO 3228	Nepal
25.	PI 316815	Ethiopia
26.	PI 356131	Ethiopia
27.	PI 382537	Ethiopia
28.	PI 382556	Ethiopia

AFLP Analysis

Plant mapping kit for regular plant genomes (500-6000 Mb) AFLP™ (PE Applied Biosystems, USA) was used for the analysis. The technique developed by Vos *et al.* (1995), was optimized for barley by modifying the protocol provided by the manufacturers. The technique is based on the selective PCR amplification of restriction fragments from digestion of total genomic DNA. ABI plant mapping protocol was followed for analysis of barley populations. The recommended DNA concentration was 500 ng per reaction. The DNA concentration was optimized for barley by testing three different DNA concentrations viz., 500, 200 and 100 ng per reaction. Similarly, two restriction enzyme concentrations viz., 5U and 3U of *EcoR* I per reaction and 1U and 0.2U of *Mse* I were tested and finally 3U of *EcoR* I and 0.2U *Mse* I enzymes were used. Pre-selective amplification was performed to reduce the overall complexity of the target DNA fragments by increasing specific target sequences so that the double digested fragments become predominant. This was performed by using pre-selective primers (Table 2).

Each peak in the electropherogram was considered as an AFLP marker. The scoring of bands was done from the electropherograms according to size (in bp.). Presence of band was treated as '1' and absence of band as '0'. The 'Genescan' and 'Genotyper' software packages (Applied Biosystems, USA) were used for processing and scoring of the results. The 1-0 matrix of cultivars X AFLP products was used to calculate pairwise Jaccard's similarity coefficient.

The similarity coefficient matrix was subjected to cluster analysis by Unweighted Pair Group Method of Arithmetic Average (UPGMA) analysis and dendrogram was generated with the help of NTSYS-pc software version 1.70 (Exeter Software, New York, USA). The 28 selected barley landraces were used in the cluster analysis.

Microsatellite (STMS) Analysis

The procedure described below was used for carrying out the PCR reactions for STMS analysis. The PCR reaction mixture consisted of Taq DNA polymerase, 10x PCR buffer, dNTPs, MgCl₂, primer and genomic DNA. Optimization of PCR component concentrations was carried out for Taq DNA polymerase, MgCl₂, genomic DNA and primer. Concentration of dNTPs (200 μM) and PCR buffer (1x) was not varied. PCR reactions were carried out in a Perkin Elmer Thermocycler with heated

lid. Thermocycling conditions were as follows: 1) denaturation at 94° C for 3 minutes; 2) 45 cycles of denaturation at 94° C for 1 minute, 3) primer annealing at 55° C for 1 minute; 4) primer extension at 72° C for 2 minutes and 5) final extension step at 72° C for 10 minutes. The selected primers after screening and their sequences are listed in Table 3. The selected five primers were used for population genetic studies.

Electrophoresis was carried out at 90 V for one hour 30 minutes till the bromophenol blue dye travelled less than 2/3rd the length of gel. The resolved amplification products were visualized under UV light after staining with ethidium bromide on a UV-Transilluminator. The gel was photographed using a Gel Documentation System.

The amplification products were scored across the lanes comparing their respective molecular weights. Each band was treated as one STMS allele. Scoring of bands was done from photographs. Homology of bands was based on distance of migration in the gel.

The STMS allele data for each population was used to calculate frequency of occurrence of a specific allele. The accessions x allele matrix for all 5 loci analysed was used to calculate the genetic diversity parameters. Genetic

diversity of the populations was described using the parameters, per cent polymorphic loci, number of alleles per locus, genetic diversity for each locus and population, the level of heterozygosity, coefficient of gene diversity, Shannon diversity index, fixation-indices and gene flow for all loci.

Results

AFLP Analysis

Primer Screening

Twelve selected primer pairs were used for detailed genetic diversity analysis for 28 barley landraces. They were selected from the list published in literature. The properties of AFLP amplicons generated by 12 primers in selected barley landraces are listed in Table 2. The selected primer pairs generated a total of 1517 amplicons ranging from 36 (E-ACC/M-CAC) to 188 (E-ACA/M-CTT) among 28 barley landraces analyzed. Of the 1,517 amplicons generated 1,318 amplicons (86.9%) were polymorphic and ranged from 34 (E-ACC/M-CAC) to 159 (E-ACG/M-CAA). The per cent polymorphism ranged from 81.1% to 98.0%. Among twelve primer pairs, four primer pairs generated above 90% polymorphism (E-ACC/M-CAA, E-ACC/M-CAC, E-ACG/M-CAA and

Table 2. Properties of AFLP amplicons generated by 12 primers in selected barley landraces

S.No.	Primer sequence	Total no. of amplicons	No. polymorphic amplicons	% polymorphism	Average no. of amplicons per accession
1	E-ACA/M-CAA	176	153	86.9	93.4
2	E-ACG/M-CAA	172	159	92.4	80.7
3	E-ACC/M-CAA	51	50	98.0	11.2
4	E-ACA/M-CAC	157	143	91.1	68.4
5	E-ACG/M-CAC	127	114	89.8	58.0
6	E-ACC/M-CAC	36	34	94.4	8.6
7	E-ACA/M-CTG	127	106	83.5	68.3
8	E-AAG/M-CTG	102	89	87.3	47.8
9	E-ACC/M-CTG	127	103	81.1	61.8
10	E-ACA/M-CTT	188	153	81.4	99.6
11	E-AAG/M-CTT	127	107	84.3	59.8
12	E-ACC/M-CTT	127	107	84.3	55.0
Total		1517	1318	86.9	712.6

Table 3. Primer sequences, repeat motif, allele size ranges (bp), and chromosomal location of 5 microsatellite primers

Primer ID	Primer sequence (5'-3')	Core motif	Allele size	Annealing temperature	Chromosomal location*
HVBKAS1	atlggeggtgaccgatatttatgtca caaaactgcugctaagcagggaaca	(CA) _n	176-204	56	2(2H)
HVM9	cttcgacaccatcaccag accaaaatcgccatcgaucaat	(TCT) ₅	218-230	54	3(3H)
HVM43	ggatlttctcaagaacactt gggtgagtgcataacatt	(CA) ₉	239	50	5(1H)
BMS90	acatcaaccctcctgctc ccgcacatagtggttaacac	(AC) ₂₀	221	55	5(1H)
HVM6	catggatgaatgattggttttg cgctccgtatgtgtatgagtaa	(GA) ₉	175	52	7(5H)

* Chromosome numbering follows barley nomenclature with the homologous chromosome group given in parenthesis (IBGS, 1996)

E-ACA/M-CAC). The average number of amplicons per accession ranged from 8.6 (E-ACC/M-CAC) to 99.6 (E-ACA/M-CTT) per primer. Of the 12 primer pairs, two primer pairs showed the average number of amplicons per accession as above ninety. AFLP profiles of two primer pairs are presented in figure 1.

Diversity Analysis

The Jaccard's similarity coefficients ranged from 0.37 to 0.72. The UPGMA dendrogram (Fig. 2) constructed from Jaccard's similarity co-efficients indicated presence of two major clusters, when cut-off value was considered as 0.546, the average similarity coefficient. The cluster I included 23 barley populations representing all regions, Uttarakhand, Jammu & Kashmir, Himachal Pradesh, Nepal and Ethiopia. The cluster could be further divided into two sub-clusters, sub-cluster Ia comprising only two accessions from Uttarakhand (IC-266944 and IC-406570). The cluster II comprised only two populations, IC-356122 and IC-406567, both from Uttarakhand. The Jaccard's similarity co-efficient between these accessions is 0.53. The three accessions, from Uttarakhand (IC- 260864 and IC-406572) and one accession from Ethiopia (PI- 382556) were not included in any of the clusters.

Microsatellite (STMS) Analysis

Primer Screening

Five primers were used for detailed population genetic diversity analysis for 28 barley landraces. These primers were selected from the list published in literature. The properties of STMS bands generated by five primers are listed in Table 3. This Table included the core motif, allele size etc. The Alleles had simple core repeat motifs viz., $(C)_n$, $(TCT)_n$, $(GA)_n$, $(CA)_n$ except two, $(AG)_{11}$, $(GA)_{14}$ and $(GA)_6$, $(GT)_4$, $(GA)_7$.

The Allele frequency per locus generated by five STMS primers among populations is listed in Table 4. The primer HVBKASI identified two alleles per locus with average allelic frequency of 0.21 and 0.79. The primer BMS90 identified two alleles per locus with average allelic frequency of 0.38 and 0.62. The primer HVM43 identified three alleles with average allelic frequency of 0.028, 0.967 and 0.003. The primers HVM9 and HVM6 identified only single allele with allelic frequency of 1.00. A representative profile generated by two STMS primers is presented in figure 3.

Diversity Analysis of STMS Data

The summary statistics of diversity analysis of selected barley landrace populations is listed in Table 5. Of the

five loci analysed by selected primers, three loci were polymorphic and two loci were monomorphic. The percentage of polymorphic loci is 60%. Of the observed number of alleles (1.8 ± 0.82) among populations, the effective number of alleles is 1.25 ± 0.34 . The populations with more effective number of alleles possessed higher diversity than the others. These populations were CHIO 3228 (Nepal), PI 572605 (Himachal Pradesh), PI 429885 (Jammu & Kashmir), PI 316815 (Ethiopia), IC 398291 (Uttarakhand), IC 356114 (Uttarakhand), IC 260864 (Uttarakhand) and PI 429941 (Himachal Pradesh). The expected heterozygosity was 0.16 ± 0.20 among populations and the observed heterozygosity was 0.01 ± 0.20 . Of the 28 barley populations, only four populations namely, PI-429885 (Jammu & Kashmir), PI-176040 (Uttarakhand), PI-316815 (Ethiopia) and PI-356131 (Ethiopia) showed higher observed heterozygosity.

Shannon's information index was high for populations CHIO 3228 from Nepal, PI 572605 and PI 429941 from Himachal Pradesh, PI 429885 from Jammu & Kashmir, and IC 260864 and IC 362256 from Uttarakhand indicating greater diversity of these populations.

The UPGMA dendrogram from population analysis (Fig. 4) constructed from Nei's genetic distances indicated presence of two major clusters I and II. Cluster I could be further divided into two sub-clusters. The sub-cluster Ia included 21 barley populations, representing accessions from all areas, Uttarakhand, Jammu & Kashmir, Himachal Pradesh, Ethiopia and Nepal. The sub-cluster Ib included only three populations, two from Uttarakhand and one from Ethiopia. The cluster II included three populations, all from Jammu & Kashmir. One accession from Uttarakhand (IC-355879) was not included in any of the clusters.

Grouped Population Descriptive Statistics

The group-wise allelic frequency per locus generated by 5 STMS primers is listed in Table 6. The group I included the accessions collected from Uttarakhand and one accession from adjoining Nepal, in these three loci out of five were polymorphic. The group II included the populations assembled from Jammu & Kashmir in which two loci out of five loci identified by selected primers were polymorphic. The group III comprised the populations from Himachal Pradesh and only two loci out of five loci were polymorphic. The group IV comprised the populations from Ethiopia where only one locus out of five loci was polymorphic.

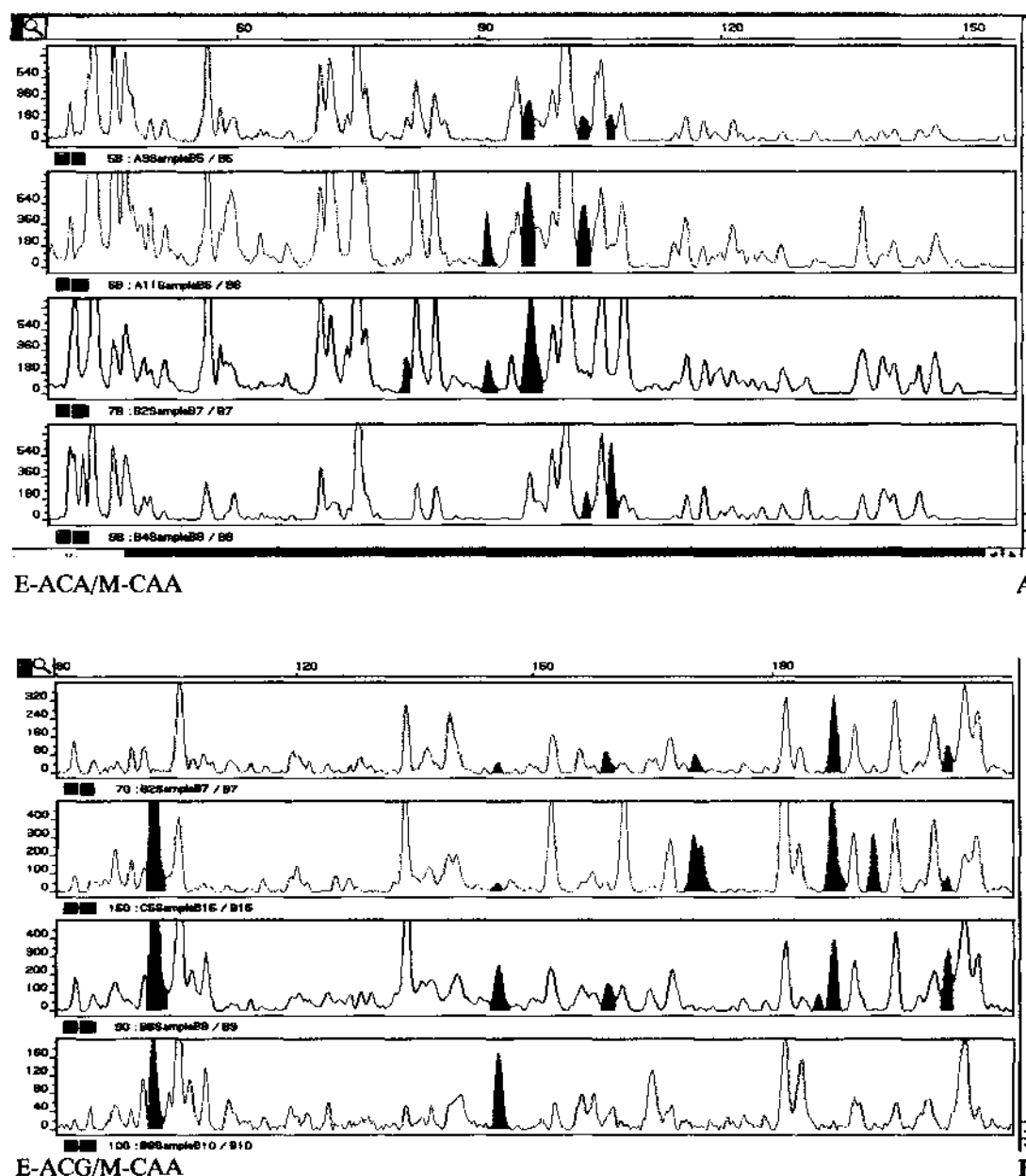


Fig 1(A,B): AFLP profiles of four barley landraces each generated by different primer pairs indicating the quality and extent of polymorphism for amplification products. The dark coloured filled bands are polymorphic and rest are monomorphic among the populations

The summary statistics for selected populations group-wise is presented in Table 7. The populations from group I (Uttarakhand and Nepal), group II (Jammu & Kashmir) and group III (Himachal Pradesh) contributed more for representation of diversity of populations with more effective number of alleles. The group I populations had all the three polymorphic loci out of five loci identified by selected primers. The per cent polymorphism of group I population is 60% and both group II and group III is 40%.

The group I, group II and group IV showed higher observed heterozygosity which was possibly the result of natural crossing among the populations. The Shannon's indices were more for group II and group III showing greater diversity of the populations in these groups.

The summary of group-wise F-statistics and gene flow for all loci identified by 5 STMS primers is listed in Table 8. The proportion of diversity among and within populations indicated that, on average 68% (F_{st}) of the variation was among populations and 32% ($1-F_{st}$) was

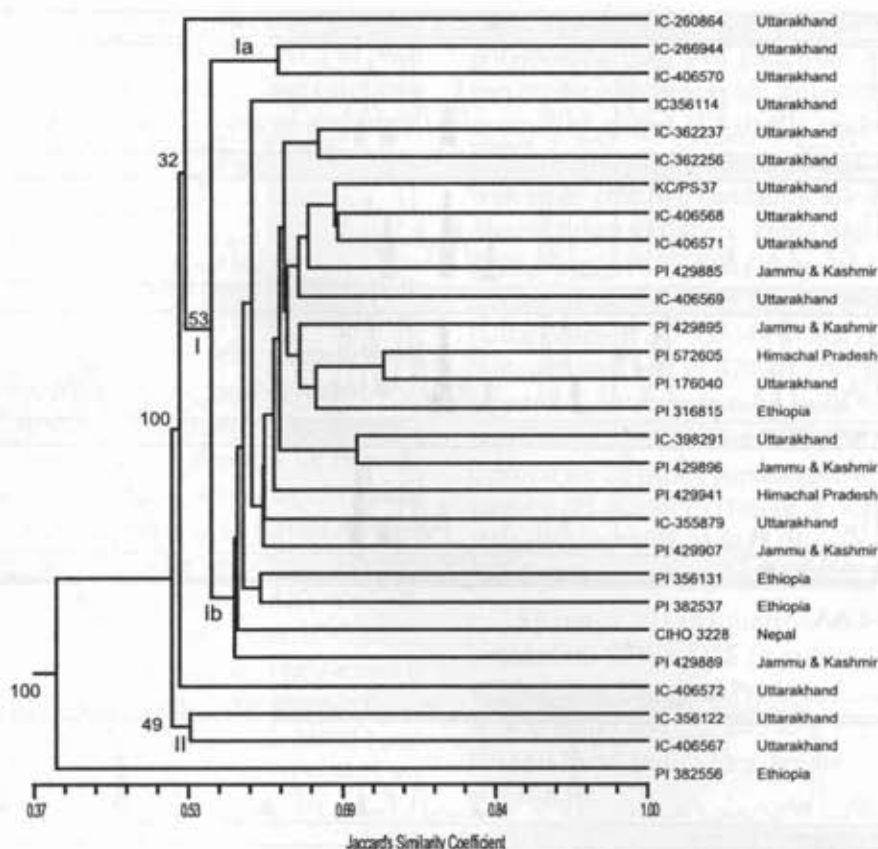


Fig. 2: UPGMA dendrogram of 28 barley landraces based on AFLP data



Fig. 3: STMS profiles of barley populations generated by the primers, HVM 43 (A) and HVBKASI (B) indicating inter-population diversity

within populations. High F_{st} values in group II (Jammu & Kashmir) and group I (all populations from Uttarakhand and one accession from Nepal) were indicative of high population differentiation in these groups. The negative F_{is} values in group II, III and IV were indicative of high degree of inbreeding among populations of these groups. High F_{it} values in group I, II and III also indicate greater population differentiations between populations.

The contribution of gene flow (N_m values) is more in group III (Himachal Pradesh) populations as compared to other groups.

Discussion

AFLP characterization

The AFLP characterisation of selected barley landraces indicated enough polymorphism to fully differentiate the inter population diversity (Table 2). The bootstrap tests on the data of figure 2 fully supported the resolution shown. Though, at the major cluster level there was no strong association between geographical origin and genetic diversity, yet at sub-cluster level this association was better revealed. Some of the Uttarakhand accessions were clearly discriminated in distinct clusters/sub-

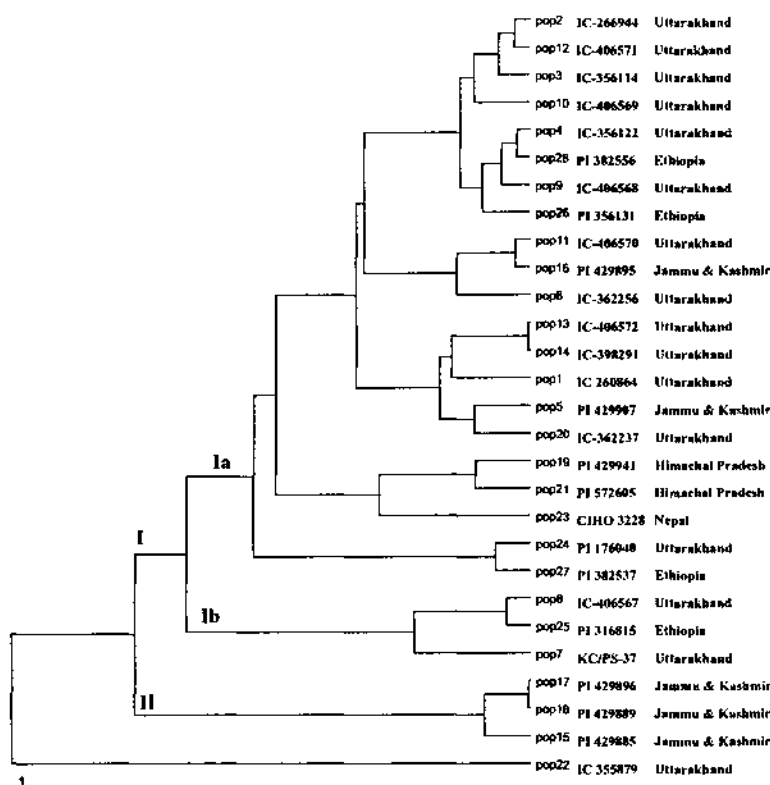


Fig. 4: UPGMA dendrogram of 28 barley landraces based on STMS data

Table 4. Allelic frequency per locus generated by 5 STMS primers

S.No.	Accession	HVBKASJ		HVM9	BMS90		HVM43			HVM6
		Allele A	Allele B	Allele A	Allele A	Allele B	Allele A	Allele B	Allele C	Allele A
1.	IC-260864	0.90	0.10	1.00	0.20	0.80	—	1.00	—	1.00
2.	IC-266944	—	1.00	1.00	0.10	0.90	—	1.00	—	1.00
3.	IC-356114	—	1.00	1.00	0.30	0.70	—	1.00	—	1.00
4.	IC-356122	—	1.00	1.00	—	1.00	—	1.00	—	1.00
5.	IC-362237	—	1.00	1.00	0.20	0.80	—	1.00	—	1.00
6.	IC-362256	—	1.00	1.00	0.90	0.10	—	0.90	0.10	1.00
7.	KC/PS-37	—	1.00	1.00	—	1.00	—	1.00	—	1.00
8.	IC-406567	—	1.00	1.00	—	1.00	0.10	0.90	—	1.00
9.	IC-406568	—	1.00	1.00	0.10	0.90	—	1.00	—	1.00
10.	IC-406569	—	1.00	1.00	0.20	0.80	—	1.00	—	1.00
11.	IC-406570	—	1.00	1.00	1.00	—	—	1.00	—	1.00
12.	IC-406571	—	1.00	1.00	1.00	—	—	1.00	—	1.00
13.	IC-406572	—	1.00	1.00	0.20	0.80	—	1.00	—	1.00
14.	IC-398291	—	1.00	1.00	0.70	0.30	—	1.00	—	1.00
15.	PI 429885	0.70	0.30	1.00	0.90	0.10	—	1.00	—	1.00
16.	PI 429895	0.10	0.90	1.00	1.00	—	—	1.00	—	1.00
17.	PI 429896	0.90	0.10	1.00	1.00	—	—	1.00	—	1.00
18.	PI 429889	1.00	—	1.00	1.00	—	—	1.00	—	1.00
19.	PI 429907	1.00	—	1.00	—	1.00	—	1.00	—	1.00
20.	PI 429941	0.20	0.80	1.00	0.20	0.80	—	1.00	—	1.00
21.	PI 572605	0.50	0.50	1.00	0.20	0.80	—	1.00	—	1.00
22.	IC-355879	—	1.00	1.00	1.00	—	—	1.00	—	1.00
23.	CIHO 3228	0.50	0.50	1.00	0.50	0.50	—	1.00	—	1.00
24.	PI 176040	—	1.00	1.00	—	1.00	0.15	0.85	—	1.00
25.	PI 316815	—	1.00	1.00	—	1.00	0.30	0.70	—	1.00
26.	PI 356131	—	1.00	1.00	—	1.00	0.25	0.75	—	1.00
27.	PI 382537	—	1.00	1.00	—	1.00	—	1.00	—	1.00
28.	PI 382556	—	1.00	1.00	—	1.00	—	1.00	—	1.00
Overall allelic frequency		0.21	0.79	1.00	0.38	0.62	0.028	0.967	0.003	1.00

Table 5. Summary diversity analysis of selected barley landraces

S.No.	Accession No.	Sample size	No. of polymorphic loci	% of polymorphic loci	Observed no. of alleles	Effective no. of alleles	Shannon's Information Index	Observed heterozygosity	Expected heterozygosity
1.	IC-260864	10	2	40	1.40±0.55	1.14±0.21	0.17±0.23	0.00	0.11±0.15
2.	IC-266944	10	1	20	1.20±0.45	1.04±0.10	0.07±0.15	0.00	0.04±0.08
3.	IC356114	10	1	20	1.20±0.45	1.14±0.32	0.12±0.27	0.00	0.12±0.27
4.	IC-356122	10	0	0	1.00	1.00	0.00	0.00	0.00
5.	IC-362237	10	1	20	1.20±0.45	1.09±0.21	0.10±0.22	0.00	0.07±0.15
6.	IC-362256	10	2	40	1.40±0.55	1.09±0.12	0.13±0.18	0.00	0.08±0.10
7.	KC/PS-37	10	0	0	1.00	1.00	0.00	0.00	0.00
8.	IC-406567	10	1	20	1.20±0.45	1.04±0.10	0.07±0.15	0.00	0.04±0.08
9.	IC-406568	10	1	20	1.20±0.45	1.04±0.10	0.07±0.15	0.00	0.04±0.08
10.	IC-406569	10	1	20	1.20±0.45	1.09±0.21	0.10±0.22	0.00	0.07±0.15
11.	IC-406570	10	0	0	1.00	1.00	0.00	0.00	0.00
12.	IC-406571	10	0	0	1.00	1.00	0.00	0.00	0.00
13.	IC-406572	10	1	20	1.20±0.45	1.09±0.21	0.10±0.22	0.00	0.07±0.15
14.	IC-398291	10	1	20	1.20±0.45	1.14±0.32	0.12±0.27	0.00	0.09±0.19
15.	PI 429885	10	2	40	1.40±0.55	1.19±0.31	0.19±0.28	0.04±0.09	0.12±0.19
16.	PI 429895	10	1	20	1.20±0.45	1.04±0.09	0.07±0.14	0.00	0.04±0.08
17.	PI 429896	10	1	20	1.20±0.45	1.04±0.10	0.07±0.15	0.00	0.04±0.08
18.	PI 429889	10	0	0	1.00	1.00	0.00	0.00	0.00
19.	PI 429907	10	0	0	1.00	1.00	0.00	0.00	0.00
20.	PI 429941	10	2	40	1.40±0.55	1.19±0.26	0.20±0.27	0.00	0.13±0.18
21.	PI 572605	10	2	40	1.40±0.55	1.29±0.44	0.24±0.33	0.00	0.17±0.25
22.	IC 355879	10	0	0	1.00	1.00	0.00	0.00	0.00
23.	CIHO 3228	10	2	40	1.40±0.55	1.40±0.55	0.28±0.38	0.00	0.21±0.29
24.	PI 176040	10	1	20	1.20±0.45	1.07±0.15	0.08±0.19	0.06±0.13	0.05±0.12
25.	PI 316815	10	1	20	1.20±0.45	1.14±0.32	0.12±0.27	0.12±0.27	0.09±0.20
26.	PI 356131	10	1	20	1.20±0.45	1.12±0.27	0.11±0.25	0.10±0.22	0.08±0.18
27.	PI 382537	10	0	0	1.00	1.00	0.00	0.00	0.00
28.	PI 382556	10	0	0	1.00	1.00	0.00	0.00	0.00
Overall	280	3	60	1.80±0.82	1.25±0.34	0.24±0.29	0.01±0.20	0.16±0.20	

Table 6. Group-wise allelic frequency per locus generated by 5 STMS primers

S.	Accession	HVBKAS1		HVM9	BMS90		HVM43			HVM6
No.		Allele A	Allele B	Allele A	Allele A	Allele B	Allele A	Allele B	Allele C	Allele A
1.	Group I (UA & Nepal)	0.08	0.92	1.00	0.32	0.68	0.01	0.98	0.006	1.00
2.	Group II (J&K)	0.62	0.38	1.00	0.72	0.28	-	1.00	-	1.00
3.	Group III (HP)	0.35	0.65	1.00	0.20	0.80	-	1.00	-	1.00
4.	Group IV (Ethiopia)	-	1.00	1.00	-	1.00	0.14	0.86	-	1.00
	Overall allelic frequency	0.26	0.74	1.00	0.31	0.69	0.04	0.96	0.002	1.00

UA=Uttarakhand, J&K = Jammu & Kashmir, H.P.= Himachal Pradesh

Table 7. Group-wise summary diversity analysis of selected barley landraces

S. No.	Group	Sample size	No. of polymorphic loci	% of polymorphic loci	Observed no. of alleles	Effective no. of alleles	Shannon's Information Index	Observed heterozygosity	Expected heterozygosity
1.	Group I (UA and Nepal)	170	3	60	1.80±0.84	1.19±0.33	0.20±0.26	0.008±0.18	0.13±0.18
3.	Group II (J&K)	50	2	40	1.40±0.55	1.32±0.44	0.25±0.35	0.007±0.01	0.18±0.24
5.	Group III (HP)	20	2	40	1.40±0.55	1.26±0.38	0.22±0.32	0.00	0.16±0.22
6.	Group IV (Ethiopia)	40	1	20	1.20±0.45	1.06±0.14	0.08±0.18	0.06±0.12	0.48±0.11
	Overall	280	3	60	1.45±0.59	1.20±0.32	0.19±0.28	0.02±0.01	0.23±0.19

UA=Uttarakhand, J&K = Jammu & Kashmir, HP= Himachal Pradesh

clusters. This provides the opportunity to select diverse accessions from distinct microclimatic niches for specific morphological adaptations. Grouping of accessions from all regions in sub-cluster Ib indicates preponderance of widespread common alleles in barley landraces under

study. The AFLP markers have also been successfully used for cultivar identification and genetic diversity analysis in barley (Ellis *et al.*, 1997; Schut *et al.*, 1997; Powell *et al.*, 1997; Davila *et al.*, 1998; Treuren and van Hintum, 2001; Turpeinen *et al.*, 2003).

Table 8. Summary of group-wise F-statistics and gene flow for all loci in selected barley landraces [See Nei (1987) *Molecular Evolutionary Genetics* (p. 159-164)]

Group	Sample Size	Fis	Fit	Fst	Nm*
Group I (UA & Nepal)	170	0.803	0.934	0.5808	0.180
Group II (J&K)	50	-16.466	0.962	0.7269	0.094
Group III (HP)	20	-16.301	1.000	0.0581	4.056
Group IV (Ethiopia)	40	-81.939	-0.159	0.1621	1.293
Mean	280	0.755	0.920	0.675	0.120

* Nm : Gene flow estimated from $F_{st} : 0.25(1 - F_{st})/F_{st}$.

UA: Uttarakhand, J&K : Jammu & Kashmir, HP: Himachal Pradesh

STMS Characterisation

At the level of the population, any particular allele at a locus occurs with a certain frequency and in self-fertilizing species like barley may attain any frequency. The amount of polymorphism within populations, the allelic richness (the total number of alleles in the population), the gene diversity or probability that two random copies of the gene will have dissimilar alleles, and the heterozygosity (the percentage of heterogeneous genotypes in a population) are all measurements of genetic diversity within a population. The informative value of microsatellite markers for genetic studies and as a powerful tool for linkage maps and barley breeding was confirmed in several studies (Saghai-Maroo *et al.*, 1994; Becker and Heun, 1995; Liu *et al.*, 1996; Struss and Plieske, 1998; Ramsay *et al.*, 2000; Pillen *et al.*, 2000; Kunzel *et al.*, 2000; Kunzel and Waugh, 2002; Holten *et al.*, 2002; Li *et al.*, 2003; Thiel *et al.*, 2003).

Among the five STMS loci, two (HVM9 and HVM6) were entirely invariant as only one allele was observed in the total 280 individuals from 28 populations analysed (Table 4). The alleles at these loci can be categorised as common and widespread according to Marshall and Brown (1975). Of the three remaining loci, BMS90 was most variant followed by HVBKASI and HVM43. All the alleles at these loci occurred with frequency $P > 0.1$ for individual populations. At locus HVBKASI, allele A was common and localized and was present in only one population (IC 260864) of the 16 populations of Uttarakhand region studied. This allele was, however, common and widespread in populations of Jammu & Kashmir and Himachal Pradesh, and also occurred in one population of Nepal (CIHO 3228). The above population from Uttarakhand (IC 260864) was collected from the adjoining overlapping areas of Uttarakhand and Himachal Pradesh. Similarly at locus HVM43, allele A and C were common and localized. Allele A at this locus occurred in

two populations of Uttarakhand (IC 406567 and PI 176040) and two populations from Ethiopia (PI 316815 and PI 358131). Allele C was present in only one population of Uttarakhand (IC 362256). The common and localized alleles occur in only one or few habitats, where they normally reach a high frequency. These alleles may be biologically specialized alleles that enhance adaptation only in certain habitats. These are often the class of alleles of most interest to breeders, because breeders are concerned with improving performance in the specialized habitats of their own ecogeographical regions. Widespread, common alleles have almost certainly been introduced into all habitats, whereas introduction of the localized alleles of special habitats is likely to have been sporadic. Such considerations led Marshall and Brown (1975) to suggest that locally common alleles are, at least conceptually, the key class of alleles in formulating sampling strategies, whether for capturing the maximal amount of useful variation within populations (within practical limits of sample size) or determining the distribution of environmentally influenced genetic variation within species. Alleles whose frequencies vary widely from population to population (common and localised categories) appear to be responsible for most of the allelic variation that exists within and among populations of barley landraces studied. Such variations in allelic frequencies are often correlated with readily observable and measurable environmental factors (rainfall, temperature, slope, exposure, soil type, etc.).

The population genetic parameters revealed high allelic richness in four of the 16 landraces from Uttarakhand (IC 260864, IC 356114, IC 398291 and IC 362256) together with high Shannon diversity indices (Table 5). Of the five populations of Jammu & Kashmir, one accession, PI 429885 had high allelic richness together with high Shannon diversity index. The two accessions from Himachal Pradesh displayed relatively high allelic richness and high Shannon diversity index. The one accession from Nepal included in the study had the highest allelic richness (effective number of alleles 1.40 ± 0.55) and Shannon diversity index (0.28 ± 0.38) of all the accessions studied. Among the four Ethiopian accessions, two accessions PI 416815 and PI 356131 had high allelic richness together with high Shannon diversity indices. Five accessions from Uttarakhand (IC 356122, KC/PS 37, IC-406570, IC-406571, IC-355879), two accessions from Jammu & Kashmir (PI-429889, PI-429907) and two accessions from Ethiopia (PI-382537,

PI 382556), did not show any polymorphism for the five STMS marker loci studied.

Group-wise summary statistics (Table 7) for various population genetic parameters indicated that accessions from Himachal Pradesh (group III) and Jammu & Kashmir (group II) had relatively more number of effective alleles and high Shannon diversity index followed by accessions from Uttarakhand and one accession of Nepal clubbed in group I and the accessions from Ethiopia in group IV. Observed heterozygosity is more for Ethiopian accessions followed by accessions from Uttarakhand and Jammu & Kashmir.

Group-wise F-statistics (Table 8) revealed greater population differentiation in group II and I. On average 68% of variation was apportioned among populations and 32% within populations. The contribution of gene flow was more for two populations from Himachal Pradesh (group III) followed by landrace populations from Ethiopia, Uttarakhand and Jammu & Kashmir.

Understanding the population genetic structure of farmers' landraces may be helpful for *in situ* (on-farm) management of these landraces. Farmers' decisions regarding the size and relative placement of their fields impact significantly on local crop diversity. Fields may be large or small, close together or widely spaced. Depending on the reproductive biology of the crops in question, this structuring can have a range of effects on the genetic diversity of the crops. It is not known whether common landraces used throughout the village or region tend to be more variable than less common varieties. It could be that the differences are related much to character differences (and possibly to the distribution of diversity) and all landraces have about the same allelic richness. Neither is known whether increasing richness of farmer varieties or number of farmer varieties and increasing genetic diversity (allele richness) are positively correlated. It could be that the genetic diversity contained in a few landraces in some villages is similar to the amount of genetic diversity contained in villages with many varieties. To make rational conservation plans, it is important to test whether villages with a few landraces are conserving as much diversity as villages with many varieties. Locally common landraces are those landraces that appear to be particularly important for conservation and particularly interesting for users.

Farmer management of gene flow impacts genetic diversity over time and space. Landraces may hybridize with other farmers' landraces. Farmer management of

crop populations according to flowering dates is another action with relevance for gene flow between varieties. When new genetic combinations arise through introgression, farmers select and maintain new combinations under specific situations.

The UPGMA dendrogram presented in figure 4 provides opportunity for selecting distinct populations from different microclimatic niches for use in crop improvement. Diversity analysis will provide information on the genetic distinctiveness of farmer-named varieties. Measurement of diversity can determine whether rare varieties are selected from common ones and whether locally common varieties have the greatest number of locally common alleles for different breeding systems. Diversity analysis at different spatial scale will enable comparisons at community and regional levels, such as whether the crop populations of one village represent all the genetic diversity in the region.

The above population genetic parameters can help measure the average genetic diversity of a field/village/region, the differences in allele frequencies among different populations, and the differences in level of polymorphism among populations.

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Genetic Resources of Linseed (*Linum usitatissimum* L.) – Conservation and Utilization in Crop Improvement

J Radhamani¹, SD Dubey², RL Srivastava³ and AK Singh¹

¹ Division of Germplasm Conservation, National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012

² ACRIP on Linseed, Kanpur, Uttar Pradesh

Linseed is one of the important oilseed and fibre-yielding crops of India. India is the third largest producer in the world. However, the average national productivity (403 Kg/ha) is far below the world average (851 Kg/ha), predominantly owing to the susceptibility of the cultivars to biotic and abiotic stresses. With the inception of Coordinated Research Project on linseed significant progress has been made in the varietal development. The development of about 56 high yielding, disease resistant varieties suitable for different agro-climatic zones has helped in improving not only the productivity but also addressing various biotic and abiotic stresses. Resistant sources have been identified for the disease like rust [*Melampsora lini* (Pers.) Lev.], wilt (*Fusarium oxysporum* f. *lini*), powdery mildew (*Oidium lini* Skoric), leaf spot (*Alternaria lini* Dey) and pests such as linseed gall midge (*Dasyneura lini* Barnes) and linseed semilooper (*Plusia orichalcea* Fabr.). Nevertheless, due to narrow genetic base of the released varieties, concerted efforts are required to breed varieties involving distant and exotic germplasm, preferably from main centres of diversity, to produce varieties with higher level of resistance and productivity. Present paper deals with the status of varietal germplasm and sources of resistance available for the effective utilization of linseed germplasm at National level.

Key words: Genetic resources, Germplasm, Varieties, Linseed/flax, *Linum usitatissimum*

Linseed or flax (*Linum usitatissimum* L.) is an annual oilseed crop of the family Linaceae. Genus *Linum* has nearly 100 species and over 200 varieties. Depending on the agro-climatic conditions there is a diverse range of variability in the crop in height (25 to 125 cm), branching pattern (sparsely and heavily branched) and maturity periods (fast-growing varieties spread in the north latitudes and mountainous regions to slower-growing varieties cultivated on irrigated soils in Asia). Commercially grown flax varieties/cultivars are grouped into two main types-fibre flax and seed flax, the former is generically referred to as long-stalked flax and the latter as crown flax. Long-stalked flax is grown for fibre and cultivated as a spring crop on primarily silt or clay loams in a moist and warm climate.

India ranks third largest producer amongst the linseed-producing countries. Germany has the highest productivity (1699 Kg/ha) followed by UK (1258 Kg/ha), Canada (1078 Kg/ha) and China (933 Kg/ha), whereas India averages 403 Kg/ha. It occupies an important position in India for its technical grade vegetable oil producing property. The acreage of linseed in India is nearly 5.26 lakh/ha with production of 2.12 lakh tones and national productivity is about 403 Kg/ha as per the 2003-04

records. Fibre yielding property from the linseed stalk is an added advantage of this crop. In India, Madhya Pradesh leads in yield and acreage, followed by Uttar Pradesh, Maharashtra, Chhattisgarh, Bihar, Jharkhand, Karnataka and West Bengal. In India *Linum usitatissimum* is the main cultivated species. However, for the ornamental purposes, species like *L. gradiflorum*, *L. mysorensense*, *L. perenne*, *L. strictum*, *L. angustifolium*, and *L. bienne* are occasionally grown in gardens. Distinct morphological features such as flower colour, seed size, plant and capsule type have been observed in different species.

Origin and Distribution

Flax is believed to be one of the most ancient agricultural crops. It is distributed throughout the world but it was never found with certainty in wild state under natural conditions. A number of workers (Planchen, 1848; Decandolle, 1904; Helbock, 1956; Richharia, 1962; Gill, 1966; Smith, 1969) have attempted to trace the origin and history of *L. usitatissimum*. It is recognized to be an old world crop and as revealed by historical and archaeological records, its cultivation was in practice long before Christian era in Europe, Africa and Asia. There seems to be no certainty about its actual time of domestication.

* Corresponding author's E-mail: jalliradhamani@yahoo.co.in

Domestication of fibre flax occurred in India and China more than 5,000 years ago. There is evidence that as far back as 3,000-4,000 years BC flax was grown for fibre in Mesopotamia, Assyria and Egypt where the finest linen cloths were spun. Flax was extensively raised in Colchis that used linen to pay tribute to the Turks. According to one account, the voyage of Argonauts from Hellas to Colchis for the Golden Fleece was in fact prompted by a desire to obtain the secret of making fine flax yarn that was treasured as much as gold and was as good as that produced in Egypt.

It is, however, generally believed that linseed originated in an area east of the Mediterranean sea, near India (Simmonds, 1976). Seed type linseed, cultivated for its oil, is believed to have developed primarily in South-eastern Asia, whereas fibre flax developed in the Mediterranean region. Botanically, these two forms are in no way different from each other. The names viz. linseed and flax are used interchangeably. There is a great variation in flax found in India and adjacent northern area. The most likely progenitor is *L. angustifolium*, but other species such as *L. bienne* also seems to have contributed in the evolution of cultivated linseed (Gill, 1987).

Morphology and Cultivation

The cultivated plant (*Linum usitatissimum* L.) has a short tap root system with fibrous branch, which may extend to a depth of 9-120 cm. in favourable soil texture. Linseed is grown in the range of latitudes between the 10th and 65th parallels, both north and south. Areas with the annual rainfall ranging from 45-75 cm are best suited for its cultivation. The seed crop does well under moderate cold, but the fibre crop grows best in cool moist climates. In India, the crop is grown in the *rabi* season from September-October to February-March. Linseed can be grown on different kinds of soils, except the sandy and badly drained heavy clays or clay loams. The crop is grown either broadcast or drilled in lines 20 to 30 cm apart. Harvesting is done when the crop ripe with a sickle or by uprooting the plants. When the fibre is also desired along with seed, the harvesting of the crop is done at the stage of capsule maturity even when the crop is slightly green. The fruit is near rounded capsule of about 5-10 mm in diameter covered by persistent sepals. Mature capsule is non-dehiscent. The seeds are oval, lenticular, smooth, shining and pointed at one end measuring 4-6 mm length and 2-3 mm breadth. The seed colour varies from pure yellow,

yellowish with brownish tinge, deep fawn and light fawn, light brown to deep brown.

Economic Importance

Linseed occupies a greater importance among oilseeds, owing to its various uses and special qualities. In India, it is grown mainly for extracting oil. The oil content of the seed varies from 33 to 47 per cent. Linseed oil is not suitable for edible purpose because of its high alpha-linolenic acid concentration (Frankel, 1991). However, it is precisely this characteristic that makes linseed oil unsurpassed as a drying oil for manufacturing paint and varnishes, oilcloth, waterproof fabric pad and printing inks, leather and soap industries and linoleum as edible oil in some areas, varnishes, printing inks, etc. (McHughen, 1992). Successful breeding through mutagenesis led to the development of linseed mutants with seed oil containing less than 2 per cent alpha-linolenic acid (Green, 1986, Rowland and Bhatti, 1991). Such an oil is of great value for edible purposes (Bickert et al., 1994). Gamma-linolenic acid is a polyunsaturated fatty acid that attracts much interest because of its many health benefits (Fan and Chapkin, 1998). Research indicates several possible human health benefits associated with consumption of flax oil. Flax contains approximately 20 per cent alpha-linolenic acid (ALA, DM basis), an essential omega-3 fatty acid that is a precursor for eicosapentaenoic acid (EPA), which in turn is a precursor for the formation of eicosanoids. Eicosanoids are hormone-like compounds that play an essential role in immune response. Seed is a bowl cleaning fibre and act as an anticancer agent effective in colon, prostate and breast tumors. Linseed-cake is a very good manure and animal feed. Linseed straw produces fibre of good quality. Linseed is used in making paper, strong twines, canvas, house pipe (water storage tubs), suiting-shirting and various indispensable products for aerospace, aeronautical and defense purposes. Rough and strong fibre is used to make low cost roofing tiles based on convertible plastics of unsaturated polymers.

Genetic Resources

Germplasm accessions are supposed to be the library of the variable plant cultures of a particular crop. In any systematic breeding programme, for improving a crop with respect to desired trait(s), potential donor/lines are the prerequisite. The main objective behind the evaluation is to isolate the potential donors for their effective utilization in subsequent breeding programmes

for creating genetic variability for yield and yield components.

Due to wide range of variability in different traits exist in linseed, worldwide exploration, collection, evaluation and maintenance are prevailing for linseed germplasm. Linseed germplasm is currently being maintained at 38 centres in 28 countries. Major holding having more than 200 accessions are located in Russian Federation (5240), China (4886–3 centres), Romania (3701–3 centres), Ethiopia (3110), Germany (2763–3 centres), Czech Republic (2032–2 centres), Argentina (1125), Ukraine (1064–2 centres), Poland (547), Sweden (357) and Japan (287) (Tiwari, 2002). The countries with more than one center have duplicates in the holdings at different centres. In India a number of landraces and exotic germplasm were collected from different states/districts and from different countries through National Bureau of Plant Genetic Resources, New Delhi.

A total of 2,730 accessions are being maintained at All India Coordinated Research Project on Linseed under Indian Council of Agricultural Research Kanpur, in India comprising 2,180 of indigenous and 550 of exotic collections. While at National Gene Bank, New Delhi, a total of 2,365 accessions are maintained which has more than 2,242 collections predominantly of indigenous and 123 of exotic collections. About 85 per cent of the total collection represents the landraces and traditional varieties originated in different agro-climate or production systems. Besides others centres viz. Mauranipur (1300), Raipur (440), Kanpur (387), Nagpur (251), Hoshangabad (146) and Jashipur (107) also have active germplasm collections.

Efforts towards Varietal Development

In India, linseed is used for both oil and fibre so breeding for dual purpose in linseed is essential. A huge quantity of quality straw is wasted as fuel. If acceptable, fibre in appreciable quantity is introduced in the variety producing seed for oil purpose there would be high demand for dual purpose varieties in the market. Incorporation of genes for resistance to insect pests and disease is also a desirable objective as this causes substantial loss in yield. Development of early maturing and fertilizer responsive cultivars may cause a breakthrough in linseed cultivation in India since a considerable amount of yield loss has been observed in shedding of flowers and capsules in the late flowering varieties due to high temperature in the later period of growth.

With the inception of Coordinated Research Project on linseed in the country, number of high yielding seed types and dual purpose varieties have been developed viz. Gaurav, Meera, Shikha, Rashmi, Nagarkot and Parvati (Table 1). Double purpose varieties can compete well with other crops. The seed Act, 1966 and the Central Sub-Committee on Crop Standards, Notification and Release of Varieties in Agricultural Crops have played a great role in bringing out varieties developed in various crops in public domain and recognition to the role of seed quality in seed production to increase crop productivity. In the initial stage of crop improvement i.e., before 1967, the improved cultivars were selected from the local populations/landraces and resulted in the release of only ten varieties. This particular trend continued until 1980 with very little efforts of breeding in varietal development and consequently, 32 cultivars were released before 2,000 but the average productivity remained stagnant until mid eighties because of poor production technology and the susceptibility of released cultivars to various biotic/abiotic stresses. This demanded breeding for resistance, involving screening of germplasm for identification of sources and hybridization breeding for incorporation of gene(s) conferring resistance.

Although, development of cultivars for higher yield initially received more attention of breeders, but later cultivars coupled with tolerance for some of the biotic stresses were also developed. A significant progress has been made in this regard and about 56 varieties have been released, so far as a result of the efforts of All India Coordinated Research Project, State Agricultural Universities or State Agricultural Departments. Amongst the 56 released varieties 13 are the state released and 43 are released under Central Variety Release Committee at National level (Table 1). Most of them have been notified under the Section 5 of the Seeds Act. It is evident that there has been a major thrust for the development of early maturing and high yielding varieties. Of the total 56 varieties developed at national level, 46 varieties have been developed through pedigree selection and 10 varieties through mass selection. About 11 per cent of varieties released have exotic germplasm in their parentage. Exotic germplasm has not been of much use as they are poor yielder compared to the indigenous, late maturing, small seeded and tall plants. Similarly wild species were also not used in varietal improvement due to their cross incompatibility, hybrid in-viability, hybrid sterility and transfer of undesirable

genes. The oil content of the varieties ranged from 40-45 per cent.

Abiotic/ Biotic Stresses

For sustainable improvement, there is an urgent need for introduction of accessions with resistance to newly arising biotic and abiotic stress. Wilt, leaf spot, powdery mildew and rust are the major diseases of linseed and have been recorded from all the linseed growing areas. Rust infection not only damages the fibre and reduces the yield but also is reported to cause significant reduction in oil content. In wilt the plants are attacked at all stages of growth. Leaf spot is found to cause heavy damage to crop particularly in low lying ill drained areas and the powdery mildew occur mainly in the crop grown in rich soils under irrigated conditions.

Linseed budfly (*Dasineura lini*) is the most serious pest of linseed. Sometimes indigo caterpillar (*Spodoptera exigua*) and thrips (*Caliothrips indicus*) also cause substantial damage. Parasitism of linseed budfly by pteromalid larval parasitoid *Habrocytus fasciatus* goes up to 23 per cent (Anand Prakash and Chaturvedi, 1978), *Systests dasyneurae* is also a key parasitoid of linseed budfly. The most effective method to control the disease is to cultivate the resistant varieties. The growing of early varieties and mixed cropping are reported to reduce the incidence of the pest. In linseed *Alternaria* blight is the most serious diseases and bud fly is a major pest and both are treated on major thrust. A special screening under saline/alkaline soils has led to the identification of resistant lines.

The yield potential of varieties was found to be 800-1000 Q/ha under rainfed and 1500-2000 Q/ha under irrigated conditions. Some of the varieties such as RLU-6, NL-142, Neelum, Shekar, Parvati, RL-914, Suyog, BS-44 showed significantly higher yields (≥ 15 Q/ha, Table 1). Although K-2, Neelum and T-397 varieties were released 25-30 years ago yet are under commercial cultivation due to their higher yield percentage. On the other hand some of the state released varieties, which have lower yields were highly resistant to pests/diseases. Unlike other crops most of the varieties have a high degree of mono or multiple disease resistance. A number of high yielding and wilt resistant varieties are available such as NP (RR) 9, BS 44, Hira, Mukta, Neelum and Jawahar Linseed-23 (Table 1). Some of the varieties were mono disease resistance such as C-429 and Jawahar-17 are rust resistant and others are multiple disease resistant. Gaurav, Binwa, Baner, BS-44, Jawahar-1, M-

10 and Mayurbhan are both rust and wilt resistant. Similarly, Jeevan, Sheela, RLC-81, Meera, Rashmi, Shubra, Shikha, Laxmi-27, Nagarkot and chambal also are resistant to all three diseases-rust, wilt and powdery mildew. Whereas Nagarkot, RLC-76, Shikha and RLU-6 were found to be resistant to all rust, wilt, powdery mildew and *Alternaria* blight (Table-2). Varieties LC-185, Jawahar-552 and Jawahar-7 were found suitable for *Utera* cultivation. Although several Institutes from different states viz. Himachal Pradesh, Maharashtra, Rajasthan and Punjab had contributed for the development of linseed varieties, the maximum number of linseed varieties have been released from Kanpur, Uttar Pradesh (29 per cent).

Very few accessions have been used for transfer of specific desirable traits. Eighty per cent of the varieties have been developed predominantly using local collections, where selections from introduced germplasm has been the main breeding methodology. Therefore, for sustainability and to increase the yield, greater emphasis is required for exploitation of germplasm, primarily exotic to breed resistance to yield reducing factors and specific agronomic traits so that varieties for specific environment and requirement can be developed. The improved varieties recommended for cultivation in different zones are listed in Table 1.

The growing of resistant varieties is recommended to control these diseases (Table 2). On saline soils Hira and Mukta performed better than others (Rai and Sinha, 1980). Therefore, there is a need for incorporation of new, diverse and more stable sources of resistance and other desirable features, including wild species in the parentage.

Future Perspectives

Incorporation of resistance against stresses in combination of desirable commercial characteristics and widening of genetic base of the cultivars is an important challenge. In this regard, extensive hybridization with exotic sources and wild species provide a unique opportunity some of which have low linolenic acid (edible grade oil with 8% linolenic acid) viz., *L. sulcatum* (3%), *L. mucronatum* (3%), *L. salsoloids* (3%), *L. suffruticosum* (3.5%), *L. tenuifolium* (6.3%). Approaches to confer resistance to bacteria, nematodes and herbicides are enumerated in the recent reviews. Considerable research is needed to apply these tool and techniques to manage biotic stresses such as development of elite breeding lines resistant to *Alternaria* blight and bud fly and to abiotic

Table 1. List of Linseed varieties released from Indian Agricultural Research System till date

Variety	National Identity	Pedigree	Developing Institute	Developer	Notification No.	Adaptation Zone*	Yield Q/ha	Specific trait(s)	Additional trait (s)
Laxmi 27 (LMH-27)	IC113105	Neelum/KP-1/Neelum/NP(RR)-9/Neelum/R-1/Neelum/Afg-8	Chandra Shekhar Azad University of Agriculture & Technology (CSAU&T), Kanpur, UP	Dr. S.L. Katiyar	165 E, 06.03.1987	III	13	Resistant to rust, wilt and Powdery mildew	Deep brown seeds, Suitable for rain fed and irrigated conditions, Oil Content 45%
Sweta (LHCK-131)	IC113107	Mukta/T-1206	CSAU&T, Kanpur, UP	Dr. R.N. Dubey	540 E, 24.07.1985	II	9	Resistant to drought, frost, Non shattering, Resistant to rust	Plant erect, Suitable for late and early sowing, Oil content 44%
Shubhra (LHCK-21)	IC113108	Mukta/K-2	CSAU&T, Kanpur, UP	Dr. R.N. Dubey	540 E, 24.07.1985	II	12	Resistant to rust, wilt & powdery mildew	Erect growth, white flowered, brown seeds, Oil Content 45%
Neelum	IC113109	T-1/NP(RR)-9	CSAU&T, Kanpur, UP	Dr. N.K. Bajpai	13, 19.12.1978	II, III	15	High yielding	Double purpose variety, Oil content 43%
T 397	IC113110	T-491/T-1103-1	CSAU&T, Kanpur, UP	Dr. L.C. Gangwar	596 E, 13.08.1984	II	9	Tolerant to rust & wilt	Erect tall, Used as national check and Oil content 44%
Gaurav (LCK-152)	IC113111	Sel-3/EC-1552	CSAU&T, Kanpur, UP	Dr. R.N. Dubey	834 E, 18.09.1987	II	11	Resistant to rust and wilt	Tall plant, bold seeds, Fawn colour seeds, Double purpose variety, Oil content 43%
LC- 54	IC113155	K-2/Kangra local	Punjab Agricultural University (PAU), Ludhiana, Punjab	Dr. T.R. Gupta	19E, 14.01.1982	I	12	Resistant to rust, Powdery mildew & tolerant to Alternaria blight, Tolerant to frost	Erect growth habit with white flowers, Medium size seeds, Oil content 42%
LC-185	IC113156	NP(RR)-37/Kangra Local	PAU, Ludhiana, Punjab	Dr. T.R. Gupta	44 E, 21.08.1975	I	8	Tolerant to frost, Suitable for <i>Utera</i> cultivation	Short stature plant, yellow seeds
Parvati (LMH-16-5)	IC305053	EC41628/III/EC77959/II (DPL-20/ Neelum) (EC-216/Hira)/ (BR-1/ NP-440)	CSAU&T, Kanpur, UP	Dr. P.K. Singh	92 E, 02.02.2001	II, III	16	High yielding, Resistant to rust & Powdery mildew, Early maturity	Medium plant height, non-shattering capsule, Dull yellow seeds, Double purpose variety, Oil content 42%
Shekhar (LCK-9313)	IC305055	Laxmi-27/EC-1387	CSAU&T, Kanpur, UP	Dr. Brahm Singh	92 E, 02.02.2001	II	16	High yielding, Resistant to powdery mildew, Prust & wilt	Shiny brown seeds, Oil content 43%
NL-97	IC305109	R-7xRLC-4	Mahatma Phule Krishi Vidyapeeth (MPKV), All India Coordinated Research Project on Oil Seeds, Jalgaon, Maharashtra	Dr. S.K. Raut	92 E, 02.02.2001	III	6	Resistant to Powdery mildew, wilt, Alternaria blight & Bud fly, Earliness	Brown seed colour, Oil content 42%

Variety	National Identity	Pedigree	Developing Institute	Developer	Notification No.	Adaptation Zone*	Yield Q/ha	Specific trait(s)	Additional trait (s)
Binwa (KL-210)	IC420772	Flak-1x SPS-4777-10-3	Ch. Sarwan Kumar Krishi Vishwa Vidyalaya (Ch.S.K.H.P.K.V.), Palampur, HP	Dr.(Mrs.) Bhataria	State. O.122 (E), 02.02.2005	I	9	Resistant to rust and wilt	Purplish blue flowers, yellow seeds, Oil content 40%
Baner (KL-224)	IC420773	EC-21741x LC-216	Ch.S.K.H.P.K.V., Palampur, HP	Dr.(Mrs.) Bhataria	State. O.122 (E), 02.02.2005	I	5	Resistant to rust and wilt	Purple flower, brown seeds, Oil content 39.29%
Kiran (RLC-6)	IC426925	Afg-8/R-1//Afg-8	Indira Gandhi Krishi Vishwa Vidyalaya (IGKV), Raipur, Chhattisgarh	Dr.S.K. Agrawal	10 E, 01.01.1988	II,III	8	Resistant to rust, Powdery mildew & wilt	Medium plant height and seed size, Oil content 43%
Jawahar-552 (R-552)	IC426926	No.55/B-67	IGKV, Raipur, Chhattisgarh	Dr.S.K. Agrawal	596 E, 13.08.1984	III	9	Resistant to wilt, suitable for <i>utera</i> cultivation	Brown and bold seeds, Oil content 44%
Sheela (LCK-9211)	IC426928	Gaurav/Janki	CSAU&T, Kanpur, UP	Dr.R.N. Dubey	92 E, 02.02.2001	I	14	Resistant to rust, wilt & Powdery mildew, Early maturity	Shiny brown seeds, Oil content 41%
Rashmi (LCK-9216)	IC426929	Gaurav/Janki	CSAU&T, Kanpur, UP	Dr.R.N. Dubey	1050 E, 26.10.1999	II,III	10	Resistant to rust, wilt & Powdery mildew	Brown and shiny seeds, Double purpose variety, Oil content 41%
Garima (LHCK-39)	IC426930	T-126/Neelum	CSAU&T, Kanpur, UP	Dr.R.N. Dubey	540 E, 24.07.1985	II	14	Resistant to rust, wilt and bud fly	Brown seeds, Oil content 42%
Padmini	IC426932	EC41628/ EC-77959// DPL-20/ Neelum	CSAU&T, Kanpur, UP	Dr. P.K. Singh	1050 E, 26.10.1999	III	9	Bold seeds with high oil content	Brown seeds, Double purpose variety, Oil content 43%
Nagarkot (KL-31)	IC426935	New River/ LC-216	Ch.S.K.H.P.K.V., Palampur, HP	Dr.(Mrs.) Bhataria	408 E, 04.05.1995	I, II, III	12	Resistant to rust, wilt, Powdery mildew and tolerant to Alternaria blight.	Moderate tillering, Bold and brown seeds, Double purpose variety, Oil content 43%.
Surabhi (KL-1)	IC426936	LC-216/LC-185	Ch.S.K.H.P.K.V., Palampur, HP	Dr. (Mrs.) Bhataria	408 E, 04.05.1995	I	10	Early maturity, Resistant to rust & wilt	Medium and yellow seeds, Oil content 44%
Meera (RL-933)	IC427794	RL-75-6-2/ RL-298// LCK8528	MPUA & T, Udaipur, Rajasthan	Dr. C.S. Dubey	340 E, 03.04.2000	II	14	Resistant to rust, wilt & Powdery mildew.	Brown seeds, Double purpose variety, Oil content 42%.
RLC 81 (Indira Alsi-32)	IC449071	Kiranx Ayogi LCK 88062	IGKV, Raipur, Chhattisgarh	Dr. S.S.Rao	29.06.2005	III	8	Resistant to rust, wilt & Powdery mildew, Early maturity.	Dark brown seeds, Oil content 39.29%
RLC 76 (Kartika)	IC512310	Kiran/ LCK 88062	IGKV, Raipur, Chhattisgarh	Dr. S.S.Rao	29.06.2005	III	8	Early maturing, moderately resistant to rust, wilt & Alternaria blight and resistant to Powdery mildew	Oil content 42.9%

Variety	National Identity	Pedigree	Developing Institute	Developer	Notification No.	Adaptation Zone*	Yield Q/ha	Specific trait(s)	Additional trait (s)
Him Alsi-1	IC520864	K-2XTLP-1	Ch.S.K.H.P.K.V, Palampur, HP	Dr.S.Bhateria	-	-	14	Bold seeds, good yield	
Him Alsi 2	IC520865	NA	Ch.S.K.H.P.K.V, Palampur, HP	Dr.s.Bhateria	-	-	13	Bold seeds, good yield	
NL-142	IC523094	R7XRLC-6	Dr.PDKV, Akola, Nagpur, Maharashtra	DR.P.B. Ghorpade	State, 2004	III	15	High yielding, Earliness, resistant to Powdery mildew and Bud fly	Oil content 41.36%
Hira	IC523799	H-342/NP(RR)-9	CSAU&T, Kanpur, UP	Dr.N.K.Bajpai	429 E, 19.12.1978	II	10	Non shattering and bold seeds	Medium tall plant, spreading, moderate tillering, white and light blue flowers, Brown and Bold seeds, Denotified
Mukta	IC5237800	H-626/NP(RR)I-9	CSAU&T, Kanpur, UP	Dr.N.K.Bajpai	429 E, 19.12.1978	II	12	Medium yield with bold seeds	Errect basal branching, Denotified
Neela	IC5237801	Local selection from WB	Pulses & Oilseeds Research Station, Berhampore, WB	Not available	19 E, 14.01.1982	II	9	Tolerant to rust & wilt	Medium, brown seeds
Chambal Alsi	IC5239802	Local/RR-45	MPUA&T, Udaipur, Rajasthan	Dr.P.K.Dixit	13, 19.12.1978	III	12	Tolerant to wilt, rust & powdery mildew	Moderately spreading type, non dehiscent fruit, brown and bold seeds
Himalini (LC-45)	IC5239803	K-2/Kangra local	Ch.S.K.H.P.K.V, Palampur, HP	Dr.N.D.Rana	295 E, 09.04.1985	I	13	Resistant to rust, wilt and bud fly, Early maturity	White flowers, Brown seeds, Oil content 42%.
Jawahar-23	IC5239804	EC-9832/Heera	All India Co-ordinated Research Project on Sesame & Niger (JNKVV), Jabalpur, MP	Dr.S.R.Srivastava	540 E, 24.07.1985	III	9	Tolerant to lodging, frost, Non shattering, Resistant to rust, wilt	White flowers, Synchronous flowering and fruiting, Brown seeds, Oil content 43%
RL-914	IC5239805	RR-9/R-93/FLAKI/LC54	Maharana Pratap University of Agriculture & Technology, Udaipur, Rajasthan	Dr. (Mrs.) Veena Bhatnager	937 E, 04-09.2002	III	16	Resistant to Powdery A mildew, wilt, Iternaria blight	Errect branching, oval capsule
Suyog (SLS-27)	IC5239806	(KiranxKL 168) Kiran	JNKVV, Jabalpur, MP	Dr. S.K.Madana	8161 E, 04.02.2004	III	15	High yielding, Resistant to rust, wilt, Powdery mildew and Bud fly	White flower, light brown seed, Oil content 41.43%
LMS-4-27	IC5239807	Shubra/J1/J1/Kiran	C.S.A.U., Mauranipur	Dr. V.P. Nagaich		III	8	Resistant to wilt, Powdery mildew and Bud fly, Early maturity	Oil content 41.10%
Shikha (LCK-8528)	IC5239808	Hira/CRISTA	CSAU&T, Kanpur, UP	Dr.R.N.Dubey	647 E, 09.09.1997	II	12	Resistant to rust, wilt & tolerant to Powdery mildew & Alternaria blight	Brown and shiny seeds, Double purpose variety, Oil content 42%.

Variety	National Identity	Pedigree	Developing Institute	Developer	Notification No.	Adaptation Zone*	Yield Q/ha	Specific trait(s)	Additional trait (s)
RLU-6 (Sarswati)	IC5239809	Acc.750/RL-29-8	MPUA&T,Udaipur, Rajasthan	Dr. (Mrs.) Veena Bhatnager	State, 2002	II	17	High yielding, Resistant to rust and Bud fly & resistant to Powdery mildew and Alternaria blight	White flowers, Brown colour seeds, Oil content 40.48%
BS-44	NA	NA	Not Known	Not available	State, 1955	II,III	15	Resistant to rust and wilt	White flower, Bold and brown seeds
C-429	NA	H-3/IP-135	Maharashtra	Not available	429 E, 03.01.1983	III	10	Resistant to rust	Moderately spreading type, non dehiscent fruit, brown seeds, Denotified
Co.4 (MS-1316)	NA	NA	Not Known	Not available	State, 1985		10	Non lodging, Tolerant to drought and shoot fly, early maturity	Heavy tillering, Shiny yellow and bold seeds
IPI-6	NA	Sel from local material in Central Province	Not Known	Not available	State, 1964		8	Bold seeds	Blue flowers
Jawahar-1 (JLS-1)	NA	Selection of KP-29	Jawaharlal Nehru Krishi Vishwavidyalaya (JNKVV), Jabalpur, MP	Dr. S.K.Agrawal	19 E, 14.01.1982	III	9	Resistant to rust and wilt	Semi spreading type, Blue, synchronous flowering and maturity, brown seeds
Jawahar-17 (R-17)	NA	Selection of No.55	JNKVV, Jabalpur, MP	Dr. S.K.Agrawal	19 E, 14.01.1982	III	13	Resistant to rust	Errect plant with medium tillering, Brown and bold seeds
Jawahar-7 (R-7)	NA	Selection of No.55	JNKVV, Jabalpur, MP	Dr. S.K.Agrawal	19 E, 14.01.1982	III	7	Resistant to rust, Suitable for <i>utera</i> cultivation	Errect plants with deep root system, blue flowers with white ring in centre, Brown and medium seeds
Jeevan (DPL-21)	NA	Summi/LC-216	Ch.S.K.H.P.K.V. Palampur, HP	Dr. H.L.Thakur	10 E, 01.01.1988	I	11	Resistant to rust, wilt and Powdery mildew	Tall plant, Brown seeds, low tillering, uniform maturity, Oil content 45%
Jawahar Linseed-9	NA	RL-102/R-7/J-23	JNKVV, Jabalpur, MP	Dr. S.K.Madaria	425 E, 08.06.1999	III	10	Earliness, Resistant to rust, wilt and Powdery mildew	Medium height, white flowers, medium maturity, suitable for both rain fed and irrigated conditions. Oil content 42%
K-2	NA	Kangra Local/Nigarkot/ Bhagvan Local	PAU, Ludhiana, Punjab	Not available	44 E, 21.08.1975	I,II	11	Resistant to rust, Powdery mildew & wilt, Frost tolerant	Tall plants with low tillering, white flowers, brown and bold seeds
M-10	NA	NA	Not Known	Not available	State, 1901	III	5	Resistant to rust and wilt	Medium and bold seeds
Mayurbhanj	NA	Local var of Mayurbhanj, Orissa	Not Known	Not available	State, 1978	III	10	Resistant to rust and wilt	Bold seeds with shiny brown colour

Variety	National Identity	Pedigree	Developing Institute	Developer	Notification No.	Adaptation Zone*	Yield Q/ha	Specific trait(s)	Additional trait (s)
No. 55	NA	Developed from local bulk at Nagpur	Not Known	Not available	State, 1985	III	6	Bold seeds	Errect and profusely branched, Medium, dark brown and Bold seeds
NP (RR) 9	NA	Derivative of NP-124 x A 17-I-I	Not Known	Not available	State, 1984	I, II, III	11	Early maturity and good yield	Errect and compact plant, white flowers
Pusa -2 (L.S.2)	NA	Selection BS-12	All India Co-ordinated Research Project on Linseed (AICRP on Linseed), Kanpur, UP	Dr. S.D.Dubey	295 E, 09.04.1985	I,III	13	Resistant to rust and wilt, bud fly, Resistant to drought, Non shattering	Errect and compact plant, Brown and lustrous seeds, Oil content 45%
Pusa -3 (L.S.3)	NA	K-2/T-603	AICRP on Linseed, Kanpur, UP	Dr. S.D.Dubey	295 E, 09.04.1985	I,III	11	Resistant to rust and wilt, bud fly, Resistant to drought, Non shattering	Errect and compact plant, brown seeds, oil content 45%
S-36	NA	Selection from local material	MPKV, All India Coordinated Research Project On Oil Seeds, Jalgaon, Maharashtra	Not available	State, 2004	III	4	Drought resistance, Tolerant to powdery mildew & Alternaria blight	Semi spreading type, Brown seed colour
S-48	NA	Selection from local material	MPKV, All India Coordinated Research Project On Oil Seeds, Jalgaon, Maharashtra	Not available	State, 1959	III	5	Medium size seeds	Tall plant, chocolate colour seeds

NA: The seed is not available in the Gene Bank;

*Zone I : Punjab, Haryana, Himachal Pradesh, Jammu and Kashmir;

Zone II: Gangetic alluvium of Uttar Pradesh, Bihar, Jharkhand, West Bengal, Assam;

Zone III: Bundelkhand region of Uttar Pradesh, Madhya Pradesh, Chattisgarh, Orissa, Karnataka, Maharashtra and Rajasthan.

UP = Uttar Pradesh; HP = Himachal Pradesh; MP = Madhya Pradesh

Table 2. Sources of resistance in linseed varieties/ strains

Abiotic/biotic stresses	Sources of resistance
Abiotic stresses/Agronomic traits	
High yielding	Shekhar, Shubhra, Parvati, BS-44, Neelum, RLU-6, Suyog, Sheela, Surabhi, Himalini, NL-142, RL-914
Early maturity	RLC-76, Jawahar-1, NL-142, JLS-9, NL-97, RLC-81, RLC-29, TLP-1
Drought Tolerant	Sweta, Co-4, Pusa-2, Pusa-3, S-36
Frost Tolerant	Sweta, LC-54, J-23, LC-185
Tolerance to salinity/ sodicity	Hira, Mukta, T-397, Sweta
Non shattering types	Sweta, Parvati, Hira, Chambal Als, Jawahar-23, C-429, Pusa-2, Pusa-3
Early maturity	Parvati, NL-97, Sheela, Surabhi, RLC-81, RLC-76, NL-142, Himalini, LMS-4-27, Jawahar linseed-9, NP (RR)9
Double purpose	Gaurav, Meera, Jeevan, Nagarkot, Shikha, Rashmi, Parvathi, Neelum, Padmini
Utera Cultivation	LC-185, Jawahar-552, Jawahar-7
Biotic stresses	
Powdery mildew	Shekhar (LCK-9313), NL-97, RLC 81, Parvati (LMH-16-5), LC- 54, Surabhi, Sheela, Rashmi, Meera, Shikha, Laxmi 27, Jeevan, Suyog (SLS-27), Nagarkot, LMS-4-27
Rust	RLC-76, JLS-9, Shekar, Swetha, Shubra, Baner, Garima, Padmini, Himalini, Parvati, RLU-6, Binwa, Kiran, LC-54, Surabhi, Sheela, Rashmi, Jeevan, Suyog (SLS-27), Nagarkot, T-397, Guarav
Wilt	JLS-9, Binwa, Kiran, Surabhi, Sheela, Rashmi, Meera, Shikha, Laxmi 27, Jeevan, Suyog, Nagarkot, LMS-4-27, RS- 552, T-397, Guarav
<i>Alternaria</i> blight	Nagarkot, LC-54, NL-97, RLC-76
Bud fly	NL-142, Suyog, LMS-4-27, Neela, NL-97

stresses viz., development of high yielding and early maturity varieties, edible grade oil varieties in linseed. Resistance to insect pests and viruses is an achievable goal in many instances. Search for novel insecticidal proteins and characterization of viruses specific to oilseed crops is an important endeavour. Recent trends indicate that management of bacterial and fungal disease to the desirable extent is also feasible.

These varieties contain important constellations of useful genes, but may need further improvement to meet the requirement of changing scenario. In order to have their effective utilization, inventorisation and conservation of these varieties is essential. The present article is an attempt in this direction. Authors hope that the preliminary information assembled on released varieties of linseed with desired information and their availability in the National Gene bank will facilitate their use in linseed improvement programme of India.

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Interrelationships Among Species of *Dioscorea* Revealed by Morphological Traits and RAPD Markers

KI Asha*, GM Nair¹, M Padmesh², MC Nair³ and JV Reji²

NBPGR Regional Station, Vellanikkara, Thrissur-680 654 (Kerala)

¹ Department of Botany, University of Kerala, Thiruvananthapuram, Kerala

² Tropical Botanical Garden and Research Institute, Palode, Thiruvananthapuram, Kerala

³ Department of Botany, Government Victoria College, Palakkad, Kerala

This present study assessed the interrelationships among the 12 species of *Dioscorea* by morphological traits and RAPD analysis using 14 decamer primers. In the molecular profiling of the 12 species of *Dioscorea* a total of 133 amplified products were obtained. Of the 133 amplified products all were found to be polymorphic showing high degree of genetic variability between species of *Dioscorea*. Morphologically related species such as *D. oppositifolia*, *D. spicata* and *D. wightii* got separated in RAPD analysis. Moreover, both RAPD and morphology separated *D. hispida* of the Section Lasiophyton from the other two species such as *D. pentaphylla* and *D. tomentosa*. Out of the 12 species studied, 9 species were grouped into 2 clusters and *D. bulbifera* remained as a separate entity. The results were in agreement with the earlier classification except *D. hispida* and *D. pubera*, which remained as distinct entities from the rest. But on the basis of RAPD data, nine species were grouped into two major clusters with each species showing distinct genetic distance with others, while the rest of the three *D. hispida*, *D. oppositifolia* and *D. wightii* remained as separate entities.

Key words: *Dioscorea* species, Interrelationship, Morphological characterization, RAPD

Yams belonging to the genus *Dioscorea* of the family Dioscoreaceae, are the major staple food in many tropical and subtropical countries and also a major source of pharmaceutical products such as diosgenin, botogenin, Kryptogenin, etc. Out of the 600 species reported, 23 species occur in the Indian subcontinent and 44% of these are endemic (Prain and Burkill, 1938). Based on the morphological characterization, the genus *Dioscorea* has been divided into different Sections viz., Borderea, Stenophora, Stenocorea, Combilium, Illigerastrum, Paramecocarpa, Shannicorea, Opsophyton, Lasiophyton and Enantiophyllum (Prain and Burkill, 1936). The present study focused on the 12 selected species of *Dioscorea* collected from Southern Western Ghats, belonging to 3 different sections. The species *D. bulbifera* which belongs to the section Opsophyton is characterized by the stem twining to the left, other three species viz., *D. hispida*, *D. pentaphylla*, *D. tomentosa* belonging to the section Lasiophyton are also characterized by left twining stem but with compound leaves and eight species belonging to the section Enantiophyllum are right twining.

Morphological variations, cytogenetic relationships, breeding systems and biochemical markers used in elucidating the relationships among species suffer some of the inherent limitations as these marker types depends on gene expression, which may be sensitive to

environmental influence, genetic background, developmental stage and tissue type. Hence more reliable protein or DNA profiling is now gradually replacing the traditional method of identifying cultivars by morphological characters. RAPD markers are suitable for determining similarities among inbreds, genotype identification, species classification, establishing phylogenies, fingerprinting varieties, tagging desirable genes and mapping plant genomes.

Materials and Methods

Materials analysed

Twenty-four accessions, two each from the twelve species, procured from National Bureau of Plant Genetic Resources (NBPGR) Regional Station, Thrissur, Kerala were grown in the green house of the Department of Botany during 2001-04 (Table 1). For RAPD analysis, one accession each from the 12 species having the species specific morphological traits was selected (Table 1). Young leaf samples were used for DNA extraction and analysis.

Methodology

Morphological Characterization

Morphological characterization was done using the standard descriptors published by the International Plant

* Corresponding author's E-mail: ashakarthy@rediffmail.com

Table 1. Materials characterized morphologically and by RAPD

Species	Accession number	Locality of collection
<i>Dioscorea pentaphylla</i> L.	IC202352	Nilambur, Malappuram, Kerala
	IC202367*	Peechi, Thrissur, Kerala
<i>Dioscorea oppositifolia</i> L.	IC202386*	Valpara, Palghat, Kerala
	IC210336	Coimbatore, Tamil Nadu
<i>Dioscorea hispida</i> Dennst	IC202369	Nilambur, Malappuram, Kerala
	IC202370*	Nilambur, Malappuram, Kerala
<i>Dioscorea tomentosa</i> Heyne	IC202376	Parambikulam, Palghat, Kerala
	IC202379*	South Canara, Karnataka
<i>Dioscorea belophylla</i> Voight	IC248181*	Devakolly, Coorg, Karnataka
	IC248181A	Thirunelli, Wynad, Kerala
<i>Dioscorea wightii</i> Hk. f.	IC210447A	Papanasam, Mundanthurai, Tamil Nadu
	IC214855*	Mundanthurai, Tamil Nadu
<i>Dioscorea intermedia</i> Thw.	IC202384*	Santhanpara, Idukki, Kerala
	IC210409	Kattappana, Idukki, Kerala,
<i>Dioscorea wallichii</i> Hk. f.	IC202312*	Courtallum, Tirunelveli, Tamil Nadu
	IC202320	Vellani Hills, Thrissur, Kerala
<i>Dioscorea hamiltonii</i> Hk.	IC202326	Courtallum, Tirunelveli, Tamil Nadu
	IC202328*	Vadakkancherry, Thrissur, Kerala
<i>Dioscorea spicata</i> Roth.	IC202383*	Thirthahally, Coorg, Karnataka
	IC248245	Uttara Kannada, Karnataka
<i>Dioscorea bulbifera</i> L.	IC202349*	Peechi, Thrissur, Kerala
	IC298648	Madathara, Trivandrum, Kerala
<i>Dioscorea pubera</i> Bl.	IC202382*	Begur, Wynad, Kerala
	IC298641	Elangium, Trivandrum, Kerala

* Accessions characterized by RAPD

Genetic Resources Institute on *Dioscorea* spp. (IPGRI, 1997). Due to the absence of flowering or erratic nature of flowering in the species under *ex-situ* conditions, only vegetative traits were taken into consideration. In order to find out the interrelationships among the 12 species, tuber raised plants at the vegetative growth stage of 120 to 180 days were scored for morphological traits. Data of above ground vegetative traits such as stem, leaves and bulbils were recorded at the maximum growth period during September-October and that of below ground tubers at the time of harvest during January.

The qualitative character states were scored as present (1) or absent (0) across all the accessions. The two-way data matrix of accessions x traits was used to calculate pair-wise similarity coefficients following Jaccard (1908). This matrix of similarity coefficients was subjected to unweighted pair-group method analysis (UPGMA) to generate a dendrogram using average linkage procedure. The numerical taxonomic analyses were carried out using the software, NTSYS-pc, Version 1.80 (Exeter Software, New York).

Molecular Profiling using RAPD

Genomic DNA Extraction

Total genomic DNA was extracted from fresh young leaves of the *Dioscorea* species using CTAB with appropriate modifications (Murray and Thompson, 1990). 1.2% PVP was added to the extraction buffer to remove phenolic contaminants followed by double chloroform extraction at 10000 rpm. DNA after ethanol precipitation was resuspended in 100 µl of 10:1 TE buffer and quantified using spectrophotometer at 260 nm.

PCR Analysis

Fourteen random 10-base primers were used in this study (Table 2). PCR was carried out in a 25 µl reaction mixture containing 2.5 µl 10x amplification buffer, 200 µM each of dATP, dTTP, dGTP, dCTP, 1.0 U Taq DNA polymerase (10 mM Tris HCl, pH 9.0, 1.5 mM MgCl₂, 50mM KCl and 0.01 % gelatine) from Finnzymes, 15 pmoles of 10mer primer (Operon Technologies Inc, USA & Biogene, USA) and 50 ng of genomic DNA. Amplification was performed in a Perkin-Elmer DNA Thermal Cycler (DTC 480). The sequential steps involved

were: 2 minutes at 94°C, 2 minutes at 36°C and 2 minutes at 72°C. This cycle was followed by 38 cycles of 1 minute at 94°C, 1 minute at 36°C and 2 minutes at 72°C. The last cycle was followed by 7 minutes extension at 72°C.

After completion of the PCR, the amplified products were resolved in 1.5% agarose gel (1xTBE) followed by ethidium bromide staining. 3 µl of the amplified sample was loaded into the wells and electrophoresis started with 94 V from a power pac (Pharmacia Biotech, USA). After electrophoresis, the bands were detected and documented using Alpha Chemi Imager Gel Documentation System. Amplified products that were reproducible and consistent in performance were chosen for data analysis. The two-way data matrix of species x traits was used to calculate pair-wise similarity coefficients following Jaccard (1908). This matrix of similarity coefficients was subjected to unweighted pair-group method analysis (UPGMA) to generate a dendrogram using average linkage procedure. The data was analyzed using NTSYS-pc, Version 1.80 (Exeter Software, New York).

Results

Simple Leaf Bearing Species

The nine different species of *Dioscorea*, which bear simple leaves, showed variations in qualitative juvenile traits. Waxy stem in *D. wallichii*, *D. oppositifolia*, *D. intermedia* and *D. bulbifera*, angular stem in *D. bulbifera* and *D. belophylla* and dense hairy stem in *D. pubera* are distinct variations in *Dioscorea* species which enable the taxonomic identity for each taxa. Stem

spines were recorded only in *D. wallichii* at early stages and at the same time stem was waxy in *D. wallichii*, *D. oppositifolia*, *D. belophylla* and *D. intermedia*. The anti clock-wise stem twining is a unique feature in *D. bulbifera*. Juvenile leaf pubescence was recorded in *D. spicata*, *D. bulbifera* and *D. pubera*.

The leaf traits of the species form important criteria in identification of the species in natural conditions. Arrangement of leaves is alternate in all except *D. oppositifolia* and *D. spicata* where it is alternate at base and opposite above. Leaf shape ranges from ovate in *D. oppositifolia* and *D. spicata*, followed by cordate long in *D. intermedia* and *D. pubera*, cordate broad in *D. bulbifera* and *D. wightii*, sagittate long in *D. hamiltonii* and *D. belophylla* and deltoid in *D. wallichii*.

The vegetative propagating unit, aerial bulbils recorded in different species also showed variation in bulbil traits. Bulbil production *in situ* was noticed only in four species studied in this group namely *D. bulbifera*, *D. hamiltonii*, *D. belophylla* and *D. pubera*. The shape ranges from round in *D. bulbifera*, callus like in *D. belophylla* and *D. hamiltonii* to ovate in *D. pubera*. The outer skin colour is grey in *D. pubera* and brown in others. Surface is rough with presence of roots in all except *D. pubera*. Bulbil flesh colour varied between orange-yellow in *D. pubera*, light green in *D. bulbifera* and *D. hamiltonii* and white in *D. belophylla*. Bulbil number ranges between an average of nine in *D. pubera*, 30 in *D. bulbifera* to small and many in *D. hamiltonii* and *D. belophylla*.

Tuber traits are the most variable among the different species of *Dioscorea*. Highly branched, elongated thin tubers, fused at knot and having prickly appearance, is a characteristic feature of *D. wallichii*. Tuber flesh colour is white in all except for orange in *D. pubera*, yellow in *D. bulbifera*, cream in *D. oppositifolia* and *D. wallichii*. Inner skin colour is white in all except for purple in *D. oppositifolia*, light yellow in *D. bulbifera*, cream in *D. wallichii* and *D. intermedia* and light orange in *D. pubera*.

Compound Leaf Bearing Species

The three different compound leaf bearing *Dioscorea* species viz., *D. tomentosa*, *D. hispida* and *D. pentaphylla* also showed distinct variations in morphological traits at various growth stages. Stem is pubescent in *D. tomentosa* but glabrous in others. Spine on the stem varied between short and curved downwards in

Table 2. Primers used for RAPD analysis and their results

#	Primers	Primer sequence 5' → 3'	No. of bands	No. of polymorphic bands
1	OPP 02	TCGGCACGCA	10	10
2	OPP 09	GTGGTCCGCA	6	6
3	C63	GGGGGTCTTT	5	5
4	C64	CCGCATCTAC	8	8
5	C66	GAACGGACTC	14	14
6	C67	GTCCCGACGA	11	11
7	C68	TGGACCGGTG	12	12
8	C69	CTCACCCTCC	9	9
9	C70	TGTCTGGGTG	10	10
10	C71	AAAGCTGCGG	8	8
11	C74	TGCGTGCTTG	13	13
12	C75	GACGGATCAG	12	12
13	C78	TGAGTGGGTG	6	6
14	C79	GTTGCCAGCC	9	9
Total number of bands			133	133
Mean per primer			9.5	9.5

D. pentaphylla, long and curved upwards in *D. hispida* to short and straight in *D. tomentosa*. The identifying unique feature of *D. pentaphylla* and *D. hispida* is the presence of coalescent spines.

The number of leaflets showed wide range of variation in this group. The leaf is trifoliate in *D. hispida*, tri- to penta-foliate in *D. pentaphylla*, while, variable with simple, bilobed and trilobed in *D. tomentosa*. The lamina and petiole are highly tomentose in *D. hispida* and *D. tomentosa*. The leaf margin is serrate in *D. tomentosa*. The shape and size of leaflets in compound leaf bearing forms is of considerable importance. In *D. pentaphylla*, the terminal leaflet is elliptic and laterals inequilateral, whereas, in *D. tomentosa* the leaflets are ovate-broadly elliptic with laterals oblique at base and in *D. hispida*, ovate to abruptly acuminate. Among these 3 species, *D. pentaphylla* alone produces aerial bulbils, is elongated in shape with dark brown rough skin having roots on the surface. The tubers were elongated and cylindrical in *D. pentaphylla* and *D. tomentosa* while spherical and amorphous with numerous hairs in *D. hispida*. In *D. hispida*, the inner and outer skin colour is cream with light yellow tuber flesh. The tuber flesh colour and inner skin colour was white to cream in *D. pentaphylla* and *D. tomentosa* and the outer surface looks prickly in appearance by the presence of stiff hairs.

Interrelationship Based on Morphology

The sections of the genus *Dioscorea* comprising of different species based on the classification by Prain & Burkill (1936) is taken as the basis for numeric taxonomic studies. The resulting dendrogram obtained by morphologic characterization is summarized in Fig. 1, which depicts the detailed clustering pattern of all the 12 species. A comparative account of the earlier classification by Prain & Burkill (1936) along with the present clustering of individual species is presented in Table 3a.

Cluster Analysis

The numerical taxonomic studies of the 12 species selected for study resulted in the identification of 2 major clusters having a single sub-cluster. The dissimilarity coefficients ranged between 7.391 and 19.12%. Based on the dendrogram formed from the similarity matrix of 143 characters, the cluster I included *D. pentaphylla* and *D. tomentosa* with a similarity coefficient of 84.22%. The II cluster included most of the species coming under section Enantiophyllum, except *D. pubera* and the

similarity level ranged between 83.8 to 92.6%. The exceptions, *D. hispida* of cluster I (Lasiophyton group) and *D. pubera* of cluster II (Enantiophyllum group), was similar to the I as well as the II cluster at a similarity level of 82.7% and 82.5%, respectively.

Interrelationships among *Dioscorea* species Based on RAPD

RAPD profiles of the representative samples of 12 species using 14 decamer primers generated 133 amplified products all of which were found to be polymorphic. Of the 14 primers, the number of scored markers produced by each primer ranged from a maximum of 14 in case of C66 (Plate) to a minimum of 5 as in the case of C63, with an average of about 9.5 markers per primers (Plate). The data showed a mean value of 9.5 products per primer (Table 2). Further the total number of products detected in individual species ranged from 13 to 51 with an average of 35.3 per primer. The maximum number of bands were produced by *D. hispida* (51) followed by *D. oppositifolia* (50), *D. intermedia* (49), *D. belophylla* (49), *D. tomentosa* (47), *D. hamiltonii* (44), *D. pentaphylla* (35), *D. wightii* (33), *D. spicata* (29) and *D. bulbifera* (13).

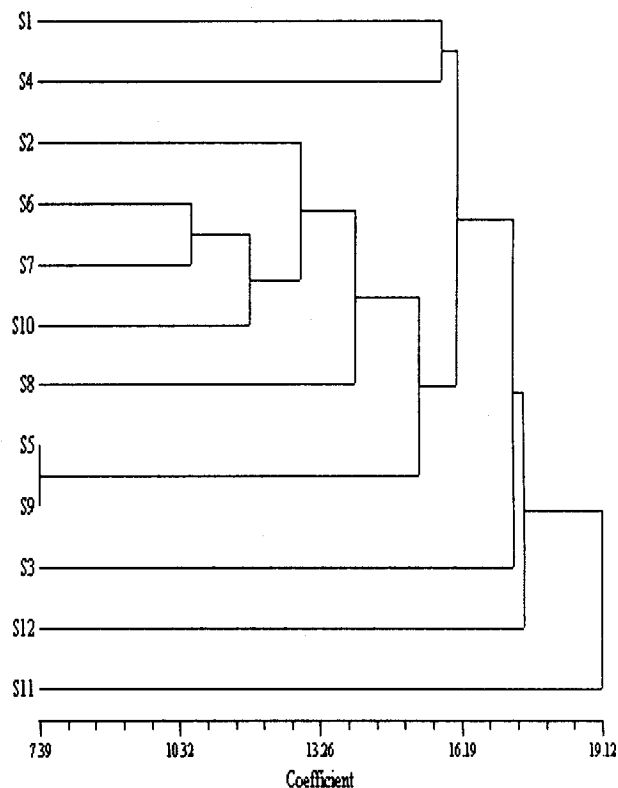
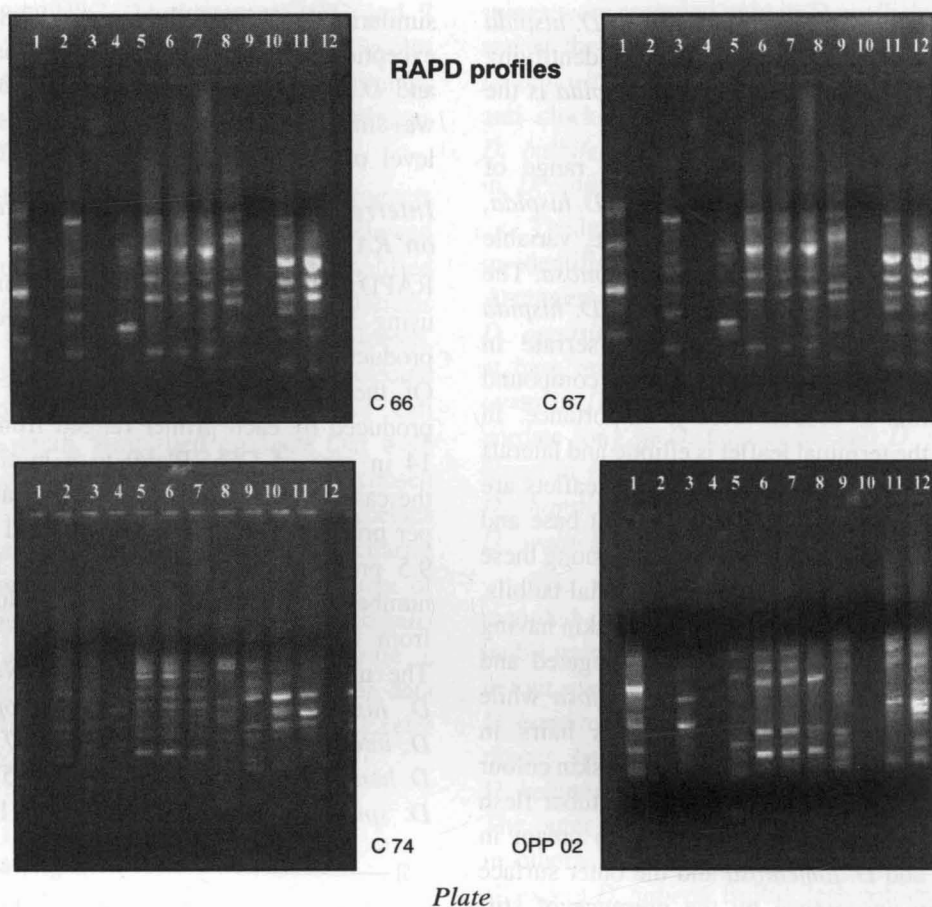


Fig. 1: Dendrogram generated by morphological characterization



Cluster Analysis

The dendrogram generated based on the genetic distance from RAPD data is shown in Fig. 2. Cluster analysis of the data shows grouping of 9 out of the 12 species into 2 major clusters. A comparative account of the earlier classification by Prain & Burkill along with the present clustering of individual species based on RAPD data is presented in Table 3b.

Cluster I

Cluster I have only 2 species *D. tomentosa* and *D. pentaphylla* of the section Lasiophyton with a similarity coefficient of 86.13%. Here *D. hispida* of the same section gets separated.

Cluster II

Cluster II comprised of 7 species viz., *D. pubera*, *D. bulbifera*, *D. wallichii*, *D. spicata*, *D. intermedia*, *D. belophylla* and *D. hamiltonii*. All the species in this cluster coming under the section Enantiophyllum and *D. bulbifera* of the section Opsophyton were grouped together within a range of 85.17 to 94.08 similarity having a ball cluster consisting of *D. intermedia* and

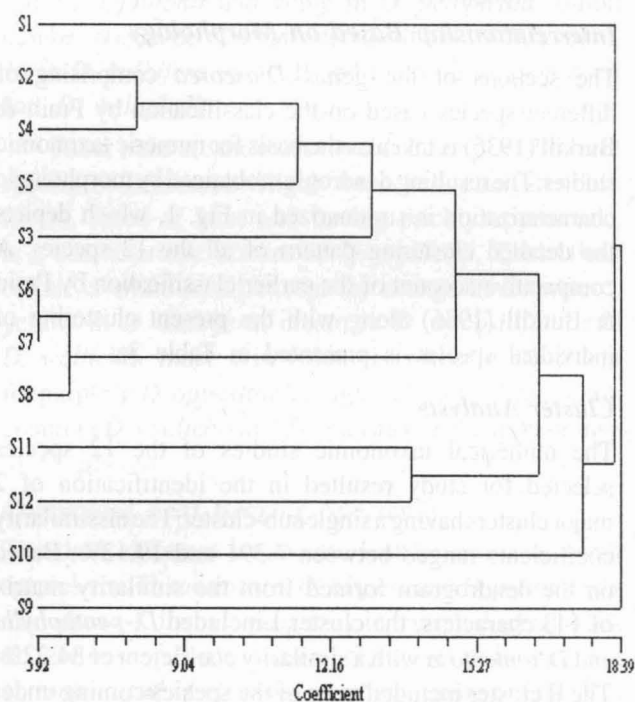


Fig. 2: Dendrogram generated by RAPD characterization

Table 3a. Comparison of Sections of *Dioscorea* based on morphology

Sections	Species	Cluster	Species
Lasiophyton	<i>D. tomentosa</i>	I	<i>D. pentaphylla</i>
	<i>D. pentaphylla</i>		<i>D. tomentosa</i>
	<i>D. hispida</i>		
	—	—	<i>D. hispida</i>
Enantiophyllum	<i>D. wightii</i>	II	<i>D. oppositifolia</i>
	<i>D. intermedia</i>		<i>D. wightii</i>
	<i>D. spicata</i>		<i>D. intermedia</i>
	<i>D. hamiltonii</i>		<i>D. spicata</i>
	<i>D. wallichii</i>		<i>D. wallichii</i>
	<i>D. belophylla</i>		<i>D. belophylla</i>
	<i>D. oppositifolia</i>		<i>D. hamiltonii</i>
	<i>D. pubera</i>		
	—	—	<i>D. pubera</i>
Opsophyton	<i>D. bulbifera</i>	—	<i>D. bulbifera</i>

D. belophylla with a similarity % of 94.084, determined to be the closest among the species studied.

The analysis of the morphovariability and interrelationships among species of *Dioscorea* at the molecular level using RAPD revealed that among the 12 species studied, 9 of them were distinctly grouped in 2 clusters and the rest 3 species viz. *D. oppositifolia*, *D. hispida* and *D. wightii* stood apart. Of the 3 divergent species, *D. hispida* shows closeness to *D. pentaphylla* and *D. tomentosa*. *D. oppositifolia* seems to be the most divergent member from all the others with a mean similarity value of 81.61%. The mean value of the coefficients of similarity for cluster II is 90.41% and for cluster I is 84.28%. Analysis of RAPD data indicated that the extend of inter specific variation in the genus is relatively less as evidenced by the coefficient of similarity values that ranges from 81.61 to 94.08, with a mean value of 87.84%.

Discussion and Conclusion

A critical observation of the present clustering showed that out of the 12 species selected for the present study, 10 of them retained their integrity as in the grouping by Prain and Burkill, except for *D. hispida* in the group Lasiophyton and *D. pubera* in Enantiophyllum. *D. bulbifera* was retained as a separate entity and is in conformity with the earlier classification. As far as the species diversity and geographical distribution are concerned, the present clustering pattern did not show any strict relation as the species from different geographical region are grouped in one cluster.

The grouping of the two varied compound leaf bearing species *D. tomentosa* and *D. pentaphylla* with similar leaf venation pattern into a single cluster depicts

Table 3b. Comparison of Sections of *Dioscorea* with RAPD cluster analysis

Sections	Species	RAPD cluster	Species
Lasiophyton	<i>D. pentaphylla</i>	II	<i>D. pentaphylla</i>
	<i>D. tomentosa</i>		<i>D. tomentosa</i>
	<i>D. hispida</i>		
	—	—	<i>D. hispida</i>
Enantiophyllum	<i>D. wightii</i>	I	<i>D. pubera</i>
	<i>D. intermedia</i>		<i>D. bulbifera</i>
	<i>D. spicata</i>		<i>D. wallichii</i>
	<i>D. hamiltonii</i>		<i>D. spicata</i>
	<i>D. wallichii</i>		<i>D. intermedia</i>
	<i>D. belophylla</i>		<i>D. belophylla</i>
	<i>D. oppositifolia</i>		<i>D. hamiltonii</i>
	<i>D. pubera</i>		
	—	—	<i>D. wightii</i>
	—	—	<i>D. oppositifolia</i>
Opsophyton	<i>D. bulbifera</i>	—	—

the importance of leaflet number in the classification of species. Wilkin (1999) on the basis of leaflet number and vein characters grouped the six African yams into two sections.

The divergence of *D. hispida* from Cluster I and *D. pubera* from cluster II needs further analysis on molecular basis to confirm its position in Prain & Burkill's Sections Lasiophyton and Enantiophyllum, respectively. In effect it can be concluded that the species holds distinct variability with respect to vegetative and tuber characteristics and there exist 2 major clusters and 3 distinct species from the rest among the 12 species available in Southern Western Ghats.

In molecular profiling using RAPD, of the 133 amplified products obtained from 14 decamer primers showing 100% polymorphism suggests a high degree of genetic variability between species of *Dioscorea*. Polymorphisms arise because sequence variations in the genome alter the primer binding sites. A similar result of high polymorphism suggesting intraspecific variability was suggested among 18 cultivars/species of *Dioscorea* (Lay *et al.*, 2001). Polymorphisms resulted from mutations or rearrangements either at or between the primer binding sites are detected as presence or absence of a particular RAPD band. Intervarietal and interspecific polymorphisms of RAPD data enabling reliable discrimination of Jamaican cultivars of *Dioscorea* were reported by Asemota *et al.* (1996). Out of the 12 species studied, 9 species were grouped into 2 major clusters, while the rest of the three remained as separate entities on the basis of RAPD data. Moreover the closely related species based

on morphological grouping such as *D. oppositifolia*, *D. spicata* and *D. wightii* gets separated in RAPD analysis.

In morphological clustering, *D. hispida*, the trifoliate species remained distinct which according to the classification by Prain & Burkill (1938) comes along with the other compound leaf bearing species such as *D. pentaphylla* and *D. tomentosa*. The separation of *D. hispida* in morphological grouping may be due to its trifoliate leaflet condition than the varied leaf nature of *D. pentaphylla* and *D. tomentosa*. The RAPD result also supports the separation of *D. hispida* from cluster I.

The grouping of the 2 compound leaf species *D. pentaphylla* and *D. tomentosa* in the same cluster shows that morphology and RAPD are equally effective in the elucidation of interrelationship of *Dioscorea* species.

In morphological grouping *D. pubera*, *D. hispida* and *D. bulbifera* are the most divergent species whereas in RAPD *D. oppositifolia*, *D. hispida* and *D. wightii* shows distinctiveness. In this *D. pubera* and *D. bulbifera*, which gets separated in morphological classification, comes along with the simple leaf forms in RAPD clustering. Moreover, *D. wightii* and *D. oppositifolia*, which were grouped together into a single group along with 5 species by morphological clustering, were found to be divergent in the RAPD analysis. Even though *D. intermedia* did not form a close cluster with *D. belophylla* and *D. hamiltonii* in morphology, they form a single group in RAPD. The results of the present study showed that RAPD analysis is a rapid and useful approach for distinguishing closely related species of *Dioscorea* as well as for estimating genetic distance among the species.

As the study reveals varied nature of interrelationships and divergences among the species, there is a need for in-depth molecular studies using more primers and also

using other molecular markers such as RFLPs, ISSRs and AFLP etc. for conclusively elucidating the genetic diversity and assessing the phylogenetic relationships among *Dioscorea* species.

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An Efficient Methodology for Processing of Herbarium Specimens of Cultivated Plants

Anjula Pandey, E Roshini Nayar and Rita Gupta

*National Herbarium of Cultivated Plants, Division of Plant Exploration and Germplasm Collection
National Bureau of Plant Genetic Resources, New Delhi 110 012*

An efficient method of processing has been developed for depicting diverse range of material represented in the National Herbarium of Cultivated Plants, National Bureau of Plant Genetic Resources (NBPGR), New Delhi. This method is especially suitable for drying herbarium specimens and economic products that are bulky, fleshy, change quality drastically (colour) or separate into parts on processing. In addition, fungal/ insect infection manifested during processing was also minimized using this method. Thus this method proves to be an efficient one, less time and labour consuming as compared to traditional processing techniques.

Key words: Herbarium methodology, Preservation, Efficient methodology

The National Herbarium of Cultivated Plants (NHCP) holds diversity of plant specimens of cultivated taxa and their wild/weedy relatives, wild economic types and the economic products referred for studies on plant genetic resources and various research and teaching programmes. The variability included in different crop-groups has been represented as cereals and pseudo-cereals, legumes, fruits, vegetables (including rhizomes, bulbs, tubers), spices and condiments, etc. The herbarium specimens are prepared by processing the plant material by placing between absorbent sheets, pressing and drying by periodically changing the sheets until it dries (Lawrence, 1951; Jain and Rao, 1976; Nayar, 1998). The processing of difficult material is generally done by use of artificial heat, slicing/sectioning and removal of extra tissue, use of hot-water. Besides, complementary collections as photographs/digital images and illustrations/ line-diagrams and wet preservation are also included to cover wide range of diversity.

Specimens of difficult to preserve plant groups are generally represented as pickled material (wet preservation) or bulky herbarium. Traditional drying techniques are prolonged, and sometimes materials do not retain original quality and features and thus have least significance for use in taxonomic identification. Getting a perfect specimen is difficult in case of fleshy materials like succulent fruits and vegetables, tubers, rhizomes, rooted materials, fleshy flowers, etc.

Techniques using high frequency waves have been frequently used in processing of living material (Brown and Gordon, 1967; Trappe, 1982; Hu, 1992). Microwaves are one of the most commonly used radiations that have demonstrated their inertness to cellulose (Brandt and

Berteaud 1987). They have been frequently used to disinfect cereals and liquid produce in food and agriculture industry (Delaney *et al.*, 1968). Use of microwave radiation for few minutes has been proved to be useful to cause mortality of fungal spores, eggs, larvae, nymphs and adults of many storage fungi/ insects (Flieder *et al.*, 1995). The microwave technique has been advantageous as it is safe to use and available as compact equipment ideal for routine handling.

Use of microwaves for preserving the plant specimens under long-term conditions is still uncommon. In the present investigation selected species that are difficult to process for inclusion as herbarium specimens have been standardized for microwave treatment. This methodology has proved to be an efficient one and may be extended to achieve good quality of specimens as well to prolong their self life by reducing bio-deterioration caused by storage fungi, insects, that infect/infest in succulents and tubers, rhizomatous material etc.

Materials and Methods

The sample specimens of the test material was cut in to appropriate size and exposed to different doses of irradiation using microwave oven (BPL-Sanyo, model no BMC-900T; 40 litre capacity; 230 vol. 50 Hz). The plant specimen was placed on the glass turntable of the microwave oven and subjected to different degree of treatment from higher to lower dosage (in alternate days). Power (from 100-750 watts) and processing time (10-120 seconds) were selected according to the type and texture of the material (Table 1). After treatment with microwave, conventional drying procedure was followed. This process was repeated till specimen was completely dried. A control set of the test material was subjected to

Table 1. Preparing herbarium specimens using different treatment with microwave

Species (Family)	Plant / part(s)	Treatments (sec.)	Days for complete drying		Observations
			Microwave	Control	
<i>Daucus carota</i> L. (Apiaceae)	Root, full plant	80, 40, 10	8	15	Time reduced, no shrinkage
<i>Allium</i> (<i>A. sativum</i> , <i>A. cepa</i> , <i>A. tuberosum</i> , <i>A. clarkei</i>) (Alliaceae)	Plant, bulb	70, 50, 20, 10	12	20	Time reduced, no infection
<i>Brassica oleracea</i> var. <i>gongylodes</i> L. (Brassicaceae)	Plant	90, 60, 20, 10	10	25	Shape retained
<i>Ribes nigrum</i> L. (Grossulariaceae)	Plant	60, 40, 10	6	10	Berries infection free, berry drop was low
<i>Sansevieria hahnii</i> (Liliaceae)	Plant	90, 40, 10	5	12	Retained colour and quality
<i>Aloe barbadense</i> Mill. (Liliaceae)	Plant, inflorescence	70, 40, 10	7	20	Retained colour and quality
<i>Cyclanthera pedata</i> L. (Cucurbitaceae)	Fruit, plant	60, 50, 20, 10	8	15	Fruit dried without losing shape
<i>Beta vulgaris</i> L. (Chenopodiaceae)	Plant	70, 60, 40, 10	12	25	Colour and plant shape was sustained
<i>Chlophytum borivilianum</i> Santapau (Liliaceae)	Plant with tubers	60, 50, 30, 10	12	20	Fsat drying with good quality tubers
<i>Musa acuminata</i> Colla (Musaceae)	Inflorescence/ fruits	120, 60, 30, 10	14	25	Fast drying with good quality fruit/inflorescence
<i>Momordica dioca</i> Roxb. ex Willd. (Cucurbitaceae)	Fruit	60, 40, 20	7	15	Retention of colour and shape of plant
<i>Nymphaea nouchali</i> Burm. f. (Nymphaeaceae)	Torus/edible seed	110, 50, 20	15	25	Colour retention and good quality
<i>Musa bulbisiana</i> Coll. (Musaceae)	Fruit	120, 60, 30, 10	10	20	Colour retention and good quality
<i>Trapa natans</i> L. var. <i>bispinosa</i> Roxb. (Trapaceae)	Plant with fruit	90, 60, 20	7	20	Colour retention and good quality
<i>Brassica juncea</i> (L.) Czern & Cess. (Brassicaceae)	Plant	40, 20, 10	5	10	Colour retention
<i>Spinacea oleracea</i> L. (Chenopodiaceae)	Plant	40, 10	10	12	Colour retention
<i>Amaranthus hypochondriacus</i> L. (Amaranthaceae)	Plant	40, 10	7	10	Colour retention
<i>Bassella rubra</i> L. (Basellaceae)	Aerial parts	60, 20, 10	7	15	Colour retention; no defoliation in treated samples
<i>Raphanus sativus</i> L. (Brassicaceae)	Plant	120, 60, 40, 10	10	22	Colour retention, root shape retained
<i>Brassica oleracea</i> var. <i>botrytis</i> L. (Brassicaceae)	Head (sectioned)	120, 60, 20, 10	12	26	Retention of shape, no infection
<i>Ipomoea aquatica</i> Forsk. (Convolvulaceae)	Leafy twig	40, 10	5	10	No leaf detachment
<i>Ficus palmata</i> Forsk. (Moraceae)	Inflorescence	60, 40	7	15	No leaf detachment
<i>Punica granatum</i> L. (Punicaceae)	Fruit twig	90, 50, 20	8	20	No detachment of parts
<i>Citrus aurantifolia</i> Sw., <i>C. chinensis</i> (Christm.) Sw. (Rutaceae)	Flowering twig	60, 40, 10	5	10	No leaf detachment
<i>Portulaca oleracea</i> L. (Portulacaceae)	Aerial parts	30, 20, 10	6	12	Colour retention; no leaf detachment
<i>Bryophyllum pinnatum</i> (Lam.) Kurz. (Crassulaceae)	Flowering twig	50, 30, 10	6	12	Colour retained
<i>Rhoeo discolor</i> (Commelinaceae)	Leafy twig	60, 30, 10	7	14	Colour retained

(* Microwave treatment on alternate days)

traditional drying using recommended methods. Result of the treated material was compared with that of the control in terms of time needed for full processing, quality of specimen and labour involved in processing.

Result and Discussion

The microwave processing was applied for processing of 30 species specimens belonging to 25 genera and 18 families under different crop-groups of cultivated plants

(vegetables, roots, tubers, leafy types; fruits, flowers, etc.). The processing time was observed to be reduced by 40-60 per cent (Table 1). Besides, quality parameters such as low infection, retention of colour of parts, less shrinkage in tissue in case of tubers/ roots, optimal breaking of plant parts (leaves, flowers in ornamentals) were also taken care. This method proved to be relatively efficient in terms of time and labour and retention of quality. High frequency microwaves disrupt the soft tissue, soften and expel extra water to the organ surface and fix plant pigment(s) in tissue. The expelled moisture is soaked by the blotter and easily removed during processing/ pressing. During this process, secondary infection caused by the microorganisms or insect, was reduced and thus the shelf- life of the specimens was increased.

During the drying process using traditional methods, materials like succulents, fleshy types, ornamentals, etc. get infested by microorganisms and thus lost or their quality gets affected. Specimens of other types such as of leafy taxa (chenopods, brassicas, amaranths), deteriorated due drastic colour change (Pandey *et al.*, 1995; Pandey and Nayar, 1996). Using treatments by microwave radiations satisfactory results were achieved. The observations in treated and control material were presented in Table 1.

In case of fleshy material like *Musa* spp., *Daucus carota*, *Portulaca oleracea*, *Cyclanthera pedata*, *Beta vulgaris*, etc. there was reduced processing time followed by retention of the original shape of fleshy succulent tissue. In others, organ detachment was minimized by application of microwave treatment- *Ribes nigrum*, *Ficus* spp., *Ipomoea aquatica*, *Punica granatum*, etc. Organ discolouration was reduced in majority of specimens particularly in *Brassica* spp., *Spinacea oleracea*, *Amaranthus hypochondriacus* and *Rhoeo*.

Conclusion

This technique appears to be more efficient as compared to traditional drying method used for difficult taxa and

can be extended for processing and inclusion of large number of species in the herbaria. However, long-term effects on the material use are under investigation.

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SDS-PAGE Seed Protein Profiles as Distinguishing Features in Certain Varieties of Field Crops

Hari Har Ram and Kavita Sharma

Pantnagar Centre for Plant Genetic Resources, G.B. Pant University of Agriculture and Technology, Pantnagar (Uttarakhand)

A total of 74 released varieties of field crops (15 in wheat, 9 in maize, 19 in soybean, 6 in mung, 7 in urd, 8 in lentil and 10 in gram) at Pantnagar, Uttarakhand were characterized using SDS-PAGE (sodium dodecyl sulphate polyacrylamide gel electrophoresis) of seed protein extracted in Tris-HCl buffer with the objective of finding certain critical bands which could be used as distinguishable features. Protein profiles of different field crops showed the number of bands ranging from 11 (urd, lentil and gram) to 16 (maize). Wheat and soybean displayed 12 bands each and mung showed 14 bands. It was possible to distinguish UP 2565 vs C 306, PBW 343, PBW 396, PBW 262, UP 1109, UP 2338, UP 2382 and UP 2425 vs Raj 3765, HD 2687, PBW 373, PBW 502 and UP 2113 vs PBW 175 in wheat; Pant Mung 1 and Pant Mung 2 from Pant Mung 3, Pant Mung 4, Pant Mung 5 and UPM 0205 in mung; Pant U 30, Pant U 35 and UPU 0031 from Manikya, UPU 97-10, Narendra Urd-1 and Pant U 19 in urd; PL 4 and PL 406 from PL 02, PL 5, PL 018, PL 023, PL 234 and PL 639 in lentil and PG 118 from PGK 23, PG K 24, PG 033, PG 034, PG 035, PG 036, PG 037, PG 038 and Pant G 114 in gram on the basis of protein profiles. SDS-PAGE could not distinguish 19 varieties of soybean and 9 varieties of maize. These critical bands could serve as additional descriptors in DUS testing.

Key words: SDS-PAGE, Field crops

The plant cultivars usually can be distinguished morphologically; however, vegetative and floral morphology does not always provide a clear basis for varietal identification. Electrophoretic separation of seed proteins has been a widely used and valuable technique for electrophoretic characterization of a taxon, assessment of species relationship and to trace origin of cultivated plants (Ladizinsky and Hymowitz, 1979).

Seed protein profile is species specific and highly stable characteristics. Accessions among cultivated plants form different geographical areas and adapted to diverse ecological zones still possess essentially the same profile (Larsen, 1967; Johnson, 1975). Seed proteins are mainly storage proteins and are not likely to be changed in dry mature seed. Thus, mature seeds of different age still possess the same profile (Robinson and Megarrity, 1975). Intrinsic changes in the plant such as chromosomal rearrangements or even doubling of the chromosome numbers have no or very small effects on the seed protein profile (Ladizinsky and Johnson, 1972; Nakai, 1977). Thus, use of protein profiles will add to a precise description of newly bred released cultivar and that is necessary to distinguish it from other cultivars of the same kind in order to protect the rights of plant breeders and producers (Arus, 1983; Bailey, 1983; Smith and Smith, 1992).

Numerous electrophoretic methods are available to identify cultivars by protein patterns. Of these methods, sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) provides the best resolution (Smith and Simpson, 1983; Heisel *et al.*, 1986). With the enactment of Protection of Plant Varieties and Farmers' Rights Act, 2001 by Government of India, molecular characterization of released cultivars has become more relevant. Therefore, present study was undertaken to find out the varietal variation of 74 different released varieties of wheat, maize, soybean, mung, urd, lentil and gram developed at Pantnagar, Uttarakhand.

Materials and Methods

The banding pattern of sodium dodecyl sulphate extracts of seed proteins were used for SDS-PAGE following Laemmili (1970).

Extraction of Protein

0.1 g seed of different released varieties of wheat (15), maize (9), soybean (19), mung (6), urd (7) lentil (8) and gram (10) was taken in pestle and mortar adding 1 ml extraction buffer (1 M Tris-HCl-pH 8.0, 2 % SDS, 10 % glycerol, 1 mM PMSF-phenyl methyl sulfonyl fluoride and 2 % mercaptoethanol). The sample was homogenized and heated in a boiling water bath for 5 minutes at 100°C. The contents were centrifuged at 10,000 rpm for 30 minutes at 4°C and supernatant containing protein fraction was stored at -20°C till further

* Corresponding author's E-mail: ashakarthy@rediffmail.com

use. Protein samples were appropriately diluted with the sample buffer (Tris-pH 7.4, 2 % SDS, 2 % mercaptoethanol and bromophenol blue) and heated in boiling water bath for 5 minute at 65°C just before loading in the gel.

Electrophoresis

The SDS solubilized protein samples were analyzed by one dimensional, discontinuous vertical SDS-PAGE with 12.5 % separating and 4 % stacking gels using Tris-glycine electrode buffer (Tris-glycine and SDS pH 8.6). Medium range molecular weight marker (Bangalore Genei, India) protein sample was used along with the samples for determining the molecular weight of separating fractions. Electrophoresis was carried out on a vertical slab gel (Atto. Corp., Japan). The samples were electrophoresed at a constant voltage of 100 V. The run was stopped when the dye was approximately 0.5 cm from the bottom of the slab gel after about three and a half hours.

Staining and Destaining of the Gel

The gels were dipped overnight in staining solution (0.25 g Coomassie Brilliant Blue R-250, 60 g TCA, 180 ml methanol and 60 ml glacial acetic acid). The staining solution was replaced the next day with destaining solutions (3 % NaCl). The gels were intermittently shaken and destaining solution was changed till the blue colour of the background of the bands disappeared. The gels were visualized on a Syngene Gel Documentation System for documentation and photography.

Results and Discussion

The protein banding patterns of different released varieties of wheat, maize, soybean, mung, urd, lentil and gram are given in Table 1.

Wheat (*Triticum aestivum*)

The protein banding pattern were divided into few distinct zones like A, B and C by bands intensity/width/distinctness and within zone, the individual bands were numbered. There were 3 distinct zones i.e. A, B and C with a total of 12 bands.

Zone A consisted of 4 thin bands (A_1 , A_2 , A_3 and A_4) however, band A_1 was absent in UP 2565 and A_2 was absent in Raj 3765, HD 2687, PBW 373, PBW 502, UP 2113 and UP 2565. The zone B consisted of five dark bands (B_1 , B_2 , B_3 , B_4 and B_5) in all the varieties except PBW 175 which lacked band B_2 . The C zone had three bands C_1 , C_2 and C_3 in all the released

varieties of wheat (Table 1). Thus, UP 2565 was distinguishable from the other 14 varieties. There were four distinguishable groups i.e. UP 2565 in first group, C 306, PBW 343, PBW 396, PBW 262, UP 1109, UP 2338, UP 2382 and UP 2425 in the second group, Raj 3765, HD 2687, PBW 373, PBW 502 and UP 2113 in third group and PBW 175 in the fourth group.

Maize (*Zea mays*)

The protein banding pattern of maize showed a total of 16 bands divided into 4 distinct zones i.e. A, B, C and D. All the varieties remained indistinguishable.

Soybean (*Glycine max*)

Nineteen varieties showed similar 12 electrophoretic bands distributed into 4 zones.

Mung (*Vigna radiata*)

Seed protein profiles were characterized by 14 bands spread over 4 zones. The 6 varieties of mung were classified into 2 distinct electrophoretic groups where Pant Mung 1 and Pant Mung 2 had 3 faint bands in A zone which were missing in the remaining 4 varieties. Further, a prominent band B_3 was present in Pant Mung 1 and Pant Mung 2 and altogether lacking in the other 4 varieties. Thus, Pant Mung 1 and Pant Mung 2 were distinguishable from the other four varieties.

Urd (*Vigna mungo*)

A total of 11 bands were present in the released varieties of urd. The distinguishable zone was A. There was no difference in zone B and C. A_1 , A_2 and A_3 bands were almost absent in Pant U 30 and Pant U 35. A_2 and A_3 bands were absent in UPU 0031.

Lentil (*Lens culinaris*)

Eight varieties of lentil (Table 1) were electrophoresed. All the varieties of lentil were alike in protein banding pattern except PL 4 and PL 406, in which C_2 , C_3 and C_3 bands respectively were absent. The zone D consisted of only one dark band in all the released varieties of lentil. Thus, on the basis of seed protein profile, PL 4 and PL 406 were distinguishable from the other varieties. Incidentally, PL 4 and PL 406 both were small seeded and the rest mostly bold seeded. Thus, the difference between small seeded and bold seeded lentil cultivars seems to be linked with certain qualitative genes having direct bearing on seed size.

Gram (*Cicer arietinum*)

All the 10 varieties of gram showed similar seed protein

Table 1. Seed protein profiles as resolved through SDS-PAGE in released varieties of field crops

Wheat												
Varieties	A ₁	A ₂	A ₃	A ₄	B ₁	B ₂	B ₃	B ₄	B ₅	C ₁	C ₂	C ₃
C 306	+	+	+	+	+	+	+	+	+	+	+	+
Raj 3765	+	—	+	+	+	+	+	+	+	+	+	+
HD 2687	+	—	+	+	+	+	+	+	+	+	+	+
PBW 175	+	+	+	+	+	—	+	+	+	+	+	+
PBW 343	+	+	+	+	+	+	+	+	+	+	+	+
PBW 373	+	—	+	+	+	+	+	+	+	+	+	+
PBW 396	+	+	+	+	+	+	+	+	+	+	+	+
PBW 502	+	—	+	+	+	+	+	+	+	+	+	+
PBW 262	+	+	+	+	+	+	+	+	+	+	+	+
UP 1109	+	+	+	+	+	+	+	+	+	+	+	+
UP 2113	+	—	+	+	+	+	+	+	+	+	+	+
UP 2338	+	+	+	+	+	+	+	+	+	+	+	+
UP 2382	+	+	+	+	+	+	+	+	+	+	+	+
UP 2425	+	+	+	+	+	+	+	+	+	+	+	+
UP 2565	—	—	+	+	+	+	+	+	+	+	+	+

Maize																
Varieties	A ₁	A ₂	A ₃	A ₄	B ₁	B ₂	B ₃	B ₄	B ₅	B ₆	C ₁	C ₂	C ₃	D ₁	D ₂	D ₃
Surya	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Amar	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Kanchan	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Gaurav	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Shweta	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Naveen	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
D 765	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Pragati	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Tarun	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+

Soybean												
Varieties	A ₁	B ₁	B ₂	B ₃	B ₄	B ₅	B ₆	C ₁	C ₂	D ₁	D ₂	D ₃
Shilajeet	+	+	+	+	+	+	+	+	+	+	+	+
PK 472	+	+	+	+	+	+	+	+	+	+	+	+
PS 1347	+	+	+	+	+	+	+	+	+	+	+	+
Bragg	+	+	+	+	+	+	+	+	+	+	+	+
PK 327	+	+	+	+	+	+	+	+	+	+	+	+
PS 1241	+	+	+	+	+	+	+	+	+	+	+	+
Pb 1	+	+	+	+	+	+	+	+	+	+	+	+
PK 1225	+	+	+	+	+	+	+	+	+	+	+	+
PS 1092	+	+	+	+	+	+	+	+	+	+	+	+
PK 416	+	+	+	+	+	+	+	+	+	+	+	+
PK 564	+	+	+	+	+	+	+	+	+	+	+	+
Ankur	+	+	+	+	+	+	+	+	+	+	+	+
PS 1042	+	+	+	+	+	+	+	+	+	+	+	+
VLS 47	+	+	+	+	+	+	+	+	+	+	+	+
PK 262	+	+	+	+	+	+	+	+	+	+	+	+
PK1029	+	+	+	+	+	+	+	+	+	+	+	+
PKB 75	+	+	+	+	+	+	+	+	+	+	+	+
JS 335	+	+	+	+	+	+	+	+	+	+	+	+
PS 1024	+	+	+	+	+	+	+	+	+	+	+	+

Mung														
Varieties	A ₁	A ₂	A ₃	B ₁	B ₂	B ₃	B ₄	B ₅	C ₁	C ₂	C ₃	D ₁	D ₂	D ₃
Pant Mung 1	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Pant Mung 2	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Pant Mung 3	-	-	-	+	+	-	+	+	+	+	+	+	+	+
Pant Mung 4	-	-	-	+	+	-	+	+	+	+	+	+	+	+
Pant Mung 5	-	-	-	+	+	-	+	+	+	-	+	+	+	+
UPM 02-05	-	-	-	+	+	-	+	+	+	-	+	+	+	+

Urd												
Varieties	A ₁	A ₂	A ₃	B ₁	B ₂	B ₃	B ₄	C ₁	C ₂	C ₃	C ₄	
Pant U 30	-	-	-	+	+	+	+	+	+	+	+	
Manikya	+	+	+	+	+	+	+	+	+	+	+	
Pant U 35	-	-	-	+	+	+	+	+	+	+	+	
UPU 97 10	+	+	+	+	+	+	+	+	+	+	+	
Narendra Urd I	+	+	+	+	+	+	+	+	+	+	+	
UPU 0031	+	-	-	+	+	+	+	+	+	+	+	
Pant U 19	+	+	+	+	+	+	+	+	+	+	+	

Lentil											
Varieties	A ₁	A ₂	B ₁	B ₂	B ₃	B ₄	B ₅	C ₁	C ₂	C ₃	D ₁
PL 02	+	+	+	+	+	+	+	+	+	+	+
PL 4	+	+	+	+	+	+	+	+	-	-	+
PL 5	+	+	+	+	+	+	+	+	+	+	+
PL 018	+	+	+	+	+	+	+	+	+	+	+
PL 023	+	+	+	+	+	+	+	+	+	+	+
PL 234	+	+	+	+	+	+	+	+	+	+	+
PL 406	+	+	+	+	+	+	+	+	+	-	+
PL 639	+	+	+	+	+	+	+	+	+	+	+

Gram											
Varieties	A ₁	B ₁	B ₂	B ₃	B ₄	B ₅	C ₁	C ₂	C ₃	D ₁	D ₂
PGK 23	+	+	+	+	+	+	+	+	+	+	+
PGK 24	+	+	+	+	+	+	+	+	+	+	+
PG 033	+	+	+	+	+	+	+	+	+	+	+
PG 034	+	+	+	+	+	+	+	+	+	+	+
PG 035	+	+	+	+	+	+	+	+	+	+	+
PG 036	+	+	+	+	+	+	+	+	+	+	+
PG 037	+	+	+	+	+	+	+	+	+	+	+
PG 038	+	+	+	+	+	+	+	+	+	+	+
Pant G 114	+	+	+	+	+	+	+	+	+	+	+
PG 118	-	+	+	+	+	-	+	+	+	+	-

[* | In-line.WMF *]

profiles except PG 118 in which bands A₁, B₅ and D₂ were missing.

Thus, on the basis of above results, seed protein profiles as resolved through SDS-PAGE were successful in distinguishing certain varieties for example UP 2565 vs C 306, PBW 343, PBW 396, PBW 262, UP 1109, UP 2338, UP 2382 and UP 2425 vs Raj 3765, HD

2687, PBW 373, PBW 502 and UP 2113 vs. PBW 175 in wheat; Pant Mung 1 and Pant Mung 2 from Pant Mung 3, Pant Mung 4, Pant Mung 5 and UPM 0205 in mung; Pant U 30, Pant U 35 and UPU 0031 from Manikya, UPU 97-10, Narendra Urd 1 and Pant U 19 in urd; PL 4 and PL 406 from PL 02, PL 5, PL 018, PL 023, PL 234 and PL 639 in lentil and

PG 118 from PGK 23, PGK 24, PG 033, PG 034, PG 035, PG 036, PG 037, PG 038 and Pant G 114 in gram. No differences could be detected in maize and soybean. Panigrahi *et al.* (2001) and Subodh *et al.* (2001) in pigeon pea, Mallick and Sawhney (2002) in lentil and Yadav and Singh (2004) in wheat have reported varietal differences on the basis of seed protein profiles in India.

The advantages of protein data in resolving varietal differences have been reviewed by Smith and Smith (1992). The protein and DNA data are in popular use because the variation for these markers is ubiquitous and this variation is desirable in genetic terms. These characters are in routine usage and are widely accepted as source of reliable data in evolution, taxonomy and genetics. There is abundant evidence to show that protein profiles can be obtained for all crop species of major importance and that these profiles are independent of environmental and storage conditions. They are reflective of genotype. In some cases quantitative variation can occur due to environmental effects, but this contribution to variation is small and can be taken into account when considering intervarietal comparisons (Smith and Smith, 1992). Therefore, the intensity of the band has not been taken into account to evaluate their degree of significance in discriminating between qualitatively similar protein profiles in the present investigation. Protein profiles of cultivated varieties, therefore satisfy one pre-requisite of providing a fingerprint in the sense that they are specific descriptors of the genotype and the information generated in this paper adds to the list of descriptors of released crop cultivars required for facilitating the implementation of the Protection of Plant Varieties and Farmer's Right acts 2001. The fact that varieties of maize and soybean were indistinguishable from each other suggests that other electrophoretic conditions should be investigated in order to differentiate between these cultivars. In conclusion, SDS-PAGE proved to be a promising method to discriminate between certain varieties of wheat, mung, urd, lentil and gram and warrants further investigation to identify other electrophoretic conditions for identifying some critical bands in distinguishing maize and soybean varieties developed at Pantnagar.

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Genetic Diversity in Cowpea

WD Lesly, MS Uma¹ and PM Salimath

Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad-580 005 (Karnataka)

¹ *Associate Professor, Super Elite Sunflower Seed Production Scheme, ZARS, UAS, GKVK, Bangalore-560 065*

In order to assess the divergence among 169 cowpea genotypes, mahalanobis D^2 statistics was applied. The analysis of variance revealed significant differences among the genotypes for all the traits. The 169 genotypes were grouped into 46 clusters, where clusters (6,8,9) were the largest, containing seven genotypes followed by the clusters 1,2,5,6 and 24 with six genotypes. The inter cluster distance was maximum between cluster 11 and 42 followed by cluster 34 and 42. Based on inter cluster distance and per se performance of genotypes, the entries viz., IC 259084, IC 259071, IC 257420, IC 257422, IC 202803, IC 97829, IC 198333, IC 97787, IC 202824 and IC 202781 were selected, which could be intercrossed to recover good recombinants and desirable segregants. The number of pods per plant contributed maximum divergence (14.75) which was followed by harvest index (14.74%) and days to flower termination (13.72 %).

Key words: Cowpea, Genetic divergence, D^2 statistics

Conventional procedure of indiscriminate hybridization on a massive scale in any crop results in an immense wastage of resources. Quatset (1979) opined that most often asked question among breeders is how to choose parents for crossing. Greater success can be achieved through judicious choice of parents for hybridization based on genetic divergence. Crosses between divergent parents usually produce greater heterosis than those between closely related ones (Moll and Stuber, 1971). Genetic divergence studies are the vital tools for the evaluation of germplasm lines and selection of parents for the breeding programme. So, the present study was undertaken to measure genetic diversity among the germplasm lines. Such information will be helpful for breeders to plan hybridization programme. Inclusive of diverse parents in hybridization programme can serve the purpose of combining desirable genes or to obtain superior recombination. Among several methods of multivariate analysis available to study genetic diversity in biological population, the D^2 analysis had been a perfect test in the quantitative estimation of genetic diversity.

Materials and Methods

The materials for the present investigation comprised 169 cowpea genotypes including 157 lines from the National Bureau of Plant Genetic Resources (NBPGR), New Delhi core collection from different parts of India, 7 from exotic collection, 3 released varieties and 2 local land races. Thus, the material represented a wide range of geographic diversity. The experiment was carried out in simple lattice square design with two replications

during *kharif* 2004 and 2005, in the Botanical garden located at University of Agricultural Sciences, Dharwad, Karnataka, India. Each accession was grown in two lines of 4 m length. The spacing adopted between rows and between plants within a row was 60 cm and 20 cm, respectively. Observations on various morphological and yield components such as germination percentage, plant height (cm), number of branches, number of clusters per plant, number of pods per plant, pod length (cm), seeds per pod, days to flower initiation and termination, days to physiological maturity, seed weight of hundred seeds (g), harvest index and seed yield per plant (g) were recorded on five randomly selected plants of each entry in each replication. The mean data of two seasons were pooled and the test of homogeneity of error variance was found to be non-significant and hence the pooled data was further subjected to statistical analysis using Mahalanobis D^2 analysis (Mahalanobis, 1936). Grouping of genotypes into various clusters was carried out following Tocher's procedure (Rao, 1952) and the relative contribution of different characters to total D^2 distance was calculated as per Singh and Choudhary (1979).

Results and Discussions

Group constellation: Analysis to estimate D^2 values was done on the basis of relative magnitude of D^2 values, all the 169 genotypes were grouped into 46 clusters (Table 1).

The highest inter-cluster distance was observed between clusters 11 and cluster 42 (349.31) followed by clusters 34 and 42 (346.10), 26 and 41 ((343.99)

Table 1. Number of clusters and their varietal composition of cowpea

Cluster number	Number of genotypes	Name of genotypes
1	6	IC243489, IC249141, IC253268, IC219594, IC257445, IC257406
2	6	IC198321, IC198355, IC257422, IC201095, IC202720, IC202779
3	5	IC208618, IC215015, IC219872, IC202901, IC202846
4	5	IC202743, IC202782, IC202803, IC202705, IC198361
5	6	IC202824, IC202868, IC202791, IC204103, IC202778, IC202718
6	7	IC198333, IC199701, IC97856, IC202707, IC202762, IC97806, IC202786
7	5	IC198359, IC201099, IC198323, IC97767, IC97834
8	7	IC201079, IC202710, IC202775, IC198342, IC91556, IC202789, IC202823
9	7	IC202854, IC202924, IC214752, IC219141, IC243312, IC249133, IC202804
10	6	IC202730, IC202781, IC202799, IC202841, IC202893, IC207813
11	5	IC68786, BIALAHONGAL LOCAL, EC394805, IC259083, IC259105
12	5	IC198335, IC199704, IC202709, IC202772, IC97806
13	4	IC97764, IC198349, IC257420, IC97830,
14	5	IC259071, IC259085, IC257452, IC201098, IC202932
15	5	IC259058, IC259078, IC253277, IC257427, IC249593
16	4	IC202927, IC214833, IC202867, IC219592
17	5	IC249586, IC253276, IC257425, IC257453, IC259072
18	5	IC247430, IC253275, IC214836, IC219640, IC249585
19	3	IC97787, IC198327, IC97838
20	5	GOA LOCAL, EC394740, IC257447, IC5969, IC259100
21	5	IC202873, IC214835, IC202835, IC206240, IC202797
22	4	IC219574, IC243353, IC214759, IC249137
23	4	IC249140, IC253255, IC253288, IC243486
24	6	IC257449, IC259069, IC259084, IC202784, IC202931, EC3947
25	1	IC259063
26	5	EC394855, GC-3, C-152, IC68786, IC259104
27	5	IC249583, IC257407, IC243501, IC253270, IC219607
28	2	IC257411
29	4	IC202787, IC202809, IC202926, IC202860
30	4	IC247435, EC394823, IC259095, IC4506
31	1	IC97764
32	1	IC249132
33	1	IC201087
34	5	V-118, EC394753, IC259084, IC202702, IC259159
35	1	IC257424
36	1	IC259064
37	5	IC253181, IC253281, IC257435, IC259061, IC259081
38	1	IC257410
39	1	IC15567
40	1	IC97830
41	1	EC394745
42	1	IC257437
43	1	EC 394691
44	1	IC257441
45	1	IC97829
46	1	IC214834

and 25 and 42 (340.54). The lowest intra-cluster distance other than the solitary clusters was in the cluster of 19 (17.19). Twenty two clusters in between minimum and maximum values were observed showing different divergence groups. While, the highest intra-cluster distance was observed in cluster 37 (30.53) followed by cluster 10 (29.77) and 34 (28.99). The number and genotype composition of different clusters are presented in Table 2. The clusters 6, 8 and 9 were the biggest clusters with 7 genotypes in each cluster. Clusters 1, 2, 5, 10 and 24 are the second largest clusters with six genotypes in each. The clusters 3, 4, 7, 11, 12, 14, 15, 17, 18, 20, 21, 26, 27, 34 and 37 consist of five genotypes in each cluster and the clusters 13, 16, 22, 23, 29 and 30 consists of 4 genotypes in each. The solitary clusters were 25, 28, 31, 32, 33, 35, 36, 38, 39, 40, 41, 42, 43, 44, 45, and 46 they showed zero cluster distances.

Two multivariate analysis using D^2 statistic revealed that number of pods per plant and harvest index contributed maximum to the divergence followed by days to flower termination and number of branches per plant. Backiyarani *et al.* (2000) also reported largest contribution to total divergence by harvest index, followed by single plant yield and earliness in flowering. But in contrary to these results Ranganayaki and Rangaswamy (1991) reported that hundred seed weight as the major contributor to the genetic divergence, followed by pod length and seed yield.

Based on the mean values of different clusters (Table 3) the mean seed yield per plant had highest mean for cluster 40 (24.53) and lowest mean for cluster

Table 2. Average intra-cluster (bold) and inter-cluster D2 values of cowpea

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
1	26.72	183.79	242.47	225.72	71.11	211.92	195.45	147.50	220.89	188.57	254.89	153.79	122.89	222.60	238.49	178.03	272.73	196.86	217.75	251.73	184.19	192.93	204.85
2		26.33	137.51	130.71	128.99	164.51	91.82	146.51	168.85	93.68	249.79	178.16	95.43	163.64	187.63	166.22	162.60	114.09	140.69	197.27	49.89	209.52	200.71
3			24.89	48.99	205.57	154.54	114.41	203.22	155.09	146.43	277.78	173.21	188.88	236.81	167.26	215.00	62.34	179.79	85.46	174.29	156.77	174.69	238.84
4				22.75	185.69	122.02	98.43	181.76	121.89	133.87	262.46	146.69	167.67	228.52	136.53	194.56	104.22	168.66	43.32	145.13	151.05	148.10	220.61
5					###	172.70	144.43	119.76	183.72	137.16	239.65	135.24	59.41	182.75	205.52	151.32	240.49	148.63	177.27	219.72	133.83	178.37	185.36
6						24.59	132.38	127.98	50.84	159.08	180.86	96.97	159.72	241.23	87.85	126.19	204.62	188.87	98.17	121.12	180.27	114.61	141.26
7							24.74	165.09	128.73	59.13	257.96	161.19	119.83	165.69	142.62	182.02	150.73	100.18	101.77	149.05	121.43	190.26	210.87
8								27.72	139.75	181.77	150.13	112.21	122.01	249.74	165.11	51.78	241.59	205.34	170.15	187.71	141.52	166.08	89.71
9									22.36	157.04	187.89	117.34	170.33	240.82	45.97	137.36	204.29	187.01	97.19	77.94	184.26	135.98	150.88
10										29.77	269.75	180.88	110.84	113.59	168.93	197.93	174.61	51.73	137.08	175.05	124.06	207.37	224.87
11											25.97	184.08	240.69	319.48	203.04	106.11	307.11	288.19	253.31	231.31	246.49	223.41	65.92
12												25.55	146.56	254.56	146.47	121.09	218.39	207.98	128.93	173.99	188.15	81.80	139.72
13													22.96	163.83	193.36	149.30	225.75	124.16	160.22	206.73	100.78	186.22	186.94
14														27.75	248.81	262.07	253.03	71.80	231.17	253.89	184.93	273.90	282.79
15															27.47	161.64	212.89	196.63	114.17	45.21	201.92	159.64	171.56
16																20.42	251.99	220.63	183.37	187.77	161.79	173.87	48.93
17																	23.79	202.99	142.39	217.43	178.99	219.77	272.57
18																		26.80	171.08	201.51	141.90	231.05	245.73
19																			###	124.89	160.48	129.02	209.90
20																				25.18	210.56	184.19	200.07
21																					27.39	219.72	197.65
22																						25.88	188.12
23																							22.87
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Table 2 Contd.

	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
1	228.34	229.84	260.40	203.79	128.46	163.77	292.60	231.64	255.01	92.68	66.37	205.67	39.09	225.82	144.33	134.11	186.17	250.39	314.62	227.71	228.14	143.47	46.72
2	149.12	234.88	271.17	99.92	139.89	183.74	183.63	175.34	140.85	117.37	238.13	135.11	213.32	241.21	170.08	163.77	38.82	183.18	206.26	174.52	212.48	118.24	160.87
3	239.04	267.35	215.09	193.86	204.85	164.95	100.61	251.50	38.61	197.48	282.36	208.78	265.37	193.89	180.91	177.17	115.16	264.76	128.69	250.90	250.42	185.94	224.33
4	234.35	251.39	194.31	188.86	183.02	137.49	143.29	243.94	78.67	176.37	268.06	197.44	250.07	170.32	155.41	151.36	109.17	259.10	171.84	239.03	232.51	163.44	206.24
5	194.86	217.14	250.47	162.15	100.49	146.19	263.15	193.91	218.76	38.17	129.35	161.01	102.56	214.93	122.98	112.14	131.93	220.78	287.73	188.32	205.10	102.04	52.88
6	252.62	170.12	182.02	212.69	143.74	94.65	239.13	254.03	179.78	167.34	252.91	210.86	235.54	144.76	104.50	99.46	151.13	272.96	268.03	244.76	154.07	131.80	193.31
7	219.38	221.83	252.44	170.16	162.69	163.52	178.39	184.20	127.97	137.37	244.35	132.54	223.18	222.16	155.00	147.74	65.96	248.35	204.17	177.63	222.79	143.14	169.09
8	185.93	126.21	245.17	157.08	43.43	130.72	267.33	259.09	217.86	114.88	188.52	224.29	167.61	203.43	96.04	92.45	149.30	203.64	292.01	252.43	114.41	49.66	141.45
9	255.83	177.64	198.64	215.87	155.30	117.15	239.61	253.79	182.34	178.18	260.61	209.63	243.43	163.36	122.47	119.42	155.34	276.29	266.79	244.31	162.62	143.82	202.45
10	219.85	255.68	265.96	173.29	178.47	182.56	197.73	132.61	156.15	133.26	239.24	81.01	217.61	237.58	175.51	165.85	79.13	252.43	221.04	127.16	235.97	161.69	160.75
11	275.94	34.55	287.99	255.96	187.07	201.98	328.72	323.86	290.33	237.62	280.24	300.42	267.42	247.12	178.38	181.46	249.02	288.19	349.31	322.08	53.17	186.48	251.02
12	254.55	166.60	269.24	218.12	120.85	45.85	248.69	266.67	195.06	135.94	185.53	227.13	171.86	222.79	37.92	37.43	165.61	274.31	276.73	259.46	159.41	118.77	145.75
13	171.47	221.83	255.79	134.39	106.85	155.97	249.86	175.96	201.86	39.81	183.10	139.03	156.01	222.18	134.88	125.46	101.26	199.65	275.27	169.60	201.19	92.09	103.14
14	257.30	306.98	320.97	222.97	246.27	255.01	267.99	34.05	241.61	185.03	268.57	39.06	249.09	198.25	251.11	239.73	166.99	292.69	285.28	41.14	291.36	235.54	198.10
15	269.57	194.11	213.53	231.24	180.14	144.71	247.83	261.43	194.97	200.42	275.34	218.30	259.19	182.09	152.07	149.12	174.79	289.59	272.76	252.17	181.71	170.35	221.25
16	202.25	85.49	251.38	175.49	86.81	141.77	277.38	269.83	229.50	145.48	216.08	237.84	196.96	208.36	107.44	107.73	167.76	218.58	301.39	264.58	68.75	83.38	171.29
17	255.03	297.57	252.91	212.61	243.43	211.16	46.73	266.32	95.40	234.23	308.83	230.09	293.38	235.34	224.89	221.27	142.60	281.33	71.27	270.82	283.49	226.17	256.45
18	230.03	274.49	284.86	187.80	201.31	208.65	223.17	89.78	187.47	147.35	246.84	39.05	225.63	259.03	203.44	192.48	110.17	264.92	243.95	83.57	255.93	187.14	169.27
19	240.91	241.72	179.24	196.81	171.29	118.39	181.74	246.89	116.82	167.94	260.35	198.38	242.31	153.30	139.03	134.75	121.63	263.88	210.54	238.05	222.35	152.99	197.83
20	275.13	222.31	231.38	237.99	198.90	170.78	252.06	266.63	202.15	213.51	287.33	223.39	271.18	204.12	178.86	175.42	185.23	294.82	275.07	257.24	209.23	188.73	234.44
21	108.80	231.13	280.15	60.59	133.40	194.52	197.93	195.69	159.32	116.73	238.86	162.37	212.81	250.53	179.74	174.11	70.29	142.24	218.39	196.02	209.61	112.65	169.59
22	278.75	209.85	92.23	245.57	171.46	49.04	252.20	285.10	200.17	177.31	220.47	248.13	209.47	49.74	113.41	104.63	198.69	297.23	280.30	279.16	204.37	169.08	185.61
23	234.63	43.10	261.88	210.41	125.74	159.71	296.39	289.28	252.18	183.21	235.66	260.78	220.04	218.70	129.51	130.99	200.54	249.34	319.14	285.26	44.01	127.25	199.87
24	26.99	261.90	328.04	56.42	176.39	259.42	269.04	263.78	240.83	175.58	276.53	242.39	250.78	303.42	248.19	243.43	173.29	46.18	283.14	266.52	244.25	164.72	227.29
25	0.00	278.35	241.22	161.87	185.36	319.41	312.04	280.13	216.88	254.33	287.39	242.54	236.21	236.21	159.18	161.19	234.56	274.86	340.54	309.71	48.37	165.52	227.31
26	28.22	300.23	248.74	133.80	248.74	133.80	283.66	330.54	239.84	248.26	282.19	298.69	274.18	55.44	202.08	192.42	262.47	343.99	309.12	326.53	274.66	246.24	254.89
27	##	278.35	241.22	161.87	185.36	319.41	312.04	280.13	216.88	254.33	287.39	242.54	236.21	236.21	159.18	161.19	234.56	274.86	340.54	309.71	48.37	165.52	227.31
28	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
29	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
30	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
31	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
32	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
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34	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
35	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
36	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
37	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
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41	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
42	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
43	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
44	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
45	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92
46	0.00	148.10	223.65	136.08	24.58	24.58	268.82	256.49	219.16	96.29	171.86	220.71	149.29	209.45	104.39	98.29	145.02	194.26	293.62	248.87	151.56	38.89	123.92

Table 3. Mean performances of different clusters of cowpea

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
1	85.50	45.64	60.83	74.50	76.58	4.94	11.93	16.23	15.38	14.02	11.15	0.18	13.58
2	81.92	44.57	60.75	74.75	77.08	4.21	10.17	15.85	13.69	12.43	11.29	0.25	19.21
3	76.90	41.51	56.70	70.80	73.10	4.13	9.59	10.14	15.20	13.35	11.42	0.18	13.55
4	79.60	39.14	58.80	70.90	73.40	3.96	10.16	16.14	13.90	11.84	11.07	0.21	16.23
5	71.25	40.69	61.25	74.50	76.92	3.79	10.38	17.84	13.94	12.35	10.45	0.23	17.03
6	78.71	45.01	61.00	73.86	76.36	4.19	10.38	17.98	15.38	13.47	11.06	0.23	17.80
7	79.10	43.67	59.90	72.50	74.80	4.20	11.84	18.61	13.44	12.24	11.65	0.22	15.42
8	78.14	45.39	59.29	72.64	74.86	4.42	11.26	17.73	15.05	13.33	11.77	0.23	17.73
9	81.93	41.59	59.14	72.00	74.71	4.45	9.93	15.20	14.95	13.24	10.44	0.19	14.12
10	50.67	42.15	60.75	74.00	76.50	4.28	10.03	12.14	13.60	12.10	11.92	0.19	13.77
11	76.10	43.24	55.90	69.20	71.70	4.47	11.81	17.63	14.59	12.83	13.34	0.28	21.79
12	80.50	41.95	58.20	72.20	74.40	4.09	12.42	18.61	15.23	13.94	10.37	0.20	15.80
13	86.25	42.21	61.00	74.13	76.75	4.41	11.69	18.24	14.08	12.51	9.20	0.25	19.75
14	74.70	45.29	63.40	77.80	80.10	4.89	10.36	14.55	14.05	12.22	11.51	0.20	16.06
15	87.00	48.43	58.40	71.10	73.60	4.93	12.98	13.04	13.17	12.10	9.05	0.17	12.27
16	77.88	44.14	59.13	71.13	74.25	4.21	9.11	15.23	14.31	12.47	10.03	0.19	12.90
17	79.70	45.15	60.60	75.30	77.40	4.43	11.28	16.61	14.12	12.65	11.79	0.23	16.54
18	74.60	47.17	63.20	74.80	77.60	4.66	10.69	14.70	14.46	13.16	11.30	0.26	18.27
19	86.00	42.50	60.50	73.67	75.00	4.32	13.38	21.52	14.45	12.58	8.60	0.25	20.84
20	55.40	45.84	58.30	72.40	75.00	4.68	9.08	13.83	14.09	12.32	14.68	0.21	16.98
21	74.80	41.54	63.30	75.10	77.10	4.03	9.39	16.39	15.97	13.80	11.31	0.25	18.14
22	78.50	41.39	60.50	72.13	74.88	4.23	10.93	17.49	14.86	13.25	11.55	0.21	15.89
23	88.38	42.64	57.00	70.00	72.80	4.59	10.30	14.00	15.22	13.13	9.79	0.20	14.86
24	75.75	43.71	57.25	71.00	73.33	5.03	10.75	15.23	13.90	12.12	12.62	0.25	18.89
25	100.00	46.40	59.00	70.00	74.00	4.50	8.80	11.50	16.05	13.66	9.44	0.18	14.06
26	65.70	45.16	57.50	70.10	73.00	5.06	12.34	19.19	15.20	13.29	12.26	0.27	21.77
27	81.00	41.44	59.60	71.90	74.00	4.41	9.02	12.19	12.64	11.64	11.03	0.19	13.89
28	97.50	45.28	64.00	76.50	81.50	4.00	12.50	14.25	12.40	11.50	8.07	0.22	19.12
29	80.75	40.04	62.88	74.75	77.13	4.14	11.60	17.09	13.43	12.33	11.21	0.21	15.24
30	72.75	40.76	57.13	71.75	74.25	4.75	9.21	13.65	12.82	11.59	12.88	0.22	16.06
31	46.00	48.85	67.50	80.00	82.50	4.90	9.30	17.90	17.90	15.75	12.05	0.27	22.80
32	97.50	46.55	59.00	74.50	77.00	3.40	13.70	22.10	18.08	16.20	12.34	0.14	13.10
33	69.00	43.75	60.50	77.00	76.50	3.20	13.75	19.40	16.27	14.40	9.86	0.22	14.62
34	80.00	41.77	56.70	71.50	73.90	4.73	11.46	16.04	15.24	13.44	12.21	0.26	20.42
35	85.00	40.85	69.50	81.00	84.00	4.45	9.00	11.15	14.64	11.96	7.73	0.15	12.57
36	94.00	45.75	55.50	69.00	72.30	3.90	9.00	10.80	8.25	8.10	10.51	0.25	16.92
37	68.10	47.58	56.80	70.30	73.10	4.83	10.85	16.10	14.05	13.13	11.71	0.22	16.13
38	84.00	37.00	61.00	74.00	76.50	3.70	11.06	16.60	12.20	11.20	8.17	0.24	16.75
39	95.00	40.55	66.00	78.00	80.00	4.15	9.70	16.85	15.85	14.70	10.90	0.19	15.15
40	47.50	40.85	62.50	75.50	78.00	4.15	11.50	23.55	13.23	12.60	10.30	0.27	24.53
41	72.00	41.65	59.00	74.50	77.50	4.90	10.85	17.10	13.36	11.90	11.76	0.29	21.71
42	74.00	43.00	62.00	74.50	76.50	5.45	13.15	20.55	16.85	14.40	12.67	0.22	21.73
43	79.00	46.65	59.50	73.00	72.50	5.40	12.90	17.85	12.70	12.02	14.48	0.27	23.61
44	91.00	46.55	65.50	78.00	81.00	4.50	12.15	11.95	14.75	13.38	7.01	0.14	13.85
45	37.50	34.65	59.00	70.50	72.50	4.10	13.00	24.00	15.72	13.09	10.85	0.28	21.21
46	43.50	37.45	59.00	74.00	76.50	4.10	8.50	15.60	14.65	13.40	9.64	0.19	15.25

X1 = Germination percentmtage

X6 = Number of branches per plant

X10 = Number of seeds per pod

X2 = Plant height

X7 = Number of clusters per plant

X11 = Hundred seed weight

X3 = Days to flower initiation

X8 = Number of pods per plant

X12 = Harvest index

X4 = Days to flower termination

X9 = Pod length

X13 = Seed yield per plant

X5 = Days to physiological maturity

15 (12.27). The cluster 35 had highest mean values for days to flower initiation (69.50), days to flower termination (81.00) and days to physiological maturity (84.00) and also the cluster 36 showed the lowest means for the same traits and that indicates early maturing genotypes grouped in this cluster. Highest cluster mean was observed for pod length (18.08) and seeds per pod (16.02) in cluster 32, whereas cluster 36 showed lowest mean values for both the characters 8.25 and 8.10 respectively. Clusters 40, 41 and 42 had higher mean values for seed yield per plant, harvest index and number of clusters per plant respectively. Clusters 20, 25 and 31 had highest mean values for hundred seed weight, germination percentage and plant height respectively.

The highest inter cluster distance was observed between clusters 11 and 42 (349.31) followed by clusters 34 and 42 (346.10). The lowest intra cluster distance other than the solitary clusters was in the cluster of 19 (17.19). Twenty two clusters in between minimum and maximum values were observed showing different divergence groups. The maximum intra cluster distance of 30.53 was observed for the cluster 37 involving the genotypes IC 253181, IC 253281, IC 257435, IC 259061 and IC 259081 followed by cluster 10 involving the genotypes IC 202730, IC 202781, IC 202799, IC 202841, IC 202893 and IC 207813. The cluster 37 included five genotypes, out of which two from IARI, New Delhi, two from NBPGR, New Delhi and one from NBPGR centre, Kerala respectively. Cluster 10 comprised of six genotypes, out of which 5 were landraces from Goa and Orissa and another one primitive cultivar from Andhra Pradesh.

The genotypes of early maturing, high yielding and disease resistance were IC 259084, IC 97834, IC 97838, IC 198333 and IC 97787 respectively which were belongs to clusters such as 24, 13, 19, 7 and 19 respectively. In future, these genotypes can be utilized for the hybridization programme to increase the grain yield per plant with desirable traits. In respect of mean values of different clusters, the highest mean seed yield of 24.53/plant was observed in cluster 40 involving only one genotype IC 97830 followed by cluster 43 involving EC 394745.

Practical utility: Based on the study of genetic divergence and disease resistance (Withanage Don Lesly *et al.*, 2005; Withanage Don Lesly and Uma, 2007) the following promising genotypes were identified, which can be used in breeding programme.

Genotypes	Desirable characteristics
IC 259084	Very Early, rust resistant
IC 259071	Very Early, rust resistant
IC 257420	High yielding
IC 257422	High yielding
IC 202803	High yielding
IC 97829	Mosaic virus resistant
IC 198333	Disease resistance-Powdery Mildew
IC 97787	Mosaic virus resistance-Powdery Mildew
IC 202824	Disease resistance-Powdery Mildew
IC 202781	Bold seeded, Bacterial leaf blight resistant

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Genetic Variability and Character Association of Yield and Related Traits in Advance Breeding Lines of Indian Mustard (*Brassica juncea* L.)

ML Meena, Manju Singh, JS Chauhan and Arvind Kumar

National Research Center on Rapeseed and Mustard, Sewar, Bharatpur-321 303 (Rajasthan)

Twenty-one advance breeding lines and four check varieties, Varuna, BIO-902, Kranti and Rajat of Indian mustard (*Brassica juncea* L.) were evaluated in Randomized Complete Block design with three replications during 2001-02 and 2002-03 *rabi* season to estimate genetic parameter and study character association for 12 quantitative characters, viz., plant height (cm), primary branches/plant, secondary branches/plant, main shoot length (cm), siliquae on main shoot, siliqua length (cm), seeds/siliqua, 1000-seed weight (g), oil content (%), biological yield/plant (g), seed yield/plant (g) and harvest index (%). The PCV and GCV varied from 8.8 (seeds/siliqua) to 48.0% (seed yield/plant) and 1.4 (oil content) to 26.0% (secondary branches/plant), respectively. The higher estimate of heritability coupled with higher genetic advance for 1000-seed weight indicated that heritability could mainly be due to additive effects and selection would be effective for this trait. Seed yield / plant had positive and significant correlations with, plant height, secondary branches/plant, main shoot length, seeds/siliqua, 1000-seed weight and harvest index. Moderate to high direct positive effects of these characters except seeds/ siliqua and main shoot length on seed yield were responsible for their positive and significant association with yield. Hence these characters merit consideration in the selection programme to improve yield. The characters under investigation could explain about 71.9% of the variability in the seed yield.

Key words: *Brassica juncea*, Genetic variability, Path analysis, Correlation coefficient, Indian mustard

Indian mustard (*Brassica juncea* L.) is the major rapeseed-mustard crop in India. Hence, the improvement of productivity of this crop will go a long way in enhancing the rapeseed-mustard production in country. Seed yield is the end product of additive and / or multiplicative interaction among various factors known as yield contributing characters. Direct selection for seed yield is usually not very effective because yield being a complex character. Therefore, selection based on component characters has been suggested to improve seed yield (Grafius, 1964) in different crops. Genetic variability is prerequisite for a meaningful selection. Genetic parameters like heritability, coupled with genetic advance largely determine the success of selection. The nature and magnitude of association among yield and its components reveal the scope for correlated response to selection. Hence, basic information on genetic parameters, extent of variability and nature of association is essential in formulating appropriate selection approaches in the mustard-breeding programme. Therefore, the present study was attempted to assess the nature of variation and characters association in Indian mustard.

Materials and Methods

The experimental material consisted of 21 advanced breeding lines and four varieties, Varuna, BIO-902, Kranti and Rajat of Indian mustard. These breeding

lines were derived from nine crosses viz., TERI (OE) M-08 x Bio-902 (BPR-2), TERI (OE) M-21 x Varuna (BPR-6), Shiva x Varuna (BPR-62), Pusa Basant x RLM-514 (BPR-83), (Pusa Bold x RLM-514) x Shiva (BPR-87), (RH-30 x PCR-3) x Shiva (BPR-95), RH-819 x PCR-3 (BPR-96), RL-1359 x PCR-3 (BPR-104), and YSRL-9 x PCR-3 (BPR-106). The experimental materials were sown in randomized complete block design with three replications during 2001-02 and 2002-03 *rabi* season. Each genotype was sown in five-row-plot and each row was 5 m long, spaced 30 cm apart. Plant-to-plant distance was maintained of 10-15 cm within a row by thinning. 40 kg N and 40 kg P₂O₅/ha was applied at the time of sowing and the rest of 40 kg N was applied after first irrigation. Two irrigations were given at 40 and 78 days after the sowing, respectively. Observations were recorded on five competitive randomly taken plants from each genotype in each replication on plant height (cm), primary branches/plant, secondary branches/plant, main shoot length (cm), siliquae on main shoot, siliqua length (cm), seeds/siliqua, 1000-seed weight (g), oil content (%), biological yield/plant (g), seed yield/plant (g) and harvest index (%). The genotypic (GCV) and the phenotypic (PCV) coefficients of variation, heritability and genetic advance were calculated by the formulae given by Johnson *et al.* (1955). The genotypic and phenotypic correlations were calculated as per the

method of Al-Jibouri *et al.* (1958). Path coefficient analysis was done according the method of Dewey and Lu (1959).

Results and Discussion

The analysis of variance indicated significant differences among the genotypes for all the characters except primary branches/plant, siliquae on main shoot, siliqua length and biological yield/plant. Therefore, these four characters were excluded from further analysis. The environmental effect was significant only for harvest index indicating thereby that all the genotypes had similar pattern of variability both the years for all the characters except harvest index. Interaction effect of year $\times$ genotypes was significant only for main shoot length. The results implied that the genotypes would behave differentially for this character during both the years. The range, mean, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability and genetic advance for eight quantitative characters are presented in Table 1. The wide range of mean was observed for almost all the characters. The range for plant height was 141.9 cm (BPR-6-91-53-4) to 191.9 cm (Kranti). Genotype BPR-166-24-1 had maximum number of secondary branches per plant. The main shoot length was the highest for the genotype BPR-96-3 (75.6 cm). Minimum and maximum of seeds/siliqua were recorded in the genotype BPR-166-24-1 and BPR-83, respectively (Table 1). Genotype BPR-6-91-52-3 had the highest 1000-seed weight (6.8 g). Harvest index ranged from 18.7 (PCR-18) to 29.4% (BPR-83). All the characters, in general, showed higher magnitude of PCV than GCV indicating the effect of environment on the expression of these characters. However, trend of GCV and PCV was similar. The PCV and GCV varied from 8.8 (seeds/siliqua) to 48.0% (seed yield/plant) and 1.4 (oil content) to 26.0% (secondary branches/plant), respectively. The PCV and GCV were high for

secondary branches/plant, seed yield/plant and 1000-seed weight (Table 1). Sikarwar *et al.* (2000) and Mahla *et al.* (2003) reported high PCV and GCV for seed yield/plant. The rest of the characters showed low PCV and GCV. Heritability values ranged from 14.4 (seed/siliqua) to 63.0% (1000-seed weight). Heritability was relatively high only for 1000-seed weight. Similar results were also reported earlier (Sikarwar *et al.* 2000; Mahla *et al.* 2003). The characters plant height, secondary branches/plant and harvest index showed moderate heritability while, the rest of characters showed low heritability. But in previous studies, high heritability was reported for plant height, secondary branches/plant and seed yield (Sikarwar *et al.* 2000; Mahla *et al.* 2003). Moderate to low estimates of broad sense heritability indicates that improvement for these characters through simple selection would be limited. Genetic advance was high for 1000-seed weight (32.4%) and secondary branches/plant (29.5%), while the other characters showed low genetic advance. Mahla *et al.* (2003) observed high genetic advance for seed yield/plant. The higher estimates of heritability coupled with higher genetic advance for 1000-seed weight indicated that heritability could be mainly due to the additive effects and selection would be effective. The results of the present study were in conformity with earlier report of Mahla *et al.* (2003). Moderate heritability accompanied with low or medium to low genetic advance for other characters indicated the involvement of non-additive gene action in the expression of these characters and moderate heritability is expressed due to favorable influence of the environment rather than genotypes. These results were similar to the finding of Sikarwar *et al.* (2000) and Mahla *et al.* (2003).

Correlations at Phenotypic Level

Estimates of correlation coefficients presented in Table 2 revealed that plant height; secondary branches/plant,

Table 1. Range, mean, phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV) heritability (in broad sense) and genetic advance (as percent of mean) of different characters in Indian mustard.

Characters	Range	Mean $\pm$ SE _m	PCV (%)	GCV (%)	Heritability (%)	Genetic advance (%)
Plant height (cm)	141.9–191.9	165.8 $\pm$ 7.1	13.2	7.6	33.0	9.0
Secondary branches/plant	2.8–10.8	7.4 $\pm$ 1.2	47.2	26.0	30.0	29.5
Main shoot length (cm)	57.0–75.6	65.9 $\pm$ 3.1	13.2	5.8	19.5	5.3
Seeds/siliqua	12.8–15.1	13.7 $\pm$ 13.7	8.8	3.4	14.4	2.6
1000 seed weight (g)	3.2–6.8	4.9 $\pm$ 0.3	24.9	19.8	63.0	32.4
Oil content (%)	39.3–42.6	40.8 $\pm$ 0.5	3.2	1.4	19.0	1.2
Seed yield /plant (g)	5.2–15.5	8.9 $\pm$ 1.5	48.0	23.7	24.3	24.0
Harvest index (%)	18.7–29.4	24.1 $\pm$ 1.7	21.3	12.2	33.0	14.5

main shoot length, seeds/silique, 1000-seed weight and harvest index had significant and positive correlations with seed yield/plant at phenotypic level. Secondary branches/plant had positive and significant correlation with seed yield/plant at phenotypic level ($r=0.306^{**}$) whereas at genotypic level both were negatively associated ($r = -0.834$), thereby suggesting the influence of environment on the correlation. Positive and significant correlations of plant height were observed with main shoot length, 1000-seed weight and harvest index while it had significant and negative association with secondary branches/plant ($r = -0.187^{*}$). Secondary branches/plant exhibited significant and negative relationships with 1000-seed weight, oil content and harvest index but its association with seeds/silique was positive and significant (Table 2). The associations of seeds/silique were positive and significant with main shoot length, 1000-seed weight and harvest index. 1000-seed weight showed significantly positive relationships with harvest index and seeds/silique.

Correlations at Genotypic Level

High positive correlations of plant height were observed with main shoot length, 1000-seed weight and harvest index but its relationship with secondary branches/plant was strong and negative ($r = -1.095$). Positive and high genotypic correlations of seed yield/plant were observed with plant height; secondary branches/plant, main shoot length, seeds/silique, 1000-seed weight and harvest index (Table 2). Mahla *et al.* (2003) also reported high positive association of seed yield with plant height.

Seed yield/plant was negatively correlated with secondary branches/plant ($r = -0.834$ and its association with oil content was weak ($r=0.206$). Secondary branches/plant, in general, had negative association with all the characters investigated in the present study. However, main shoot length showed positive correlation with 1000-seed weight, seeds/silique, oil content and harvest index. Seeds/silique had relatively weak positive correlation with oil content and harvest index. 1000-seed weight showed positive relationship with harvest index and oil content (Table 2).

In general, the pattern of associations between yield and its attributes were similar at both genotypic and phenotypic levels except for secondary branches/plant, which showed variable nature of association with seeds/silique and seed yield. The results suggest that $g \times e$ interaction played important role in the expression of these relationships.

Path Analysis at Phenotypic Level

Correlation coefficients generally describes association between the characters in statistical terms, they are inadequate in interpreting the cause and effect relationship. Hence, correlation coefficients between various characters are partitioned into direct and indirect relationship by path analysis considering seed yield as dependent variable and the rest of the characters as independent variables. Highly significant correlation of seed yield with plant height was due to its moderate positive direct effect and low indirect effects via secondary branches/plant and 1000-seed weight (Table 3). Secondary branches/

Table 2. Correlation coefficients at phenotypic (P) and genotypic (G) levels.

Characters		Secondary branches/plant	Main shoot length	Seeds/silique	1000-seed weight	Oil content	Harvest index	Seed yield / plant
Plant height	P	-0.187*	0.444**	0.009	0.354**	0.060	0.185*	0.469**
	G	-1.095	0.670	0.021	0.952	0.159	0.880	0.725
Secondary branches/	P		-0.142	0.280**	-0.556**	-0.256**	-0.189*	0.306**
	G		-0.929	-0.086	-0.985	-0.347	-0.917	-0.834
Main shoot length	P			0.176*	0.33**	0.252**	0.097	0.358**
	G			0.664	0.810	0.362	0.687	0.673
Seeds/silique	P				0.6**	0.062	0.231**	0.351**
	G				0.084	0.329	0.289	0.434
1000 seed weight	P					0.102	0.498**	0.330**
	G					0.220	0.839	0.811
Oil content	P						0.040	0.006
	G						0.206	0.206
Harvest index	P							0.510**
	G							0.998

*, ** Significant at 5% and 1% level of probability

plant had a strong positive direct effect (0.6397) in building its positive association with yield, which was partially neutralized, by low negative indirect effects via rest of the characters. Satyavathi *et al.* (2000) and Mahla *et al.* (2003) also reported that the number of branches/plant is an important character contributing directly to seed/yield. Low positive direct and indirect effects of main shoot length and seeds/silique were the cause of their positive and significant association with seed yield (Table 3). Moderate positive direct effect and low indirect effects via harvest index and oil content resulted in positive and significant association between 1000-seed weight and seed yield. Gupta and Thakur (2000) also reported that 1000-seed weight had significant positive correlation and positive direct effects on seed yield in karan rai (*Brassica carinata*). Harvest index also showed highly significant correlation with seed yield due its moderate positive direct effect (0.3666). The characters together could explain 71.9% of the variability in the seed yield. Further, in the present study, direct positive effects of plant height, secondary branches/plant, main shoot length, 1000-seed weight and harvest index were observed on seed yield (Table 3). Therefore, selection based on plant height, secondary branches/plant, main shoot length, 1000-seed weight and harvest index should bring forth the desired improvement in seed yield in Indian mustard.

Path Analysis at Genotypic Level

Strong negative direct effect (-1.0247) of plant height and its negative indirect effects via secondary branches/plant and seeds/silique were neutralized by equally strong

positive indirect effect via harvest index (1.5007) and moderate positive effects through main shoot length and 1000-seed weight, resulting into positive association between plant height and seed yield. High negative indirect effect of secondary branches/plant through harvest index and moderate indirect effects via 1000-seed weight and main shoot length was the cause of its negative association with seed yield. Nevertheless, secondary branches /plant had moderate positive direct effect on seed yield (Table 3). Similarly, positive association between main shoot length and seed yield was the result of its moderate direct effect and strong indirect effect via harvest index, which were partly negated, by indirect effects via seeds/silique (-0.2077). Although, seeds/silique had negative direct effects which were compensated by positive indirect effects via rest of the characters (Table 3). Direct and indirect positive effects of 1000-seed weight and via harvest index were the main reasons for its positive association with seed yield. The correlation between harvest index and seed yield was due to its strong positive direct effect. The study revealed that harvest index is the major component in building associations of seed yield with other yield contributing characters as it had high direct as well as indirect effects through them.

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Table 3. Path analysis at phenotypic (P) and genotypic (G) level taking yield as dependent variable (direct effects in bold).

S. No.	Characters		Plant height	Secondary branches/plant	Main shoot length (cm)	Seeds/silique	1000 seed weight	Oil content	Harvest index	Seed yield / plant
1	Plant height	P	0.329	0.1194	0.0543	0.0007	0.1222	0.0038	0.0678	0.4594
		G	-1.0247	-0.4719	0.2696	-0.0067	0.4548	0.0032	1.5007	0.7249
2	Secondary branches/plant	P		0.6397	-0.0173	0.0218	-0.1917	-0.0165	-0.0693	0.3050
		G		0.4309	-0.3735	0.0268	-0.4707	-0.0069	-1.5632	-0.8343
3	Main shoot length	P			0.1222	0.0137	0.1140	0.0162	0.0355	0.3576
		G			0.4031	-0.2077	0.3870	0.0072	1.1720	0.6733
4	Seeds/silique	P				0.0778	-0.0194	0.0040	0.0845	0.3506
		G				-0.3129	0.0400	0.0065	0.4922	0.4339
5	1000 seed weight	P					0.3443	0.0065	0.1826	0.3301
		G					0.4777	0.0044	1.4298	0.8112
6	Oil content	P						0.0643	0.0146	0.0052
		G						0.0199	0.3506	0.2062
7	Harvest index	P							0.3666	0.5103
		G							1.7047	0.9983

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Exploiting Genotypic Variability in Relation to Genetic Divergence Among Advanced Lines of Soybean [*Glycine max* (L) Merrill]

VK Sood*, OP Sood, Anju Pathania and Kushal Chandel

Department of Plant Breeding and Genetics, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062 (Himachal Pradesh)

Sixty eight advanced soybean lines derived from 19 crosses, involving diverse parents, along with two varieties, were evaluated for seed yield and its components to assess genotypic variability in relation to genetic divergence. Analysis of variance revealed significant differences among the lines for all the traits studied. On the basis of D^2 analysis, the lines were grouped into 14 clusters. The patterns of distribution of genotypes in different clusters indicated that genetic divergence was not related to parentage. Maximum intercluster distance was obtained between clusters II and VIII followed by clusters VIII and IX. These clusters included the genotypes Himso 1610, Himso 1629, Himso 1630, Himso 1631, Himso 1606, Himso 1655, Himso 1636, Himso 1650, Himso 1609 and Himso 1669, derived from the crosses Himso 330 x Punjab-1, Himso 1520 x Himso 330, Punjab -1 x DS 74-22, P7-1-1 x Punjab-1, PK 1053 x Punjab-1 and Himso 330 x Hardee. These genotypes may be utilised in the future breeding programme.

Key words: Genetic divergence, Soybean, Advanced breeding lines

The success in genetic improvement of a crop depends on extent of genetic variability. It is evident that genetically diverse parents are likely to produce high heterotic effects and yield desirable segregates. Soybean is the world's most important oilseed crop in terms of total production and trade. A considerable amount of the existing genetic variability in this crop has been exhausted in developing improved varieties in the country. Since the development of a variety is based on the extent of variability for desired characters, the locked genetic variability in respect of linked genes can be released by hybridization and thus breaking gene linkages by crossing over (Fahr, 1978). Earlier studies have revealed the genetic diversity in soybean only of germplasm lines of different geographic origin. Whereas, information on genetic diversity among soybean lines generated through hybridization is meager, therefore, the present investigation was undertaken to unzip the genetic divergence among the advanced lines of soybean following Mahalanobis D^2 statistics which is a powerful tool to quantify the variability at genotypic level.

Materials and Methods

Sixty eight advanced lines of soybean derived through hybridisation from 19 different crosses, along with two commercial varieties, were grown in a randomized block design with two replications during *kharif*, 2004 at the experimental farm of the Department of Plant Breeding & Genetics, Chaudhary Sarwan Kumar (CSK) Himachal Pradesh Krishi Vishvavidyalaya, Palampur. Selection in

the segregating generations was practiced on the basis of yield contributing traits and as a result more than one breeding line having different combination of traits from the same cross were isolated. Each line was sown in a single row plot of 2m length with row- to- row spacing of 30 cm and plant- to- plant spacing of 5 cm. Recommended package of practices were followed for raising the crop. Observations on different traits were recorded on five random competitive plants from each genotype in each replication. To assess the genetic divergence among the lines, Mahalanobis D^2 statistics (Singh and Chaudhary, 1977) was used and grouping of lines was done following Tocher's method (Rao, 1952).

Results and Discussion

Analysis of variance indicated significant variability between the lines for all the traits under study, thereby revealing that sufficient genetic variability has been generated through hybridisation in the present material. Based on the magnitude of D^2 values, sixty eight lines were grouped into 14 clusters, the lines present in the same cluster have smaller D^2 values among themselves than those belonging to different clusters. The parentage of different advance lines have been given in Table 1. As many as 26 lines were grouped in cluster I; 12 in cluster III; 6 each in cluster II and IV; 4 in cluster V, 3 each in cluster VI and X, 2 each in cluster VII, VIII and IX and one each in cluster XI, XII, XIII and XIV (Table 2). The pattern of distribution of genotypes in different clusters indicated that genetic divergence was not related to parentage. Many advanced

* Corresponding author's E-mail: vkspbg23@rediffmail.com

Table 1. Parentage of different soybean lines

Parentage	Number of lines	Code of lines
DS83-20 x Punjab-I	2	Himso 1607, Himso 1608
Himso 330 x Hardee	2	Himso 1609, Himso 1668
Himso 330 x Punjab-I	1	Himso 1610
Himso 333 x NRC2	17	Himso 1611, Himso 1612, Himso 1613, Himso 1614, Himso 1615, Himso 1616, Himso 1617, Himso 1618, Himso 1619, Himso 1620, Himso 1621, Himso 1622, Himso 1623, Himso 1624, Himso 1625, Himso 1626, Himso 1627
Himso 558-A x Bragg	1	Himso 1628
Himso 1520 x Himso 330	4	Himso 1629, Himso 1630, Himso 1631 Himso 1606
Himso 1520 x Punjab-I	3	Himso 1632, Himso 1633, Himso 1634
NRC2 x Hardee	1	Himso 1635
P7-1-1 x Punjab-1	5	Himso 1636, Himso 1637, Himso 1638, Himso 1639 Himso 1640
PK 1053 x Himso 107	7	Himso 1641, Himso 1642, Himso 1643 Himso 1644, Himso 1645, Himso 1646 Himso 1647
PK 1053 x Punjab-1	4	Himso 1648, Himso 1649, Himso 1650 Himso 1651
Punjab-1 x VLS2	3	Himso 1652, Himso 1653, Himso 1654
Punjab-1 x DS 74-22	1	Himso 1655
VLS 2x Lee	2	Himso 1656 Himso 1657
SL 284 x Bragg	6	Himso 1658, Himso 1659, Himso 1660, Himso 1661, Himso 1662 Himso 1663
SL 284 x Punjab-1	3	Himso 1664, Himso 1665 Himso 1666
Palam Soya x PK 416	1	Himso 1667
Hardee x JS 78-53	2	Himso 1669 Himso 1670
Hardee x Punjab-1	3	Himso 1671, Himso 1672 Himso 1673
Palam Soya, Bragg (Commercial varieties)	2	69, 70

Table2. Clustering of 68 soybean lines based on D² statistics

Cluster	Number of lines	Code of lines
I	26	Himso 1611, Himso 1616, Himso 1618 Himso 1624, Himso 1626, Himso 1627 Himso 1635 Himso 1637 Himso 1639 Himso 1641 Himso 1642 Himso 1643 Himso 1644 Himso 1645 Himso 1646 Himso 1647 Himso 1649 Himso 1651 Himso 1652 Himso 1653 Himso 1654 Himso 1658 Himso 1659 Himso 1666 Himso 1670 Himso 1672
II	6	Himso 1610, Himso 1629, Himso 1630, Himso 1631, Himso 1606, Himso 1655
III	12	Himso 1612, Himso 1619, Himso 1620, Himso 1621, Himso 1622 Himso 1628 Himso 1638 Himso 1660 Himso 1661 Himso 1662 Himso 1664 Himso 1669
IV	6	Himso 1607, Himso 1608, Himso 1663, Himso 1668, Palam Soya, Bragg
V	4	Himso 1613, Himso 1617, Himso 1640, Himso 1665
VI	3	Himso 1632, Himso 1634, Himso 1671
VII	2	Himso 1623, Himso 1625
VIII	2	Himso 1636, Himso 1650
IX	2	Himso 1609, Himso 1669
X	3	Himso 1614, Himso 1615, Himso 1657
XI	1	Himso 1633
XII	1	Himso 1648
XIII	1	Himso 1656
XIV	1	Himso 1673

lines derived from the same cross were grouped into different clusters and *vice-versa*. Such type of clustering may have been resulted from recombination coupled with selection for different combinations of desirable traits in segregating generations.

Intra-cluster distances ranged from zero (in monogenotypic clusters) to 37.21 (cluster among genotypes of cluster X), indicating that the lines present in this cluster have maximum genetic dissimilarity among themselves. The intra-cluster distances of clusters III, IV and V (28.68, 29.58 and 29.19, respectively) indicated close relationship and almost parallel genetic diversity among the genotypes included in the respective clusters. Similarly, intra-cluster distances of clusters I and II (31.56 and 32.95), clusters VIII and IX (26.20 and 27.58), clusters VI and X (36.90 and 37.21) exhibited narrow genetic diversity among the genotypes in the respective clusters.

Maximum inter-cluster distance (Table 3) was observed between clusters II and VIII (656.61), followed by clusters VIII and IX (587.99), indicating thereby that the progenies derived from crossing the lines of these clusters, will be expected to throw out a broad

Table 3. Intra-cluster (diagonal and bold) and inter-cluster distances among fourteen clusters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	31.6													
II	253.7	32.9												
III	55.5	298.0	28.7											
IV	80.2	128.8	74.1	29.6										
V	78.8	394.8	129.7	205.5	29.2									
VI	140.7	249.7	244.6	228.4	95.9	36.9								
VII	66.9	437.5	61.6	141.9	117.4	294.4	12.8							
VIII	209.0	656.6	319.8	445.5	71.9	151.8	261.5	26.2						
IX	352.0	121.5	499.7	297.2	422.8	212.7	575.9	587.9	27.6					
X	58.9	393.8	69.2	161.3	56.0	161.2	92.6	159.1	526.9	37.2				
XI	80.7	103.7	110.6	68.5	131.4	84.3	206.2	305.1	208.6	123.8	0.0			
XII	97.4	358.4	58.1	132.5	136.2	226.0	127.8	307.1	567.9	53.1	104.0	0.0		
XIII	158.1	427.5	221.6	302.2	69.6	84.6	276.2	89.2	469.4	108.1	148.6	193.7	0.0	
XIV	94.5	315.4	207.5	216.1	50.6	50.5	187.6	94.2	245.3	129.7	125.8	228.7	117.9	0.0

spectrum of genetic variability and thus providing greater chances for isolating high- yielding segregates in the succeeding generations. New and hitherto unknown gene combinations could be produced by crossing genotypes from highly diverse groups. Hybridization between genetically diverse groups to generate promising breeding material has been suggested frequently (Raut *et al.*, 1984). The minimum inter- cluster distance was observed between clusters XIV and VI (50.48), followed by clusters XIV and V (50.62), indicating the minimum diversity between the genotypes included in these clusters. Such results suggest to avoid selection of parents from these clusters (genetically closer) which may narrow down the genetic base and result in inbreeding depression.

Cluster means showed that maximum and minimum values for different characters were; 72.50 days (cluster XIII) and 60.50 days (cluster VII) for days to flowering; 128 days (cluster IX) and 119.17 days (cluster X) for days to maturity; 18.15g (cluster II) and 8.88 g (cluster VIII) for 100-seed weight, 45.50 (cluster XII) and 23.83 (cluster II) for pods per plants, 235g (cluster IX) and 155 g (cluster VIII) for seed yield (Table 4). As such, it was observed that the 100-seed weight was maximum in cluster II but the number of pods per plant the minimum in cluster II, indicating thereby inverse relationship between these traits. So, lower the pod number, bolder the seed. Cluster VIII had the minimum 100-seed weight (8.88g) and simultaneously the lowest yield (155g)

Table 4. Cluster mean values for different traits among the lines

Cluster/Trait	Plant height	Days to flowering	Days to maturity	Pods per plant	100 seed weight	Seed yield
I	65.8	64.0	121.0	29.5	12.0	225.5
II	73.0	64.0	122.0	23.8	18.2	226.7
III	64.7	62.0	118.0	30.5	12.1	221.3
IV	66.0	61.0	120.0	27.4	14.5	233.3
V	70.4	68.0	122.0	32.1	10.8	208.8
VI	67.8	70.0	124.0	31.5	13.8	181.7
VII	66.3	61.0	120.0	29.8	9.6	165.0
VIII	63.3	71.0	124.0	31.0	8.9	155.0
IX	81.3	66.0	128.0	25.0	17.6	235.0
X	88.3	66.0	119.0	35.8	11.2	221.7
XI	75.0	67.0	121.0	33.0	15.2	190.0
XII	65.0	65.0	118.0	45.5	12.8	190.0
XIII	64.0	73.0	120.0	24.5	10.9	150.0
XIV	73.5	68.0	126.0	34.0	11.9	240.0

among all clusters which indicated direct relationship between 100-seed weight and seed yield. Genetic divergence studies in soybean has been carried out by earlier workers only on germplasm lines of soybean of different geographic origin (Raut *et al.*, 1984; Ghatge and Kadu, 1993; Kumar and Nagarajan, 1994; Mehetre *et al.*, 1994), suggesting that majority of economically important characters including seed yield and its components are amenable for genetic improvisation through intense breeding, among genetically diverse parents.

In the present study, maximum intercluster distance was observed between clusters II and VIII followed by clusters VIII and IX. These cluster involved the genotypes Himso 1610, Himso 1629, Himso 1630, Himso 1631, Himso 1606, Himso 1655, Himso 1636, Himso 1650, Himso 1609 and Himso 1669, derived from the crosses Himso 330 x Punjab-1, Himso 1520 x Himso 330, Punjab -1 x DS 74-22, P7-1-1 x Punjab-1, PK 1053 x Punjab-1 and Himso 330 x Hardee. These genotypes may be utilised in the future breeding programme as hybridisation between divergent genotypes

is likely to produce wide variability and transgressive segregants.

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Characterization and Evaluation of Sorghum [*Sorghum bicolor* (L.) Moench] Germplasm from Andhra Pradesh, India

M Elangovan, Prabhakar and D Chandra Sekara Reddy

National Research Centre for Sorghum, Rajendranagar, Hyderabad-500 030 (Andhra Pradesh)

This paper discusses results of the preliminary characterization and evaluation of 95 accessions of sorghum germplasm collected from Andhra Pradesh under the National Agricultural Technology Project (Mission Mode-Plant Biodiversity). A total of 28 agro-morphological and one biochemical character were studied. The accessions exhibited good variability in both qualitative and quantitative traits. In qualitative traits, maximum diversity was observed in earhead compactness, glume colour, seed size, and seed colour. The days to 50% flowering (60–121), plant height (103–270 cm), earhead length (8.96–39.65 cm), stem fresh weight (50–940 g), stem dry weight (30–290 g) and grain yield (14–83 g) showed good variability in quantitative traits. The correlation coefficients of the quantitative traits were also analysed.

Key words: Characterization, Evaluation, Germplasm, Sorghum

Sorghum, [*Sorghum bicolor* (L.) Moench] also known as Jowar was originated and domesticated in Africa about 5000–8000 years ago (De Candolle 1890; Zeven and Zhukovsky 1975). The Indian subcontinent is the secondary centre of origin of this most important cereal. The diversity in sorghum is distributed throughout India. Appa Rao *et al.* (1999) and Elangovan (2004) indicated that the racial diversity of sorghum is maximum in the state of Andhra Pradesh followed by Maharashtra.

Though a number of surveys were conducted earlier leading to a collection of about 1,100 accessions earlier, to re-collect the landrace diversity from unsurveyed and under-surveyed areas, four explorations were undertaken during 2002–2003 in Andhra Pradesh under the National Agricultural Technological project (Mission Mode-Plant Biodiversity). A total of 95 accessions were collected by National Research Centre for Sorghum (NRCS), Hyderabad, Andhra Pradesh.

Characterization and evaluation of germplasm are the pre-requisites for the utilization of the available diversity in the crop improvement programme. Hence, the accessions were characterized to assess the variability and identify the promising accessions for different traits.

Materials and Methods

The preliminary characterization and evaluation of 95 accessions of sorghum were carried out at the National Research Centre for Sorghum (NRCS), Rajendranagar, Hyderabad and Solapur during *rabi* 2002–03 and 2003–04. The centres are located at 17°19' N latitude and 78°24' E longitude and at an altitude of 538 m above MSL and 17°04' N latitude and 75°54' E longitude

respectively with temperature varying from 10° C to a maximum of 30° C during the cropping season. The soil type was of red sandy. The accessions were raised in an Augmented Randomized Block Design (ARBD) with check varieties (M35-1, Swati and CSV-15) in each block. The accessions were grown in 4 m rows with a row spacing of 60 cm and plant to plant spacing of 10 cm. Standard agronomic and plant protection practices were followed during the cropping season. The data on qualitative and quantitative descriptors were recorded using minimal descriptor developed by NBPGR (Mahajan *et al.*, 2000) and list of sorghum descriptors released by IBPGR/ICRISAT (1980, 1993). Five representative plants in each accession were tagged for recording the qualitative and quantitative characters. Brix percentage of each accession was estimated by refractometer. The quantitative data were analysed statistically.

Results and Discussion

The 95 accessions of sorghum accessions were characterized and evaluated for 28 agro-morphological and one biochemical character. Wide range of variability was recorded in both qualitative and quantitative characters. Majority of the accessions showed tan type, dark green leaf colour, erect leaf orientation, and stay green types (non-senescence). However, variation was observed in seedling vigour, midrib colour, earhead shape, earhead compactness, glume colour, glume covering, seed size, seed colour, and races. Sorghum landraces are consistent for morphological characters, the importance of the midrib color, grain color, grain

size, glume color, glume hairiness, and grain shape were used by the farmers in naming the sorghum landraces (Teshome *et al.*, 1997). Twenty-two sorghum genotypes evaluated for grain mould response showed that harder grain, higher levels of seed phenols, and darker glumes contributed to grain mould resistance (Audilakshmi *et al.*, 1999). The variability of glume colour available in the present study may be utilized for screening for grain mold resistance in sorghum.

The quantitative characters also showed wide variation in the evaluated sorghum germplasm. The results of descriptive statistical analysis are presented in Table 1. The characters of days to 50% flowering (60–121), plant height (103–270 cm), earhead length (8.96–39.65 cm), stem fresh weight (50–940 g), stem dry weight (30–290 g) and grain yield (14–83 g) are the highly variable based on the variance. The brix

percentage ranged from 6–22. The chance of deriving sweet stalk sorghum may be possible from the high brix accessions. The variability presents in the leaf length, plant height, stem fresh weight and stem dry weight can be used to derive fodder sorghum.

Evaluated was done for over 4000 accessions from 11 major sorghum growing states in India for morphological and agronomical characters Appa Rao *et al.*, (1999). Characters as days to flowering, plant height, panicle length, erect and compact panicles were more frequent. Racial diversity was maximal in the state of Andhra Pradesh followed by Maharashtra state. The present study also observed similar variability in days to 50 % flowering and plant height. Analysis of variance (Table 2) revealed significant differences among the characters within a location and across the locations.

Table 1. Statistical analysis of quantitative characters in sorghum accessions

Characters	Minimum	Maximum	Mean	SE	SD	Sample Variance
Days to 50% flowering (days)	60	121	83.63	0.97	9.45	89.30
Number of leaves	6	18	9.92	0.21	2.06	4.25
Leaf length (cm)	47.25	91.55	63.00	0.87	8.50	72.31
Leaf width (cm)	3.09	10.20	6.42	0.12	1.12	1.26
Plant height (cm)	103	270	183.47	2.94	28.64	820.24
Earhead length (cm)	8.96	39.65	18.60	0.63	6.15	37.85
Earhead width (cm)	4.45	10.25	7.25	0.12	1.15	1.32
Stem thickness (cm)	1.06	2.90	1.60	0.03	0.32	0.10
Stem fresh weight (g)	50	940	239.95	13.33	127.11	16157.88
Stem dry weight (g)	30	290	126.32	5.32	50.46	2545.89
Brix (%)	6	22	14.36	0.37	3.53	12.43
Grain yield (g)	14	83	41.94	1.81	16.95	287.24
100-seed weight (g)	1.77	4.71	3.06	0.06	0.57	0.32

Table 2. Analysis of variance for different characters

Source of variation	Variance		
	Location I (Solapur)	Location II (Hyderabad)	Pooled over I & II
d.f	12	11	12
Days to 50% flowering (days)	154.84	92.24	89.30
Number of leaves	10.28	2.88	4.25
Leaf length (cm)	137.52	82.79	72.31
Leaf width (cm)	1.45	2.12	1.26
Plant height (cm)	1731.55	1082.07	820.24
Stem thickness (cm)	0.10	NA	0.10
Earhead length (cm)	47.50	32.58	37.85
Earhead width (cm)	1.30	3.10	1.32
Stem fresh weight (g)	403946.90	395951.12	16157.88
Stem dry weight (g)	63835.40	62174.56	2545.89
Brix (%)	13.40	13.57	12.43
Grain yield (g)	378.70	470.16	287.24
Seed weight (g)	0.30	0.30	0.32

* All characters significant at P = 0.05

The correlation coefficients of grain yield/fodder yield vs. some major yield attributing characters were analysed. The grain yield and some minor grain-yield attributing characters *viz.*, number of leaves and leaf width showed positive correlation and 100-seed weight also showed positive correlation with number of leaves and grain yield. The dry fodder (stem dry weight) yield and some major fodder-yield attributing characters showed high positive correlation with stem fresh weight, number of leaves, leaf width, days to flowering, stem thickness. Amsalu Ayana, Endashaw Bekele (2000), also reported similar results. Negative correlation was observed in case of days to 50% flowering with earhead width, brix with leaf width and plant height, grain yield and earhead length, days to maturity with earhead width, and 100-seed weight with brix.

Promising lines identified performing better than the check varieties are listed in Table 3.

Table 3. Promising accessions of sorghum identified from evaluation

Trait	Promising accessions
Days to 50% flowering (=60 days)	IC-347591
Number of leaves (>17)	IC-347576, 347583
Leaf length (>82 cm)	IC-347574, 347576, 347583, 347585, 347591
Leaf width (>8 cm)	IC-347592, 392142, 392147, 392149, 392150, 392159
Plant height (>240 cm)	IC-347517, 347583, 347585
Earhead length (>30 cm)	IC-347581, 347583, 347584, 347585
Earhead width (>9 cm)	IC-369123, 369125, 369130, 345705, 345710, 345714, 347582
Stem thickness (>2 cm)	IC-347574, 347576, 347581, 347582, 347583, 347585
Brix (>19%)	IC-347517, 345722, 345725, 347570, 347576, 347587, 347594, 347595
Grain yield (>70 g)	IC-345705, 345710, 345715, 345719, 345724, 345731, 347569, 392144
100-seed weight (>4 g)	IC-345708, 345709, 345710, 345711, 392141
Days to maturity (=98days)	IC - 347579

Preliminary characterization and evaluation of 95 accessions of sorghum germplasm for 28 agro-morphological and one biochemical characters exhibited good variability in both qualitative and quantitative traits. In qualitative traits, maximum diversity was observed in earhead compactness, glume colour, seed size, and seed colour. The days to 50% flowering (60–121), plant height (103–270 cm), earhead length (8.96–39.65 cm), stem fresh weight (50–940 g), stem dry weight (30–290 g) and grain yield (14–83 g) showed good variability in quantitative traits. Promising accessions identified in the study for various characters will be helpful in sorghum improvement programmes. The high yielding accessions viz., IC Nos.- 345705, 345710, 345715, 345719, 345724, 345731, 347569, 392144 and high brix

percentage lines viz., IC Nos. - 345717, 345722, 345725, 347570, 347576, 347587, 347594, 347595 will be highly useful in the yield and sweet stalk sorghum improvement programmes.

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Comparative Manifestation of Genetic Diversity for Grain Yield and Its Component Traits in Urdbean under Two Cropping Systems

Mohar Singh and SK Sharma¹

Department of Plant Breeding & Genetics, CSK HPKV, Palampur-176 062 (Himachal Pradesh)

¹ National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012

Nature and magnitude of comparative genetic diversity was assessed using Mahalanobis's D^2 statistics in 64 genotypes (16 parents and 48 F_2 crosses) of urdbean genotype grown in monoculture and in association with maize. All the genotypes were grouped in 9 clusters in case of monoculture, while 7 clusters were formed for intercropping. Some genotypes had consistently the similar clustering pattern in both the cropping systems while others were affected by the cropping system in expressing the genetic diversity. The performance of some genotypes varied from cropping system to another, while that of others remained unaffected. Breeding programme to develop varieties suitable for monoculture, intercrop and both the cropping systems has been suggested.

Key words: Urdbean, Cropping system, Genetic divergence, Cluster analysis

Urdbean is cultivated in India as a sole or monoculture crop. However, its intercropping with maize is a common practice in some hilly tracts of North India. This practice aims at (i) ensure against total crop failures under abnormal weather conditions, (ii) increase in total productivity per unit land area and (iii) equitable and judicious utilization of land resources and farming inputs. The Indian Urdbean Breeding Programme has concentrated mainly on the development of high yielding varieties adapted to sole cropping. The varieties developed to date are also being intercropped with maize under the assumption that correlated improvement will occur in the intercrop. However, significant genotype x cropping system interactions have been reported in climbing bean genotypes (Francis *et al.*, 1978a, 1978b) and segregating soybean populations (Gupta *et al.*, 1981). Most of the available information on genetic divergence of urdbean was only under monoculture or sole crop and we have no information as to how the genetic diversity of the urdbean genotypes is altered when intercropped with maize. The selection of genetically diverse parents belonging to distant groups lead to a wide spectrum of gene combinations for polygenically inherited traits. The present study aims at analyzing the genetic divergence of 48 F_2 crosses and their parents under both the cropping systems using Mahalanobis's D^2 statistics, a powerful tool in discerning divergence among groups based upon multiple characters and assessing the relative contribution of different components to the total divergence (Rao, 1952, Murty and Annachalam, 1966). Such a measure will eventually help in breeding programmes by intermating of unlikes leads to greater opportunity for crossing over which releases latent variation by breaking

up the predominantly repulsion phase linkages (Thoday, 1960) at evolving superior genotypes required for different cropping systems.

Materials and Methods

The material for the present study consisting twelve genetically diverse lines of urdbean (HPU-1, VB-17, HPBU-124, HPBU-125, HPBU-126, HPBU-128, HPBU-129, HPBU-130, HPBU-131, HPBU-133, UL-338 and MX-17) were crossed with four diverse pollen parents (T-9, PDU-1, UG-218 and Palampur-93) in a line x tester mating design (Kempthorne, 1957). The resultant 48 F_2 crosses alongwith 16 parents were evaluated for their performance at the Regional Research Station, Himachal Pradesh Agricultural University Bajaura (31°48'N, 77°00'E, 1099 amsl). The experiment was conducted in Randomized Block Design with three replications under two sets of cropping systems *viz* monoculture and intercropping with maize. Each entry in sole crop, sub-plots comprised two rows of urdbean each 2m long and 30 cm apart. Under associated cropping, sub-plot treatments were identical except that a row of a locally recommended variety of maize (Early Composite) was added between successive two rows of urdbean. The plants of urdbean and maize were spaced at 8 and 20 cm within rows, respectively. All the recommended agronomic practices were followed for raising the crop.

Observations were recorded on 5 and 20 randomly selected plants/replication for parents and F_2 's, respectively on X_1 : seed yield/plant (g), X_2 : harvest index (%), X_3 : 100-seed weight (g), x_4 : seeds/pod, X_5 : pods/plant, X_6 : biological yield/plant (g), X_7 : plant

height (cm), X_8 : pod bearing branches/plant, X_9 : days to 50% flowering, X_{10} : days to maturity. Data were analyzed based on the procedure described by Rao (1952), the values of D^2 between pairs of genotypes were computed. The composition of groups was formed according to Tocher's method.

Results and Discussion

The composition of each cluster in two cropping systems are presented in Table 1. As many as 13 genotypes were grouped in cluster I under monoculture, followed by 10 in clusters II and IX, 9 in clusters VI and VIII and 8 in cluster III, 2 each in IV and V and 1 in cluster VII. In case of intercropping, 16 genotypes were grouped in cluster I followed by 12 in clusters II and VII, 10 in cluster IV, 9 in cluster V, 4 in III and 1 in cluster VI. The clustering pattern of progenies was independent of parental cross combinations, i.e., progenies of cross and there parents were grouped in different clusters under two cropping systems. The clustering pattern of some genotypes was not consistent. This can easily be attributed to the effect of cropping system on the genotypes in expressing the genetic diversity. This also demonstrated simultaneously that the conclusions drawn on the basis of a study of genetic diversity of parents and progenies in monoculture cannot be applicable in intercropping. Grouping of populations into clusters have been reported to alter from environment to environment (Somayajulu *et al.* 1970, Upadhyaya and Murty 1970, Jatasra and Paroda, 1983).

Intra-cluster average D^2 values for monoculture ranged from 10.10 to 16.47 while 9.78 to 12.84 under intercropping system (Table 2). Relatively low values of intra-cluster average D^2 suggested the presence of narrow genetic variation within a cluster. Inter-cluster D^2 is a measure of genetic distance between two clusters and was observed to be the highest (58.09) between clusters IV and V and the lowest (17.05) between clusters II and III in monoculture, while it was the highest (98.33) between cluster I and VI and the lowest (14.27) between cluster I and IV in the intercropping. Intra- and inter-cluster average D^2 values were higher in magnitude under monocropping than intercropping except cluster VI of intercropping. The cluster means for all the characters were higher in magnitude under monoculture than the intercrop (Table 3). It was due to the effect of intercropping on urdbean genotypes.

The urdbean breeding for higher seed yield is of great significance for both cropping systems. Direct relationship between progeny mean and number of superior genotypes to the best check has been reported by Bakshi Ram *et al.* (1996). Therefore, the mean performance of progenies is very important in deciding which of the crosses should be repeated or not in order to get better segregants. The mean performance of seed yield of diverse cluster combinations in two cropping systems indicated that means of cluster combination I (6.48) and III (6.58) were lower in magnitude under monoculture, while cluster combination V (4.34) in intercropping system. Hence, the hybridization among genotypes from these cluster combination might result in enhancement in genetic variability towards negative direction. Hybridization among genotypes from these cluster combinations may not improve the population mean performance but the variance and the range of frequency distribution are expected to increase (Allicchio and Palenzona, 1974) due to crossing over which releases latent variation by breaking up the predominantly repulsion phase linkage (Thoday, 1960).

Further, mean of cluster combination IV (HPBU-131 x PDU-1 and HPBU-133 x UG-218), followed by cluster VII (HPBU-130 x PDU-1) was the maximum in monoculture, whereas, similar clusters also consisting various genotypes under intercropping system. Therefore, subsequent cross-breeding programme among genotypes of these cluster combinations for important seed yield and component traits is expected to increase variability in the further mapping population with desirable mean performance suitable for both the cropping systems could be undertaken.

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Table 1. Distribution of parents and their progenies in different clusters under two cropping systems

Monoculture				Intercropping			
Cluster	Number of genotypes	Parents	Progenies	Cluster	Number of genotypes	Parents	Progenies
I	13	T-9, PDU-1	HPU-1 x Palampur-93, HPBU-124 x T-9, HPBU-125 x T-9, HPBU-126 x T-9, HPBU-128 x UG-218, HPBU-128 x Palampur-93, HPBU-130 x UG-218, HPBU-133 x PDU-1, UL-338 x UG-218, MX-17 x Palampur-93	I	16	MX-17, T-9, PDU-1, UG-218	HPU-1 x T-9, HPU-1 x Palampur-93, VB-17 x PDU-1, VB-17 x UG-218, VB-17 x Palampur-93, HPBU-124 x T-9, HPBU-124 x PDU-1, HPBU-125 x T-9, HPBU-126 x UG-218, HPBU-128 x T-9, HPBU-129 x T-9, HPBU-131 x Palampur-93
II	10	HPU-1, HPBU-130, HPBU-131, MX-17, UL-338	VB-17 x T-9, VB-17 x PDU-1, HPBU-126 x Palampur-93, HPBU-128 x PDU-1, HPBU-130 x T-9	II	12	VB-17, HPBU-124, HPBU-125, HPBU-126, Palampur-93	HPBU-125 x UG-218, HPBU-125 x Palampur-93, HPBU-129 x Palampur-93, HPBU-130 x T-9, HPBU-130 x UG-218, MX-17 x T-9, MX-17 x PDU-1
III	08	—	HPU-1 x UG-218, HPBU-124 x UG-218, HPBU-126 x UG-218, VB-17 x UG-218, HPBU-128 x T-9, HPBU-129 x UG-218, HPBU-129 x Palampur-93, UL-338 x T-9	III	04	—	HPBU-125 x PDU-1, HPBU-128 x Palampur-93, UL-338 x T-9, UL-338 x Palampur-93
IV	02	—	HPBU-131 x PDU-1, HPBU-133 x UG-218	IV	10	UL-338	VB-17 x T-9, HPBU-126 x PDU-1, HPBU-126 x Palampur-93, HPBU-128 x PDU-1, HPBU-129 x PDU-1, HPBU-130 x PDU-1, HPBU-130 x Palampur-93, HPBU-131 x T-9, MX-17 x UG-218
V	02	—	VB-17 x Palampur-93, HPBU-125 x Palampur-93	V	09	—	HPU-1 x UG-218, HPBU-129 x UG-218, HPBU-131 x PDU-1, HPBU-131 x UG-218, HPBU-133 x T-9, HPBU-133 x PDU-1, HPBU-133 x UG-218, HPBU-133 x Palampur-93
VI	09	HPBU-128, HPBU-129, VB-17	HPBU-1 x PDU-1, HPBU-131 x T-9, HPBU-131 x UG-218, HPBU-131 x Palampur-93, HPBU-133 x PDU-1, MX-17 x PDU-1	VI	01	HPU-1	—
VII	01	—	HPBU-130 x PDU-1	VII	12	HPU-1, HPBU-128, HPBU-129, HPBU-130, HPBU-131, HPBU-133	HPU-1 x PDU-1, HPBU-124 x UG-218, HPBU-126 x T-9, HPBU-128 x UG-218, UL-338 x PDU-1, MX-17 x Palampur-93
VIII	09	HPBU-126	HPBU-125 x PDU-1, HPBU-125 x UG-218, HPBU-126 x PDU-1, HPBU-129 x T-9, HPBU-124 x Palampur-93, HPBU-130 x Palampur-93, MX-17 x T-9, MX-17 x UG-218				
IX	10	HPBU-124, HPBU-125, HPBU-133, UG-218, Palampur-93	HPU-1 x T-9, HPBU-124 x PDU-1, HPBU-129 x PDU-1, HPBU-133 x T-9, UL-338 x Palampur-93				

Table 2. Intra- and inter- cluster VD² values under two urdbean cropping systems

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
Monoculture									
I	10.10	24.96	24.28	40.23	39.51	18.68	39.25	20.27	17.73
II		15.64	17.05	43.35	21.80	25.05	38.76	19.46	21.17
III			16.47	47.31	30.16	30.02	46.61	30.81	17.22
IV				12.53	58.09	25.62	47.09	43.15	37.57
V					13.02	38.89	48.56	28.55	40.99
VI						11.22	35.54	21.20	22.74
VII							–	34.45	41.38
VIII								13.90	29.15
IX									13.71
Intercropping									
I	9.78	19.36	31.29	14.27	16.23	98.33	15.11		
II		9.88	18.71	15.87	17.22	95.64	15.67		
III			11.89	23.94	21.94	97.23	24.89		
IV				11.79	18.64	97.17	17.86		
V					12.84	97.29	20.29		
VI						–	96.10		
VII							12.43		

Table 3. Cluster means of characters under two urdbean cropping systems

Character	Cluster								
	I	II	III	IV	V	VI	VII	VIII	IX
Monoculture									
X ₁	6.48	9.04	6.58	11.34	7.15	8.63	9.97	8.61	8.01
X ₂	38.83	41.90	37.15	24.00	41.39	32.64	40.86	42.36	38.58
X ₃	5.04	4.96	4.87	5.20	4.88	5.11	4.92	4.82	4.88
X ₄	5.21	5.24	5.33	5.79	5.44	5.25	4.68	5.14	5.18
X ₅	26.40	35.53	25.21	37.35	28.44	31.06	44.71	35.90	31.95
X ₆	18.34	23.86	18.37	50.62	21.29	30.35	24.65	22.05	21.78
X ₇	45.44	48.26	44.80	57.26	50.25	56.60	56.28	47.83	47.55
X ₈	8.02	9.21	8.25	8.79	8.43	9.31	10.44	9.55	9.15
X ₉	41.84	40.90	41.06	42.70	41.15	41.71	42.00	41.46	40.86
X ₁₀	89.13	89.40	91.78	93.35	91.00	90.69	92.50	88.13	89.60
Intercropping									
X ₁	5.68	5.96	5.74	6.37	4.34	5.55	5.49		
X ₂	36.64	38.18	36.27	39.86	33.07	4.29	38.13		
X ₃	4.74	4.27	4.93	4.42	4.55	4.23	4.39		
X ₄	4.99	4.70	4.56	4.83	4.99	4.99	4.75		
X ₅	26.50	28.26	27.20	36.05	29.83	37.40	24.45		
X ₆	14.66	15.00	14.23	16.55	12.12	12.27	13.69		
X ₇	40.85	45.41	32.98	36.72	33.46	46.44	46.25		
X ₈	7.20	7.75	7.75	7.52	6.57	6.69	7.59		
X ₉	44.47	45.26	44.15	43.02	42.26	45.20	44.63		
X ₁₀	96.50	94.54	94.13	95.38	95.89	96.00	94.65		

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Genetic Divergence for Yield and its Component Traits in Groundnut Germplasm

TN Lakshmidhevamma, M Byre Gowda*, P Mahadevu and G Lakshmi

AICRP on Pigeonpea, University of Agricultural Sciences, GKVK, Bangalore-560 065 (Karnataka)

Eighty-one genotypes of groundnut (*Arachis hypogaea* L.) representing different groundnut centres were studied for genetic divergence analysis utilizing Mahalanobis D^2 analysis. Based on the genetic distance (D^2 value) groundnut accessions were grouped into 16 clusters. Of the 16 clusters formed, cluster I was the largest with 47 accessions followed by cluster II with 10 accessions. Test weight, days to maturity and oil content were the most potential traits contributing to the total divergence. Cluster XI and XVI had maximum inter-cluster distance suggesting wide diversity and by utilizing these accessions from these clusters desirable segregants may be evolved through hybridization. Cluster XII has genotype with most favorable characters and hence can be involved as potential parent for development of superior genotypes.

Key words: *Arachis hypogaea*, Clusters, Divergence, Groundnut, D^2 technique

Groundnut (*Arachis hypogaea* L.) is an important oilseed crop of India. The information on genetic diversity in a crop is essential in order to have breeding programmes for higher yield potentials. Choosing genetically diverse parents will enable the expansion of genetic base and development of superior types. In this regard, Mahalanobis (1936) generalized distance (D^2) technique has been extensively used to measure the genetic divergence in breeding programmes. Intercrossing between more divergent parents is expected to generate a broad spectrum of variability and selection can be adopted in the segregating generations. Hence, an attempt was made the magnitude of genetic divergence in groundnut accessions and to identify genetically divergent parents, which can be utilized in hybridization programmes.

Materials and Methods

Eighty-one genotypes of groundnut representing different parts of India were grown in 9 x 9 simple lattice design with two replications at GKVK Farm, University of Agricultural Sciences, Bangalore. Observations were recorded on five randomly chosen plants in each replication for 13 quantitative characters. The mean values were transformed into uncorrelated linear functions using Mahalanobis group distance (D^2) analysis [Rao, 1952]. The D^2 values corresponding to all possible pairs of genotypes were calculated to determine group constellations. The genetic divergence was assessed and the genotypes were grouped on the basis of generalized distance using the Tocher's method as suggested by Rao (1952).

Results and Discussion

The analysis of variance revealed highly significant differences among the genotypes for all the characters studied, indicating the existence of wide genetic divergence among them. Based on relative magnitude of values, all the genotypes were grouped into 16 clusters (Table 1). Among the 16 clusters, cluster I was the largest having 47 genotypes followed by cluster II with 10 genotypes.

Table 1. Distribution of 81 Groundnut genotypes into different clusters

Cluster no	No of genotypes	Accession Name/ Number
I	47	J-41, J-46, Dh-88, JL-24-2, K-1240, J-39, J-45, JSSP-7, J-42, JL-24, J-47, ICGS-30, TVG-9363, K-1257, ICGV-86325, AK-135, SAMRAT, TNAU-97, Dh-55, AK-107, JL-286, R-8806, Dh-87, AK-159, K-134, VRI-2, IC-1224, R-9214, VG-9521, TMV-2, Dh-53B, J-40, K-134 x D-8-29, ICGV-92242, OG-931, TNAU-325, J-48, Bagepalli Local, TG-36B, TAG-24, Dh-10 x R-847259, R-9217, TG-37C, TG-26, HNG-35, J-38, KGN-20
II	10	VG-9516, CSMG-919, Dh-53A, VG-9513, KGN-35, JL-274, ALG-75, Dh-56, ICGV-23, SB-11
III	1	JSSP-28
IV	4	M-335, JSSP-30, ICGS-76, JSSP-15
V	5	JSSP-13, RG-369, JSSP-29, TG-37D, TNAU-281
VI	1	LGN-1
VII	2	VG-9711, JSSP-17
VIII	3	ICGV-86590, ICGV-86532, JL-24-B
IX	1	J-54
X	1	TG-37F
XI	1	R-9248
XII	1	JSSP-18
XIII	1	Dh-992
XIV	1	JSSP-16
XV	1	TNAU-269
XVI	1	M-13

* Corresponding author

Ten clusters were found to be solitary with one genotype each. The clustering pattern of genotypes from different centres was of random nature. The tendency of genotypes from different centres to group together in one cluster may be due to similarity in requirements and selection approach followed under domestic cultivation. The results are in accordance with the findings of Nadaf *et al.* (1986), Katule *et al.* (1992), Nayak and Patra (1997) and Venkataravana *et al.* (2000).

Another feature that came to light was that genotypes from the same centre were placed in separate clusters indicating wide diversity among genotypes originating from the same place. The clustering pattern, thus failed to indicate any relationship between the genetic divergence and the centres of development of these accessions. Similar results were obtained by Katule *et al.* (1992), Nayak and Patra (1997) and Venkataravana *et al.* (2000).

The intra and inter cluster D^2 values among the 16 clusters are presented in Table 2. Cluster VIII had the maximum intracluster distance of 69.2 followed by cluster II with a distance of 66.5. Ten clusters, which were solitary, had no intra cluster distances. Theoretically, crossing of genotypes belonging to the same cluster

is not expected to yield superior hybrids or segregants. A general notion exists that the larger the divergence higher will be the variability generated in the segregating generation. In this context, inter-cluster distances were worked out considering 13 quantitative characters. The inter-cluster distance was the maximum between clusters XI and XVI (1117.5) followed by cluster X with XVI (901.4). The minimum inter-cluster distance was between the VI and XI (60.8). Hence, the genotypes included in the cluster VI, X, XI and XVI may be selected for more effective crossing programme and should result in wide spectrum of variability to operate selection in segregating populations.

The per cent contribution of each character in grouping the genotypes was worked out and presented in Table 3. Since each genotype produced 80 combinations with all the genotypes, 3240 D^2 values were obtained. Based on these D^2 values, per cent contribution of different characters towards divergence was obtained. Test weight ranked first i.e., 1337 times with a maximum contribution of 41.27 per cent to the total divergence followed by days to maturity (21.11%) and oil content (11.67%). These characters can be given greater

Table 2. Intra-cluster (diagonal) and inter-cluster distances for 16 clusters in groundnut

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	56.15 (7.493)	169.52 (13.02)	115.33 (10.739)	214.15 (14.634)	317.59 (17.821)	102.17 (10.108)	208.2 (14.429)	119.99 (10.954)	114.85 (10.717)	118.83 (10.901)	175.22 (13.237)	210.63 (14.513)	188.02 (13.712)	362.86 (19.049)	278.05 (16.675)	605.11 (24.599)
II		66.5 (8.156)	210.77 (14.518)	248.9 (15.777)	168.79 (12.992)	119.7 (10.941)	140.49 (11.853)	157.75 (12.56)	148.18 (12.173)	298.22 (17.269)	271.85 (16.488)	246.24 (15.692)	111.87 (10.577)	443.01 (21.048)	320.23 (17.895)	446.86 (21.139)
III			0.000	193.66 (13.916)	333.17 (18.253)	204.03 (14.284)	284.19 (16.858)	137.17 (11.712)	190.19 (13.817)	143.07 (11.961)	230.95 (15.197)	302.66 (17.397)	191.43 (13.836)	352.91 (18.786)	308.04 (17.551)	706.07 (26.572)
IV				51.37 (7.167)	192.82 (13.886)	361.3 (19.008)	106.15 (10.303)	292.03 (17.089)	191.05 (13.822)	346.03 (18.602)	553.71 (23.531)	131.24 (11.456)	281.03 (16.764)	100.02 (10.001)	168.56 (12.983)	324.68 (18.019)
V					52.1 (7.218)	385.4 (19.632)	138.6 (11.773)	266.57 (16.327)	141.47 (11.894)	564.68 (23.763)	661.67 (25.723)	178.28 (13.352)	318.23 (17.839)	248.54 (15.765)	173.03 (13.154)	170.22 (13.047)
VI						0.000	253.16 (15.911)	124.9 (11.176)	211.03 (14.527)	129.96 (11.4)	60.81 (7.798)	312.58 (17.68)	81.59 (9.033)	609.79 (24.694)	465.52 (21.576)	733.49 (27.083)
VII							36.9 (6.075)	279.09 (16.706)	170.56 (13.060)	378.96 (19.467)	477.03 (21.841)	135.79 (11.653)	226.02 (15.034)	193.82 (13.922)	179.18 (13.386)	265.27 (16.287)
VIII								69.21 (8.319)	149.06 (12.209)	190.27 (13.794)	214.83 (14.657)	250.08 (15.814)	169.65 (13.025)	421.36 (20.527)	289.85 (17.025)	553.61 (23.529)
IX									0.000	297.7 (17.254)	389.39 (19.733)	132.69 (11.519)	291.08 (17.061)	276.32 (16.623)	163.41 (12.783)	362.14 (19.03)
X										0.000	106.63 (10.326)	380.17 (19.498)	201.89 (14.209)	561.03 (23.686)	497.69 (22.309)	901.44 (30.024)
XI											0.000	546.25 (23.372)	173.37 (13.167)	857.2 (29.278)	684.82 (26.169)	1117.56 (33.43)
XII												0.000	333.9 (18.273)	138.79 (11.781)	143.4 (11.975)	231.92 (15.229)
XIII													0.000	562.83 (23.724)	489.07 (22.115)	641.96 (25.337)
XIV														0.000	93.01 (9.644)	254.95 (15.967)
XV															0.000	253.89 (15.934)
XVI																0.000

* Parenthesis : D value

** Outside the Parenthesis : D^2 value

Table 3. Percentage contribution of each character towards genetic divergence in groundnut

Characters	Times Ranked first	Contribution (%)
Days to 50 % Flowering	225	6.94
Days to maturity	684	21.11
Plant height	247	7.62
No. of Branches/plant	13	0.40
No. of pegs/plant	28	0.86
No. of matured pods/plant	16	0.49
No. of immature pods/plant	35	1.08
Pod yield per plant	24	0.74
Kernel yield	10	0.31
Shelling %	197	6.08
Test weight	1337	41.27
Oil content	378	11.67
Oil yield/plant	46	1.42
TOTAL	3240	100

Table 4. Mean values for 13 quantitative characters of 16 clusters in groundnut

Cluster No.	Day to 50% flowering	Days to maturity	Plant Height (cm)	Number of branches / plant	No. of pegs / plant	No. of mature pods / plant	No. of immature pods / plant	Pod yield / plant (g)	Kernel yield / plant (g)	Shelling (%)	Test weight (g)	Oil content (%)	Oil yield / plant (g)
I	36	110	35.90	9.0	32	21	11	20.43	15.96	78.59	41.58	44.49	7.08
II	39	121	37.10	7.0	29	21	8	21.45	16.26	75.90	46.23	42.44	6.89
III	41	109	29.10	12.0	34	22	13	18.15	13.04	71.81	42.00	41.90	5.45
IV	43	113	33.78	10.0	32	19	12	21.88	16.74	76.41	56.13	43.53	7.22
V	41	121	38.68	7.0	29	19	11	22.60	16.69	73.93	58.90	34.84	5.82
VI	36	116	41.10	6.0	28	22	6	20.85	15.90	76.31	35.25	48.10	7.65
VII	40	120	36.65	8.0	29	21	8	21.40	16.75	78.41	55.50	47.26	7.93
VIII	36	112	37.72	6.0	31	19	12	22.93	15.55	67.77	41.25	41.36	6.38
IX	36	113	36.40	7.0	28	20	18	20.95	17.15	81.96	50.75	34.61	5.88
X	36	109	30.80	8.0	32	19	13	14.25	10.45	73.31	34.25	52.52	5.49
XI	35	113	36.30	7.0	37	28	10	20.75	15.50	74.83	27.00	51.18	7.93
XII	38	111	45.50	11.0	39	28	11	31.40	24.00	76.33	55.25	39.48	9.46
XIII	44	120	31.60	5.0	28	20	8	21.10	14.60	70.92	38.75	47.69	6.97
XIV	40	109	32.90	11.0	35	22	13	26.80	19.45	72.47	64.25	42.03	8.17
XV	37	110	35.30	7.0	40	23	12	24.65	17.85	72.45	59.75	39.59	7.07
XVI	39	120	43.50	6.0	36	17	19	30.50	18.65	73.12	67.25	36.20	6.72

(JSSP-18) was highly promising since it was comparatively early with tall growth habit, maximum pod yield, kernel yield and oil yield. Shelling percentage and test weight was also relatively high. Therefore, it is available to select this genotype for various desirable characters. Similarly the genotypes can be involved as potential parents for various desirable characters.

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Character Association Studies in Yard Long Bean (*Vigna unguiculata* ssp. *sesquipedalis* L. Verdc.)

B Lovely and DS Radhadevi

Department of Plant Breeding and Genetics, Kerala Agricultural University, College of Agriculture, Vellayani, Thiruvananthapuram-695 522 (Kerala)

Fifty genotypes of yard long bean collected from various agro-climatic regions of Kerala were characterized during 2001-2005. Yield per plant showed strong positive genotypic correlation with pods per cluster, pods per plant, pod weight, pod length, pod breadth and seeds per pod. The present investigation revealed high positive direct effects of pods per plant on yield per plant.

Key words: Yard long bean, Genotypic correlation, Direct and indirect effects

Vigna unguiculata sp. *sesquipedalis* (L.) Verdc. (yard long bean) is a distinct form of cowpea grown as a vegetable crop in southern Asia and Far East for its immature pods. The crop is grown throughout India and most extensive cultivation in Kerala. A knowledge on the degree of association among quantitative characters would help the breeder to pinpoint character(s) whose selection would automatically result in an overall progress of correlated characters and elimination of negatively correlated characters with the yield. Hence the present study was undertaken to estimate the character association of various yield contributing characters in yard long bean.

Materials and Methods

The investigation was conducted in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2001-2005. Fifty genotypes of yard long bean collected from various agro-climatic regions of Kerala were used as study material. Observations were recorded on days to 50 per cent flowering, days to first harvest, clusters per plant, pods per cluster, pods per plant, primary branches per plant, pod yield per plant, pod weight, pod length, pod breadth, seeds per pod, length of harvest period, crop duration and main stem length. Analysis of Variance (ANOVA) and Covariance (ANCOVA) for randomised block design (RBD) in respect of the various characters was done. The correlation coefficient (phenotypic, genotypic and environmental) was worked out. The direct and indirect effects of component characters on yield were estimated through path analysis technique (Wright, 1954).

Results and Discussion

A knowledge on the degree of association among quantitative characters would help the breeder to pinpoint

a character or characters whose selection would automatically result in an overall progress of positively correlated characters and elimination of negatively correlated characters with the yield.

The genotypic correlation coefficients of various characters are presented in Table 1. In the present study yield per plant showed strong positive genotypic correlation with pods per cluster, pods per plant, pod weight, pod length, pod breadth and seeds per pod. A negative correlation was noted for days to 50 per cent flowering, days to first harvest and primary branches per plant.

A positive correlation of pods per plant with yield per plant was noticed in the present study. Similar results were reported by Ajith (2001) and Philip (2004) in cowpea negative correlation for days to 50 per cent flowering with yield per plant was noticed in the present investigation, which was supported by the findings of Oseni *et al.* (1992) and Tyagi *et al.* (2000) in cowpea.

Various direct and indirect effects of the characters on yield per plant has been depicted Table 2. The characters pods per cluster, pods per plant, pod weight, pod length, pod breadth, seeds per pod and main stem length had positive direct effects while length of harvest period had negative direct effect. For selection of genotypes those characters with positive direct effects are useful. The maximum direct effect was observed for pods per plant followed by pod weight, pods per cluster, pod length, seeds per pod, length of harvest period, main stem length and pod breadth.

The present investigation revealed high positive direct effects of pods per plant on yield per plant. Similar observations have been reported by Vidya (2000), Parmer *et al.* (2003) and Philip (2004) in cowpea.

Table 1. Estimates of genotypic correlation coefficients

	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
x ₁	1.0000**													
x ₂	0.8897**	1.0000**												
x ₃	-0.0373	0.0547	1.0000**											
x ₄	-0.4121**	-0.3636**	-0.3597*	1.0000**										
x ₅	-0.5458**	-0.3255*	0.5145**	0.4689**	1.0000**									
x ₆	-0.0654	-0.0514	0.1051	-0.1283	-0.0741	1.0000**								
x ₇	-0.1528	-0.1296	0.0513	0.4671**	0.4798**	-0.0610	1.0000**							
x ₈	0.4116**	0.2913*	-0.4363**	-0.0713	-0.4613**	-0.1433	0.3927**	1.0000**						
x ₉	0.5618**	0.4936**	-0.3736**	-0.0867	-0.4924**	-0.2684	0.3399*	0.8948**	1.0000**					
x ₁₀	0.2692	0.1768	-0.1630	0.0637	-0.0438	-0.2253	0.5338**	0.7124**	0.6120**	1.0000**				
x ₁₁	0.2536	0.3665**	0.1592	0.0007	0.2165	0.1822	0.3992**	0.1098	0.1583	0.2556	1.0000**			
x ₁₂	-0.3262*	-0.2918*	0.0786	0.4678**	-0.45338**	-0.3751**	0.2422	-0.1038	-0.0814	-0.0397	-0.2312	1.0000**		
x ₁₃	0.4187**	0.6793**	0.0668	0.1144	0.0659	-0.3043*	0.1055	0.1552	0.3118*	0.0678	0.0768	0.7638**	1.0000**	
x ₁₄	0.0244	-0.0598	0.1281	-0.1186	0.1110	-0.2169	0.02330	0.1346	0.1051	0.0524	0.2005	-0.0303	-0.1100	1.0000**

** significant at 1 per cent level; * significant at 5 per cent level

x₁ - Days to 50% flowering; x₂ - Days to first harvest; x₃ - Clusters per plants; x₄ - Pods per cluster; x₅ - Pods per plant; x₆ - Primary branches per plant; x₇ - Pods yield per plant; x₈ - Pod weight; x₉ - Pod length; x₁₀ - Pod breadth; x₁₁ - Seeds per pod; x₁₂ - Length of harvest period; x₁₃ - Crop duration; x₁₄ - Main stem length

Table 2. Direct and indirect effects of component characters on yield

Characters	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	Total correlation
Pods per cluster - X ₁	0.2306	0.3287	-0.0338	-0.0197	0.0023	0.0001	-0.0331	-0.0079	0.4672
Pods per plant - X ₂	0.1081	0.7010	-0.2189	-0.1160	-0.0016	0.0261	-0.0307	0.0074	0.4754
Pod weight - X ₃	-0.0164	-0.3234	0.4745	0.2028	0.0256	0.0132	0.0073	0.0090	0.3926
Pod length - X ₄	-0.0200	-0.3452	0.4246	0.2267	0.0220	0.0191	0.0058	0.0070	0.3400
Pod breadth - X ₅	0.0147	-0.0307	0.3381	0.1387	0.0360	0.0308	0.0028	0.0035	0.5339
Seeds per pod - X ₆	0.0002	0.1518	0.0521	0.0359	0.0092	0.1204	0.0164	0.0134	0.3994
Length of harvest period - X ₇	0.1079	0.3041	-0.0493	-0.0185	-0.0014	-0.0278	-0.0708	-0.0020	0.2422
Main stem length - X ₈	-0.0273	0.0778	0.0639	0.0238	0.0019	0.0241	0.0021	0.0667	0.2330

Residue = 0.2269

Direct effects - diagonal elements

Indirect effects - off diagonal elements

The positive direct effect of pod length on yield as observed in the study was supported by Panicker (2000), Bastian *et al.* (2001) and Neema and Palanisamy (2001).

From the present study it was evident that selection of genotypes based on pods per plant, pod length and pod weight can be effective for improving yield of the crop.

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Genetic Variability and Correlation Studies in Pomegranate (*Punica granatum* L.)

MM Mir, AA Sofi*, Nelofar¹ and FN Bhat²

Central Institute of Temperate Horticulture, Srinagar-190 007 (Jammu & Kashmir)

¹ Division of Floriculture, Medicinal and Aromatic Plants, Sher-e-Kashmir University of Agricultural Science & Technology, Shalimar-191 121 (Jammu & Kashmir)

² Division of Olericulture, Sher-e-Kashmir University of Agricultural Science & Technology, Shalimar-191 121 (Jammu & Kashmir)

Genetic variability studies in ten cultivars including one local check of pomegranate (*Punica granatum* L.) revealed that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits. High heritability coupled with high genetic gain were recorded for plant height, fruit volume, fruit set percentage, acidity, gross fruit yield, rind weight and number of fruits/plant. Moderate to high heritability with low genetic gain were observed for fruit diameter, rind thickness, rind weight, TSS, total sugars and juice content. The genetic correlation were higher than corresponding phenotypic ones for most of the characters implying inherent relationship among them. Gross fruit yield expressed positive and significant genotypic and phenotypic correlation with fruit weight, fruit diameter, fruit volume, juice content, fruit set percentage and number of fruit/plant.

Key words: Correlation, Genetic variability, Pomegranate, Yield

Pomegranate (*Punica granatum* L.) locally known as 'Anar' belong to family Punicaceae. It is one of the favourite table fruits of tropical and sub-tropical regions of the world. It is highly valued for its delicious fruits and possesses ornamental and pharmaceutical properties. The species however, can adopt a wide range of agro-climatic conditions. It is deciduous in low winter temperature areas but evergreen or partially deciduous in tropical and sub-tropical regions. However, its production is very low and unstable. Systematic efforts are lacking in genetic improvement of the crop. Improvement in any crop depends on the magnitude of genetic variability association between various characters and the extent of transmission of characters from one generation to the next. Therefore, it is essential to partition the overall variability into its heritable and non-heritable components, which will enhance the precision of selection.

Gross fruit yield is a complex trait influenced by several factors interacting with environment. Success of any breeding programme for its improvement depends on the existing genetic variability in the base population and on the efficiency of selection. However, knowledge on the inter-relationship of characteristics of a crop is of paramount importance as it helps in selecting appropriate components which would result in the improvement of complex characteristics that are correlated with each other. Hence, studies on genetic variability, and correlation studies among various plant and fruit characteristics in

pomegranate crop were conducted.

Materials and Methods

The plant material consisting of 10 pomegranate cultivars including one Local check, viz. Kabuli Kandhari, Chawla, Ganesh, Mridula, Jyoti. G-137, Dholka, Bedana, Kandhari and Local check were used in the present investigation. The experiment was carried out at Research Farm of Central Institute of Temperate Horticulture (CITH), Srinagar (Jammu & Kashmir) in a Randomized Block Design with three replications during 2005. Six year old plants were selected at a distance of 2.5 m x 2.5 m. The recommended cultural practices were followed during the studies. Observations were recorded on fifteen characteristics viz. plant height (cm), plant spread (cm), days to first flowering, fruit weight (g), fruit diameter (cm), fruit volume (cm³), rind thickness (mm), rind weight (g), TSS (%), acidity (%), TSS/acid ratio, juice content (%), fruit set (%) and number of fruits/plant and gross fruit yield (kg/plant). The genotypic and phenotypic coefficients of variation, heritability in a broad sense and expected genetic gain as per cent of mean were calculated by standard statistical procedure (Burton and De Vane 1953; Johnson *et al.*, 1955). The correlation coefficients were calculated by a method described by Singh and Choudhary (1979).

Result and Discussion

The analysis of variance for fifteen quantitative characters revealed that mean sum of squares were significant for

* Corresponding author

all. Based on the mean performance of fruit yield, cv. Dholka was found higher yielder followed by Bedana, Kandhari, Kabuli Kanhdari and G-137 (Table 1). The range and mean values revealed higher variation for plant height, plant spread, fruit weight, fruit volume and rind weight while as for rest of the traits it was medium to low. A perusal of the data depicted in Table 2 revealed that phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high for gross fruit yield, fruit set, number of fruits/plant, acidity and fruit volume. The low PCV and GCV were observed in traits viz. TSS, juice content and fruit diameter. The remaining traits showed medium range of PCV and GCV. This indicated that the characters showing higher magnitude of coefficient of variation offer a better opportunity for improvement through selection. These results are in broad conformity to those of Manohar *et al.* (1981) and Meena *et al.* (2003).

The estimates of heritability indicate the effectiveness with which selection can be expected to exploit the existing genetic variability (Burton and Devane (1953); Johnson *et al.* (1955). In the present study, generally estimates of heritability were high for all the characters. Fruit diameter, plant height, fruit volume, rind weight, plant spread, gross fruit yield, number of fruits/ plant, fruit set, days to first flowering and fruit weight recorded the highest heritability while the other traits showed low to moderate heritability. High heritability in broad sense indicated that large proportion of phenotypic variance was attributed to the genotypic variance and that

difference for these characters among the cultivars were real and traits were less influenced by the environment and selection based on phenotypic performance for these traits would be effective. The results obtained from the present study are in agreement with the findings of Attri *et al.* (1999), Pandey and Bist (1998) and Meena *et al.* (2003).

Heritability is not an absolute parameter because it could be high even when genetic variance is low. However, expected genetic gain can be high only if the genetic variance is high (Allard, 1960). Burton (1953) advocated that GCV along with heritable estimates would furnish a better picture of the amount of progress expressed by phenotypic selection. The characters exhibiting comparatively lower heritability accompanied by low genetic gain indicate that dominance or epistatic effects are of considerable value for these characters and hence little improvement in these characters is possible through selection. The results are in accordance with the findings of Panse (1957). The expected genetic gain (% of mean) was high for gross fruit yield, fruit set, number of fruits/plant, acidity, fruit volume and plant height. High genetic gain for acidity and low for TSS was reported by Manohar *et al.* (1981) and Meena *et al.* (2003). The results also coincide with the findings of Pandey and Bist (1998).

The GCV estimates are useful in studying the extent of variability in different characters as it measures the range of genetic variability. The high values of heritability coupled with high GCV and expected genetic gain were observed for gross fruit yield, fruit set, number of fruits/

Table 1. Range, mean, variance, coefficients of variation, heritability and expected genetic gain for different important characters in pomegranate

Character	Range	General mean	Variance		Coefficient of variation (%)		Heritability in broad sense (%)	Expected genetic gain (%) of mean)
			Genotypic	Phenotypic	Genotypic	Phenotypic		
Plant height (cm)	85.77-180.99	132.48	850.03	861.51	22.01	22.05	98.7	45.03
Plant spread (cm)	79.20-135.33	114.99	332.48	334.30	15.86	16.14	96.6	32.09
Days taken to first flower opening	50.00-76.66	59.06	59.84	66.00	13.10	13.75	90.7	25.68
Fruit weight (g)	111.29-232.92	181.15	1375.36	1522.68	20.47	21.54	90.3	40.08
Fruit diameter (cm)	5.77-7.65	6.88	0.32	0.33	8.29	8.34	98.8	17.00
Fruit volume (cm ³)	100.80-234.85	173.74	1688.43	1711.86	23.65	23.81	98.6	48.38
Rind thickness (mm)	2.94-4.24	3.76	0.28	0.40	14.10	16.83	70.2	24.44
Rind weight (g)	50.57-75.20	64.80	96.37	97.83	15.15	15.26	98.5	30.97
TSS (%)	13.72-15.85	14.99	0.50	1.07	4.72	6.90	46.8	6.66
Acidity (%)	0.43-0.82	0.54	0.02	0.03	26.09	28.57	83.4	49.27
TSS/ acid ratio	19.43-34.87	28.99	26.60	42.76	17.78	22.55	62.2	28.89
Juice content (%)	42.23-50.93	47.81	9.57	10.76	6.47	6.86	88.9	12.56
Fruit set (%)	26.15-67.46	39.74	219.56	241.79	37.25	39.13	90.5	73.19
Number of fruits plant ⁻¹	14.21-43.10	216.34	82.46	89.15	34.48	35.85	92.5	68.29
Gross fruit yield (kg/plant)	1.57-9.38	5.01	6.13	6.62	49.27	51.20	92.6	97.69

Table 2. Genotypic (r_g), Phenotypic (r_p) and Environmental (r_e) correlation coefficients among different important characters in pomegranate

Character	Plant height (cm)	Plant spread (cm)	Days taken to flower opening	Fruit weight (g)	Fruit diameter (cm)	Fruit volume (cm ³)	Rind thickness (mm)	Rind weight (g)	TSS (%)	Acidity (%)	TSS/acid ratio	Juice (%)	Fruit set (%)	Number of fruits plant ⁻¹	Gross fruit yield (kg plant ⁻¹)
Plant height (cm)	r_g 1.000	0.902**	-0.663*	0.328	0.372	0.333	0.760*	0.326	-0.228	-0.155	0.035	0.371	0.176	0.542	0.405
	r_p 1.000	0.877**	-0.663*	0.306	0.371	0.331	0.641*	0.318	-0.124	-0.141	0.038	0.342	0.169	0.517	0.384
	r_e 1.000	-0.156	-0.153	-0.103	0.265	0.221	0.125	-0.273	0.364	-0.001	0.145	-0.149	0.076	-0.032	-0.086
Plant spread (cm)	r_g 1.000	1.000	-0.736*	0.550	0.535	0.502	0.698*	0.442	-0.197	-0.166	0.071	0.580	0.403	0.691*	0.595
	r_p 1.000	1.000	-0.673*	0.480	0.521	0.488	0.586	0.429	-0.127	-0.177	0.093	0.543	0.384	0.649*	0.545
	r_e 1.000	1.000	0.287	-0.586	-0.107	-0.100	0.108	-0.070	0.041	-0.381	0.338	0.083	0.120	-0.077	-0.333
Days taken to first flower opening	r_g 1.000	0.902**	1.000	-0.006	-0.023	0.007	-0.603	-0.225	0.657*	0.752*	-0.736*	-0.195	-0.074	-0.315	-0.153
	r_p 1.000	0.877**	1.000	-0.014	-0.024	0.004	-0.467	-0.206	0.404	0.589	-0.485	-0.160	-0.062	-0.294	-0.152
	r_e 1.000	-0.094	1.000	-0.094	-0.052	-0.068	0.089	0.188	-0.106	-0.520	0.359	0.151	0.059	-0.064	-0.149
Fruit weight (g)	r_g 1.000	0.870**	0.891**	1.000	0.870**	0.891**	0.156	0.775**	0.596	0.283	-0.268	0.926**	11.831**	0.823**	0.914**
	r_p 1.000	0.721*	0.735*	1.000	0.721*	0.735*	0.055	0.732**	0.272	0.307	-0.276	0.870**	0.728*	0.779**	0.908**
	r_e 1.000	0.426	0.429	1.000	0.426	0.429	-0.408	0.021	-0.507	0.484	-0.394	0.382	-0.263	0.322	0.693
Fruit diameter (cm)	r_g 1.000	0.870**	0.891**	1.000	0.870**	0.891**	0.206	0.801**	0.537	0.324	-0.326	0.910**	0.783**	0.800**	0.894**
	r_p 1.000	0.721*	0.735*	1.000	0.721*	0.735*	0.150	0.787**	0.371	0.305	-0.258	0.870**	11.740*	0.771**	0.859**
	r_e 1.000	0.426	0.429	1.000	0.426	0.429	-0.375	-0.231	0.071	0.244	-0.027	0.454	-0.063	0.194	0.355
Fruit Volume (cm ³)	r_g 1.000	0.870**	0.891**	1.000	0.870**	0.891**	0.166	0.797**	0.564	0.345	-0.340	0.904**	11.811**	0.799**	0.868**
	r_p 1.000	0.721*	0.735*	1.000	0.721*	0.735*	0.114	0.782**	0.389	0.324	-0.269	0.864**	0.767**	0.770**	0.866**
	r_e 1.000	0.426	0.429	1.000	0.426	0.429	-0.373	-0.204	0.064	0.242	-0.040	0.451	-0.041	0.209	0.378
Rind thickness (mm)	r_g 1.000	0.870**	0.891**	1.000	0.870**	0.891**	0.102	0.102	0.671*	0.038	-0.191	0.366	0.123	0.230	0.136
	r_p 1.000	0.721*	0.735*	1.000	0.721*	0.735*	0.093	0.093	-0.242	-0.025	-0.074	0.259	0.063	0.134	0.052
	r_e 1.000	0.426	0.429	1.000	0.426	0.429	0.119	0.119	0.359	-0.240	0.157	-0.169	-0.211	-0.346	-0.353
Rind weight (g)	r_g 1.000	0.870**	0.891**	1.000	0.870**	0.891**	0.480	1.000	0.480	0.055	0.036	0.31	0.520	0.560	0.628
	r_p 1.000	0.721*	0.735*	1.000	0.721*	0.735*	0.305	1.000	0.305	0.046	0.010	0.594	0.501	0.540	0.605
	r_e 1.000	0.426	0.429	1.000	0.426	0.429	-0.233	-0.063	1.000	0.853**	-0.847**	0.138	0.548	0.437	0.550
TSS (%)	r_g 1.000	0.870**	0.891**	1.000	0.870**	0.891**	0.479	1.000	0.479	0.038	-0.242	0.071	0.241	0.171	0.174
	r_p 1.000	0.721*	0.735*	1.000	0.721*	0.735*	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174
	r_e 1.000	0.426	0.429	1.000	0.426	0.429	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174
Acidity (%)	r_g 1.000	0.870**	0.891**	1.000	0.870**	0.891**	0.479	1.000	0.479	0.038	-0.242	0.071	0.241	0.171	0.174
	r_p 1.000	0.721*	0.735*	1.000	0.721*	0.735*	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174
	r_e 1.000	0.426	0.429	1.000	0.426	0.429	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174
TSS/ acid ratio	r_g 1.000	0.870**	0.891**	1.000	0.870**	0.891**	0.479	1.000	0.479	0.038	-0.242	0.071	0.241	0.171	0.174
	r_p 1.000	0.721*	0.735*	1.000	0.721*	0.735*	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174
	r_e 1.000	0.426	0.429	1.000	0.426	0.429	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174
Juice (%)	r_g 1.000	0.870**	0.891**	1.000	0.870**	0.891**	0.479	1.000	0.479	0.038	-0.242	0.071	0.241	0.171	0.174
	r_p 1.000	0.721*	0.735*	1.000	0.721*	0.735*	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174
	r_e 1.000	0.426	0.429	1.000	0.426	0.429	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174
Fruit set (%)	r_g 1.000	0.870**	0.891**	1.000	0.870**	0.891**	0.479	1.000	0.479	0.038	-0.242	0.071	0.241	0.171	0.174
	r_p 1.000	0.721*	0.735*	1.000	0.721*	0.735*	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174
	r_e 1.000	0.426	0.429	1.000	0.426	0.429	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174
Number of fruits plant ⁻¹	r_g 1.000	0.870**	0.891**	1.000	0.870**	0.891**	0.479	1.000	0.479	0.038	-0.242	0.071	0.241	0.171	0.174
	r_p 1.000	0.721*	0.735*	1.000	0.721*	0.735*	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174
	r_e 1.000	0.426	0.429	1.000	0.426	0.429	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174
Gross fruit yield (kg plant ⁻¹)	r_g 1.000	0.870**	0.891**	1.000	0.870**	0.891**	0.479	1.000	0.479	0.038	-0.242	0.071	0.241	0.171	0.174
	r_p 1.000	0.721*	0.735*	1.000	0.721*	0.735*	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174
	r_e 1.000	0.426	0.429	1.000	0.426	0.429	0.038	0.038	-0.242	-0.063	-0.242	0.071	0.241	0.171	0.174

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

plant and acidity. This might be attributed to additive gene action controlling their expression and phenotypic selection for their amelioration could be brought about by simple method like mass selection or bulk method after hybridization in early generations. Moderate to high estimates of heritability accompanied by low GCV and expected genetic gain were noticed for TSS, juice content, fruit diameter and days taken to first flowering. It may be inferred that these characters were conditioned by non-additive gene action and high genotypic environment interaction. The heritability is being exhibited due to favourable influence of environment rather than the genotypic and simple selection would be rewarding. The present results confirm to those of Rekha and Prasad (1993) and Meena *et al.* (2003).

Correlation coefficients of important economic characters between gross fruit yield and its component traits were estimated at genotypic (g), phenotypic (p) and environmental (e) levels (Table 2). In the present study, the genotypic correlation coefficients were higher in magnitude than their respective phenotypic ones for most of the associations. This suggested that there was inherited relationship between the traits under study and environment had not played much role in reducing their actual association. From these association, it appeared that gross fruit yield was significantly and positively correlated with fruit weight, fruit diameter, fruit volume, juice content, fruit set and number of fruits/plant. Positive association of plant height with plant spread have also been reported by Ram Asrey and Shukhla (2003) and fruit weight with fruit diameter by Pandey and Bist (1998).

Fruit weight and number of fruits have an important contribution to gross fruit yield. In the present investigation, fruit weight had positive and significant correlation with fruit diameter, fruit volume, juice content, fruit set and number of fruits/plant and gross fruit yield; fruit diameter and volume with fruit volume (only for fruit diameter), rind weight, juice content, fruit set, number of fruits/plant and gross fruit yield; juice content with fruit set, number of fruits/plant and gross fruit yield; fruit set with number of fruits/plant and gross fruit yield;

and number of fruits/plant with gross fruit yield. Verma *et al.* (2002) in strawberry reported positive correlations of fruit weight with fruit diameter and fruit volume. Results of present study showed that plant height, fruit weight fruit diameter, fruit volume, juice content, fruit set and number of fruits/plant had positive significant correlation with gross fruit yield. Hence, these characters contribute towards the yield efficacy of a pomegranate plant. Therefore, these characters are ideal criterion for selection of pomegranate crop regarding yield.

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Horticultural Evaluation of Garden Pea Germplasm under Humid Sub-temperate Environment of Northwestern Himalaya

Akhilesh Sharma, NK Pathania and Pritam Kalia¹

Department of Vegetable Science, COA, Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062 (Himachal Pradesh)

¹ Division of Vegetable Science, Indian Agricultural Research Institute, Pusa, New Delhi-110 012

Identification of new promising genotypes is essential for boosting the production and productivity of a crop. Involving seventy-five progenies or test cultures with five checks in augmented block design by replicating checks after 15 test cultures carried out the present investigation. The observations were recorded on ten horticultural traits viz., days to first flowering, days to first picking, pod length (cm), seeds/ pod, shelling percentage, total soluble solids (%), plant height (cm), branches/ plant, pods /plant and pod yield/ plant (g). Significant differences between the checks and the test culture genotypes were observed for all the traits studied except for days to first flowering, shelling percentage and TSS. Amongst the test cultures, PMR 10 and JP Plufela were found to be the high yielding. Similarly, JI 2432, VP 8005, JI 2436 and Arkel were observed as early maturing genotypes with good pod length, total soluble solids, shelling percentage and fairly high yield.

Key words: *Pisum sativum* L., Augmented design, Germplasm screening, Economic traits

Garden pea (*Pisum sativum* L.) is an important leguminous vegetable crop that provides us proteins and other valuable health building substances. It is a winter season crop of tropical and subtropical areas. However, in temperate and sub-temperate regions, it is cultivated during summer months. Evaluation of germplasm is important to identify horticulturally superior genotypes for utilization in breeding programmes or used as such as varieties in their own right after conducting preliminary yield evaluation trials. While evaluating a large array of germplasm, limited homogeneous land block is always a bottleneck; therefore such large collections cannot be accommodated in randomized block design due to soil heterogeneity. However, Federer (1956) proposed Augmented design to surmount this problem (Sharma, 1998). Therefore, the present investigation was aimed to identify promising genotypes having high yield and other desirable horticultural traits from 75 genotypes/breeding lines of garden pea developed/ introduced at Palampur, Himachal Pradesh for assessing their breeding potential in mid hills of sub-temperate zone of northwestern Himalaya.

Materials and Methods

The experimental material for the present investigation was comprised of eighty entries involving 75 progenies or test cultures and 5 checks. These progenies were grown in five blocks, each block accommodating 15 test cultures and 5 checks during cool season of 2004-05 at Vegetable Research Farm, Himachal Pradesh Krishi Vishvavidyalaya, Palampur, Himachal Pradesh. The

checks were repeated in all the five blocks. Two rows of each entry were sown with inter- and intra-row spacing of 45 cm and 10 cm, respectively. A recommended package of local practices followed for the crop included the application of 20 tonnes farmyard manure; 50 kg N: 60 kg P; and 60 kg K per hectare at the time of field preparation prior to seed sowing. Sufficient moisture was maintained during the crop growth span by applying irrigation at fortnightly interval. Besides two earthing ups were carried out at monthly intervals during early crop growth to check weeds and ensure better plant root aeration. The observations were recorded on five randomly selected plants of each genotype for days to first flowering, days to first picking, pod length (cm), seeds/pod, shelling percentage, total soluble solids (%), plant height (cm), branches/plant, pods /plant and pod yield/plant (g). The data was analysed by following standard procedure of Federer (1956).

Results and Discussion

The analysis of variance (Table 1) revealed that the block effects ignoring treatments were significant for days to first picking, pods per plant, seeds per pod, shelling percentage and plant height, while the effects eliminating treatments were significant for only three traits viz., pod length, seeds per pod and branches per plant. The mean squares due to the entries were significant for days to first flowering, pod length, seeds per pod and plant height irrespective of the fact whether the analysis was done eliminating or ignoring the treatments, thereby indicating the significant differences for these traits among the

Table 1. Analysis of variance for horticultural traits in garden pea

df	Source of variation							
	Blocks ignoring treatments 4	Blocks eliminating treatments 4	Entries ignoring blocks 79	Entries eliminating blocks 79	Checks 4	Test cultures 74	Check Vs test cultures 1	Error 16
Trait								
Days to first flowering	90.61*	17.74	83.61*	87.55*	5.44	90.99*	161.32*	15.44
Days to first picking	95.91	55.74	63.91	65.94	40.14	67.12	82.03	40.54
Pod length (cm)	4.44*	0.82*	0.70*	0.89*	0.13	0.86*	6.18*	0.25
Seeds / pod	4.00*	0.90*	0.68*	0.83*	0.08	0.73*	11.21*	0.15
Shelling percentage	104.15*	43.67	22.04	25.10	4.95	26.40	9.30	16.26
Total Soluble Solids (%)	5.72	4.67	2.68	2.73	0.94	2.75	9.33	2.95
Plant height (cm)	401.38*	79.31	236.14*	252.45*	90.44	260.51*	304.25*	51.74
Branches / plant	0.14	0.19*	0.08	0.08	0.23*	0.06	0.27*	0.05
Pods / plant	16.46*	1.63	6.16	6.91	4.70	6.64	35.71*	5.43
Yield / plant (g)	355.15	76.31	169.96	184.07	19.43	157.58	2803.59*	235.06

*Significant at P=0.05

Table 2. Mean performance of test cultures and checks for pod yield and related horticultural traits in garden pea

S.No.	Entry	Days to first flowering	Days to first picking	Pod length (cm)	Seeds/ pod	Shelling (%)	Total soluble solids (%)	Plant height (cm)	Branches/ plant	Pods/ plant	Pod Yield/ plant (g)
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)
1	DPP 9411	91	126	6.8	4.0	40.00	14.0	49.00	1.4	5.6	21.6
2	DPP 9414	100	132	7.2	4.2	44.20	16.4	33.60	1.8	4.8	19.8
3	DPP 9415-1	80	126	7.0	3.2	37.50	15.0	32.40	1.8	7.6	32.4
4	DPP 13	95	132	6.6	2.6	47.14	17.2	27.00	1.4	8.0	21.0
5	DPP 13-1	93	126	6.4	2.5	45.00	14.0	73.00	1.0	5.6	23.1
6	DPP 13-2	93	139	6.3	3.0	43.50	16.5	65.80	1.0	5.4	13.5
7	DPP 19	94	126	6.8	3.5	45.00	18.0	42.40	1.8	4.4	12.6
8	DPP 25G	94	147	6.4	3.6	42.00	15.0	17.40	1.0	4.0	15.0
9	DPP 54	99	126	6.5	3.2	42.00	20.0	51.60	1.2	4.8	15.0
10	DPP 62	94	126	7.4	4.2	50.00	20.0	37.00	1.6	9.2	36.0
11	DPP 80	94	126	6.1	4.2	43.00	16.0	22.4	1.0	3.2	10.2
12	DPP 89	87	126	8.1	3.6	46.67	18.0	47.20	1.2	8.8	50.0
13	DPP100	102	126	6.7	3.5	40.00	18.0	21.20	1.2	6.8	31.8
14	DPP102	94	139	5.3	3.0	42.00	16.5	77.4	1.2	3.6	9.69
15	DPP-102-1	94	126	5.8	4.0	40.00	18.0	51.6	1.2	3.6	10.8
16	DPP 107	94	132	5.7	3.5	43.50	15.4	71.20	1.0	7.0	21.0
17	DPP 107-1	99	139	6.8	3.6	42.00	16.0	44.40	1.0	5.4	17.1
18	DPP 120	94	132	7.0	4.0	43.00	16.4	73.00	1.4	8.0	25.2
19	DPP 127W	102	132	5.5	3.0	41.00	16.0	46.40	1.2	2.4	7.2
20	DPP 362	94	126	6.5	2.8	46.67	20.0	17.60	1.0	8.0	22.5
21	EC 381854	93	126	4.2	2.3	40.00	17.0	37.40	1.0	5.0	12.0
22	EC 381855	91	126	5.5	3.0	41.20	18.0	44.40	1.4	2.0	7.2
23	EC 381856	90	126	7.0	3.5	42.00	16.4	38.80	1.2	3.2	10.8
24	EC 381857	94	126	6.5	3.2	40.00	19.0	33.40	1.0	5.6	16.2
25	EC 381858	93	126	6.4	3.0	50.00	20.0	20.20	1.4	4.8	15.6
26	EC 381860	98	126	7.5	3.1	43.50	18.0	20.40	1.0	5.6	22.8
27	EC 381865	93	126	6.4	3.0	45.00	17.0	32.80	1.2	6.0	21.0
28	EC 381856-1	93	126	5.9	2.7	38.00	19.0	30.60	1.0	7.2	16.2
29	EC 381866	89	126	5.8	2.6	40.00	17.0	21.00	1.0	2.4	8.4
30	NDVP 9	93	130	7.5	4.5	45.00	18.5	25.20	1.0	6.2	30.9
31	NDVP 10A	93	126	8.5	6.0	44.50	20.0	40.20	1.0	3.2	17.4
32	NDVP 10B	94	132	6.6	2.4	40.00	13.5	26.80	1.0	4.4	13.2
33	NDVP 250	103	132	8.3	4.0	42.86	16.2	35.20	1.4	8.4	28.2
34	VP 8005	71	126	9.3	4.4	45.45	20.2	35.80	1.0	4.8	44.4
35	Green Pearl	99	132	8.4	5.5	50.00	15.4	47.60	1.2	4.0	27.6
36	KT 8	101	126	7.5	4.7	41.67	19.0	41.00	1.2	4.8	15.0
37	GC 477	98	126	7.6	4.2	40.00	20.0	46.60	1.6	10.4	43.2
38	Arka Ajit	89	126	8.9	4.0	42.00	18.0	36.20	1.4	6.8	30.0
39	KS 245	98	147	7.1	3.5	43.00	16.5	46.80	1.2	4.0	12.0
40	MA-6	65	126	7.1	4.2	40.00	19.0	23.00	1.0	3.2	15.0

Table 2. (Contd.)

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)
41	C-400A	94	147	7.0	3.6	42.00	17.5	18.4	1.2	2.0	6.0
42	Arkel	73	126	6.7	3.8	41.57	20.0	31.8	1.0	8.0	31.8
43	FC 2	98	126	6.5	3.6	42.00	18.0	40.0	1.6	9.2	31.8
44	JI 2432	67	126	9.1	5.6	58.33	18.0	22.4	1.0	4.4	34.8
45	KS 268	103	147	6.8	3.4	46.00	16.5	36.8	1.4	8.8	36.0
46	PB 29B	93	126	6.4	4.8	41.67	16.0	32.2	1.0	6.0	22.8
47	S 143	94	126	6.0	3.2	40.00	18.0	31.8	1.4	6.0	19.2
48	JI 2431	97	126	6.8	3.0	47.00	17.0	32.6	1.0	4.4	21.6
49	JI 1766	103	147	6.9	3.1	45.50	16.0	35.2	1.2	7.6	27.0
50	C 96	80	126	7.2	3.0	42.00	18.0	36.0	1.2	7.2	22.8
51	JI 2439	71	126	6.9	3.6	37.78	18.0	22.6	1.0	5.0	15.0
52	JI 2436	73	126	6.6	1.6	37.50	16.5	33.8	2.0	12.1	46.2
53	JP Afla	98	132	6.0	2.4	38.00	15.7	23.2	1.4	6.0	22.2
54	Acacia	98	132	5.8	2.5	42.00	14.8	89.8	1.2	9.6	33.6
55	JP Plufela	99	126	5.6	2.7	40.00	18.0	59.0	1.2	14.0	63.6
56	JP 501-Ak	109	147	5.3	2.0	38.00	16.0	61.6	1.8	5.0	12.0
57	JP 20	98	147	6.1	3.0	40.00	16.1	38.6	1.0	5.0	18.0
58	JP 15	111	147	6.4	2.2	35.50	16.0	61.0	1.2	6.0	12.0
59	JP 141	103	132	6.5	2.6	37.00	15.0	64.6	2.0	6.6	9.9
60	JP 825	90	126	5.7	2.8	38.57	19.0	66.4	1.4	6.8	20.4
61	T 10V	98	132	5.6	2.1	35.00	16.5	74.2	1.4	5.4	10.8
62	Green Arran	100	147	5.2	2.3	34.50	16.0	43.4	1.0	2.0	6.0
63	JP 625	107	147	5.1	1.8	33.33	15.2	48.00	1.2	5.0	9.0
64	JM 1	99	147	6.2	2.7	40.00	16.5	36.80	1.0	4.4	15.0
65	Lincoln (Bilaspur)	108	147	6.3	3.0	41.67	16.2	51.80	1.2	7.6	21.0
66	Bonneville	82	147	7.3	4.1	42.50	17.0	59.20	1.0	12.4	36.0
67	PM2	99	126	6.4	3.0	41.57	16.2	32.33	1.0	4.8	20.4
68	SL 82	99	126	5.7	2.2	38.00	16.0	28.40	1.6	5.6	14.4
69	PMR 4	101	147	6.0	2.8	40.00	16.5	33.60	1.0	6.8	18.0
70	VL 7	102	126	6.3	2.0	40.00	20.2	18.60	1.0	5.0	23.7
71	PMR 10	102	126	6.2	3.2	42.00	20.2	40.60	1.4	14.4	67.8
72	Pb 29G	93	126	6.0	3.6	37.77	19.0	29.20	1.4	5.0	15.0
73	Pb 88	98	126	6.6	3.3	39.50	19.0	32.00	1.0	5.6	19.8
74	PMR 21	93	126	6.0	3.8	36.84	19.0	37.80	1.0	4.0	15.6
75	Triton RS 497	70	126	6.1	3.7	41.50	20.0	38.60	1.2	5.2	20.1
CHECKS											
C1	Palam Priya	100.2	128.40	7.6	3.6	46.67	18.4	34.6	1.8	12.0	63.6
C2	VL 8	92.6	126.50	7.0	3.6	46.90	18.0	48.4	1.4	9.6	48.6
C3	VL 3	100.4	132.0	6.7	4.2	50.00	14.4	38.0	1.8	6.4	28.2
C4	Azad Pea 1	95.6	126.0	7.6	4.6	40.00	19.0	45.0	1.2	9.2	49.2
C5	Lincoln	95.4	126.0	7.1	4.0	45.00	16.2	31.0	1.2	7.2	39.6
CD1	Between two check means	4.34	7.03	0.55	0.43	4.45	1.90	8.02	0.25	2.58	16.93
CD2	Between two means in same block	9.70	15.72	1.23	0.96	9.96	4.24	17.76	0.55	5.77	37.86
CD3	Between two means in different blocks	10.63	17.22	1.35	1.05	10.91	4.65	19.46	0.60	6.32	41.47
CD4	Between test culture and check mean	8.23	13.34	1.05	0.81	8.45	3.60	15.07	0.47	4.89	32.12

Significant at P=0.

entries (75 test cultures and 5 checks). Significant variability among different genotypes for various horticultural traits in peas has been reported earlier also by Ramesh *et al.* (2002), Kumar and Jain (2003), Sharma *et al.* (2003) and Singh *et al.* (2003).

The checks varied for number of branches per plant. Palam Priya and VL 3 showed significantly higher values

(1.8) for this trait, while Azad P-1 and Lincoln both had significantly lowest number of branches per plant (1.2).

The progenies or test cultures exhibited significant mean squares for four traits namely, days to first flowering, pod length, seeds per pod and plant height. Single degree freedom analysis for checks vs. test cultures showed significant mean squares for all the traits studied

except for days to first flowering, shelling percentage and total soluble solids. Thus, it revealed that there were significant differences between the checks and the test culture genotypes for almost all the traits.

The mean values among the test cultures ranged from 65 days (Matar Ageta-6) to 111 days (JP 15) for days to first flowering, 126 days (in 45 test cultures) to 147 (in 14 test cultures) for days to first picking, 6.0 (C 4000A and Green Arran) to 67.8g (PMR 100) for pod yield per plant, 2.0 (C 400 A and Green Arran) to 14.4 (PMR 100) for number of pods per plant, 4.2cm (EC 381854) to 9.35cm (VP 8005) for pod length, 1.6 (JI 2436) to 6.0 (NDVP 10 A) for seeds per pod, 33.33 (JP 625) to 58.33 % (JI 2432) for shelling percentage, 13.5 (NDVP 10 B) to 20.2% (PMR 10, VP 8001 and VL 7) for TSS and 17.40 (DPP 25 G) to 89.8 cm (Acacia) for plant height. These results further corroborate the findings of Sureja and Sharma (2000), Kumar and Jain (2003), Sharma *et al.* (2003) and Singh and Dhillon (2004) for majority of the horticultural traits.

On the basis of present study, the test culture PMR 10 was found to be the highest yielder (67.8g) followed by JP Plufela (63.6g) and DPP 89 (50.0g), though they were late maturing. Matar Ageta-6, JI 2432, Triton RS 497, JI 2436, JI 2439, VP 8005 and Arkel were found to

be early maturing genotypes, of which JI 2432, VP 8005, JI 2436 and Arkel were also found to be promising with respect to high yield, pod length, total soluble solids and shelling percentage.

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Evaluation of Date Palm Germplasm Under Hot Arid Ecosystem

RS Singh, R Bhargava and DG Dhandar

Central Institute for Arid Horticulture, Bikaner-334 006 (Rajasthan)

The introduction of date palm germplasm in the arid region is essential to enrich genetic resources for crop improvement. A rich genetic diversity in date palm is available in Kachchh region of Gujarat and its exploitation is essential. The performance evaluation study indicates that cultivar Halawy is the most suitable with respect to growth, early maturing, regular bearing and fruit quality for cultivation under Indian arid ecosystem. However, the initial performance also showed that cultivars Khadrawy, Zahidi, Khuneizi, Dayari and Sabiah are better with respect to fruiting. The study reveals that introduction of date palm offshoots from warm arid and semi-arid parts of the world is useful for better establishment, growth and production.

Key words: Date palm, *Phoenix dactylifera*, Germplasm, Genetic diversity

Date palm (*Phoenix dactylifera* L. Family - Arecaceae) is an important drought hardy fruit tree of semi-arid and arid regions. Doka fruits, chuhhara (dry dates) and Pind khajoor (soft dates) are in high demand as dessert in our country. Due to meagre production in India, majority of dates are imported from Gulf countries to meet the domestic requirements (Singh *et al.* 2003).

The extremely dry areas comprising Jaisalmer, Barmer, Bikaner and Jodhpur in Rajasthan, Bhatinda, Fazilika, Abohar in Punjab Sirsa, Hisar, Mahendergarh and Bhiwani in Haryana and Kachchh region in Gujarat are the potential areas for date palm cultivation in India. However, some natural groves of date palm are found on the coastal belt extending from Anjar to Mandvi in Kachchh region of Gujarat. The selection of promising date palm genotypes from groves of Kachchh and adopting improved practices can enable a good profit per hectare annually in arid region (Pareek and Sodagar, 1986; Singh *et al.* 2004).

In order to exploit the potential of the north-western dry areas of the country for date palm production, a number of varieties have been introduced from Middle east countries, USA and Egypt and some have performed well (Chandra and Choudhary, 1990). Introduction of new varieties having better traits is a continuous process to enhance productivity of crops. Evaluation studies in date palm have been conducted at Chandan, Jaisalmer (Mertia and Vashishtha, 1985). Bhojaka, Jaisalmer (Chandra and Pareek, 1992), Bikaner (Chandra *et al.*, 1990) and Abohar, Punjab (Thatai, 1997). However, for commercial cultivation in hot-arid region, there is a need to have genotypes/cultivars, which are early to medium maturing, tolerant, capable of tolerating high temperature and salinity condition. Hence, the present study was undertaken to screen date palm germplasm

in order to identify the suitable genotypes for cultivation in hot-arid parts of western Rajasthan.

Material and Methods

The germplasm evaluation of date palm was carried out at CIAH, Bikaner (Rajasthan) which is located at 28°N and 73.18°E latitude and altitude of 234.84 m above mean sea level in north-western India. The soil of the region is sandy, poor in water holding capacity and fertility, having pH 8.3 to 8.5, EC 0.10 to 0.15 dS/m and 0.08 to 0.09 per cent organic carbon. The annual average rainfall is 240 mm, which is erratic and distributed between July and September. The mean monthly maximum temperature ranges from 42.9°C in May in summer to 23.7°C in January in winter and the minimum monthly mean temperature range from 29.6 to 7.1°C. However, the summer temperature may be as high as 49°C and the winter temperature as low as - 2°C. The morning relative humidity ranges from 78% in January to 45% in April and the evening RH from 50 to 18% in these months. The wind velocity may be as high as 17km/hr and as low as 3km/hr respectively, in June and January.

Introduction and collection of date palm germplasm was initiated during the year 1997-98 from available sources to develop repository. The offshoots were collected from Regional Fruit Research Station, Abhor; Date palm Research Station, SDAU, Tundra, Kachchh, Gujarat; Date Palm Research Centre, RAU Bikaner; CAZRI, Jodhpur and Central State Farm, Jetsar. The date palm offshoots were planted at 8m x 8 m distance in well prepared pits of 1x1x1 m size and filled with soil mixtures of sand + clay + FYM (1:1:1) and methyl parathion dust 2 % (50g /pit). Three plants of each genotype were maintained in the field repository.

One sucker of each exotic date palm cultivars viz. Braim (EC 402388) and Chip chap (EC 402389) was also introduced from Iraq to CIAH, Bikaner through NBPGR, New Delhi during the year 1997. The survival and growth performance of these cultivars under arid environment was evaluated. At planting, suckers were treated with Carbendazim (0.1%) and IBA 1000 ppm for better survival and growth. The plantations were maintained with recommended cultural practices during course of evaluation. Initially plant growth in date palm was slow. A total of 55 indigenous as well as exotic collections are maintained at CIAH farm. 22 germplasm flowered after four years of planting and rest are in vegetative growth stage.

The vegetative growth parameters were studied included plant height, spread of palm in north - south, east - west directions, trunk girth and number of suckers per palm. Trunk girth was recorded from 25-30 cm above ground level. The date of spathe emergence and opening of spathe/flowering, fruiting behaviour, maturity (*doka* stage) and fruit characters were recorded during 2003 and 2004.

Results and Discussion

The data on the performance of 22 date palm germplasm with respect to vegetative growth is presented in Table 1.

Plant Growth

The plant growth basically depends upon genetic composition as well as soil and climatic features of the region. In general, 1.80 to 3.50 m height was observed after five years of planting. The palm had good foliage, vigorous growth and 4 to 15 offshoots per palm. Maximum tree height was recorded in cultivar Halawy (3.55 m) followed by Muscat, (3.35 m), Dayari (3.25 m) and Sabiah (2.90 m). Minimum tree height was recorded in cultivars Nagal (1.80 m) followed by Hayani, Medjool, Sayer, Suria and Hamara. The highest plant spread (4.50 x 4.75 m) was noted in cv. Muscat followed by Halawy, Sabiah, Sedami, Chip chap and Khadrawy, while it was minimum (2.20 x 2.50 m) in cv. Nagal followed by Zahidi. The cultivar Halawy attained maximum spread (4.15 x 3.75 m) and trunk girth (1.40 m) at an age of five years. Superior performance in Halawy has also been reported by Mertia and Vashshitha (1985) under Chandan, Jaisalmer conditions. Similar results have also been reported by Chandra *et al.*, (1990) and Thatai (1997) under Bikaner and Abohar conditions, respectively. However, cultivar Sedami was at par in trunk diameter and spread with Halawy. Out of three new introductions, Braim and Chip chap grew well and the palm height was around 3.00 m. These plants have started flowering and fruiting after four years of establishment while, offshoot of variety Shakkar could

Table 1. Vegetative growth parameters of date palm genotypes (2004)

Cultivar/genotype	Average height of palm (m)	Trunk girth (m)	No. of suckers per palm	Spread (m)	
				N-S	E-W
Halawy	3.5	1.4	12.0	4.15	3.75
Khadrawy	2.9	1.0	12.0	4.00	4.00
Shamran	2.6	1.0	10.0	3.50	3.60
Zahidi	3.0	1.0	9.00	2.50	2.70
Braim	3.0	1.0	11.0	3.00	3.10
Chip chap	3.0	1.0	8.00	4.10	4.00
Sewi	2.6	1.2	6.00	3.00	3.10
Khuneizi	2.8	0.9	6.00	2.60	2.70
Medjool	2.0	0.8	10.0	2.40	2.50
Sabiah	2.9	1.0	10.0	4.30	4.50
Dayari	3.2	1.0	14.0	3.60	4.00
Muscat	3.3	1.2	16.0	4.50	4.75
Tayer	2.3	1.0	12.0	3.00	3.40
Umshok	2.5	0.9	8.00	3.00	3.40
Hayani	2.3	0.8	7.00	3.20	3.20
Hamara	2.2	0.9	14.0	3.50	3.50
Sedami	3.0	1.4	5.00	4.20	4.30
Medini	2.5	1.1	12.0	3.80	4.00
Sayer	2.2	0.7	8.00	3.00	2.50
Bikaner Local	3.0	1.2	15.0	3.00	3.00
Nagal	1.8	0.9	4.00	2.20	2.50
Suria	2.1	1.0	8.00	3.50	3.00
C.D. at 5%	0.12	0.25	1.73	0.15	0.51

not survive. It may possible be due to small size or lack of roots in the suckers. The appropriate size and weight of sucker is required for better establishment (Pareek, 1984). The sucker of cultivar Sakkar was small in size and rootless while other two were appropriate in size/weight with 3-4 roots. According to Mohammad (1978), the offshoots weighing 8-10 kg gave the maximum rooting. Wellrooted medium size sucker (10 - 12 kg) are better in survival and growth under field conditions as compared to poorly rooted small sized or over sized offshoots.

Growth in palm also depends on the size and weight of planting material besides environmental factor of the region and management practices. The sucker production in date palm is a genetic features of the variety coupled with growing conditions. A dat palm tree produces 10-30 suckers in the whole life. More than 10 suckers per plant were observed in cvs. Halawy, Khadrawy, Braim, Dayari, Muscat, Tayer, Hamara, Medini and Bikaner local, which show vigorous suckering habit of these cultivars.

Spathe Emergence and Opening/Flowering

The spathe emergence and opening/flowering is mainly governed by environmental factors particularly temperature. However, it also depends on the genotype. The period of spathe emergence to opening also varied from 9 (Hamara) to 21 days (Khadrawy). Early spathe emergence i.e. 15 February was observed in Halawy and Sayer. Emergence of spathe was late in cvs. Medjool, Dayari, Sedami, Tayer and Umshok during 2003. In 2004, the pattern of spathe initiation greatly varied, which may possibly be due to the environmental factors. The emergence of spathe was recorded in the last week of January in cvs Muscat, Tayer, Sayer and Nagal. Though, in most of the genotypes it was observed during mid February. The spathe initiations vary from year to year even at a particular location (Mertia and Vashishtha, 1985). During 2003, there was no spathe initiation in Nagal and Suria while in 2004, Chip chap, Sewi and Braim did not bear flower/fruit. It may possible be due to young age of plantation as well as prevailing environmental conditions. The early and late opening

Table 2. Spathe emergence/opening and fruit characters of date palm germplasm under hot arid conditions (2003)

Cultivar genotype	Spathe		Bunch per palm			No. of (cm) Stand/ bunch	No. of berry/ strand	Weight of fruit (g)	Fruit size		Fruit yield (kg/plant)	Stone weight (g)
	Date of emergence	Date of opening	No.	Length (cm.)	Av. bunch weight(g)				Length	Width		
Halawy	15.2.2003	1.3.2003	8.5	92.0	2.8	37.5	18.5	7.85	3.33	2.40	25.2	0.9
Khadrawy	18.2.2003	12.3.2003	7.0	56.6	3.0	26.7	14.3	7.42	3.23	2.15	21.0	0.76
Shamran	22.2.2003	13.3. 2003	3.0	75.3	3.0	28.5	18.3	8.30	3.33	2.10	9.0	0.74
Zahidi	1.3. 2003	15.3. 2003	1.0	35.0	3.0	21.0	20.0	7.25	3.00	2.16	3.0	0.86
Braim	2.3. 2003	19.3. 2003	4.0	45.0	1.5	21.0	15.0	7.74	3.34	2.10	6.0	1.09
Chip chap	7.3. 2003	21.3.2003	1.0	35.0	0.5	16.0	10.0	8.32	3.56	2.26	1.0	1.25
Sewi	1.3. 2003	17.3.2003	4.0	57.5	2.5	25.0	14.5	7.50	2.82	2.00	10.0	0.89
Khuneizi	13.3.2003	21.3.2003	6.0	33.0	1.0	16.0	10.0	7.40	2.80	1.70	6.0	0.61
Medjool	14.3. 2003	22.3. 2003	2.0	63.0	1.5	21.0	08.0	10.5	4.90	3.30	3.0	0.78
Sabiah	17.2.2003	12.3. 2003	2.0	70.0	2.2	35.0	14.0	8.60	3.03	1.90	4.7	0.60
Dayari	15.3. 2003	22.3. 2003	9.0	85.6	1.7	23.3	07.0	9.25	4.10	2.30	15.5	1.14
Muscat	17.2. 2003	28.2. 2003	6.0	72.6	1.0	34.0	14.0	7.30	3.23	1.57	6.0	0.75
Tayer	14.3.2003	24.3. 2003	3.0	44.0	0.5	27.5	11.0	7.00	2.93	1.80	1.6	0.80
Umashok	17.3. 2003	28.3. 2003	3.0	46.0	2.0	35.0	14.0	6.10	3.10	2.10	6.0	0.76
Hayani	12.3. 2003	19.3. 2003	3.0	28.0	0.6	22.0	06.5	7.50	3.00	1.67	1.7	0.56
Hamara	25.2. 2003	5.3. 2003	5.0	50.0	0.5	19.0	05.0	7.42	3.20	1.80	.6	0.79
Sedami	20.3. 2003	1.4. 2003	3.0	70.0	.5	3.5	10.0	7.00	3.00	1.60	4.5	1.10
Medini	17.2.2003	07.3.2003	2.0	51.0	2.0	26.5	11.0	8.50	3.76	2.00	4.0	0.96
Sayer	15.2.2003	07.3.2003	6.0	48.0	2.2	33.5	15.0	5.60	3.00	1.75	13.8	0.70
Bikaner Local	4.3. 2003	5.3.2003	3.0	55.0	3.0	28.0	20.3	6.40	2.83	2.10	10.0	0.86
* Nagal	-	-	-	-	-	-	-	-	-	-	-	-
* Suria	-	-	-	-	-	-	-	-	-	-	-	-
C.D. at 5% -	-	-	0.16	14.3	0.30	3.2	2.2	0.49	0.44	0.23	2.14	0.18

* No flowering/fruiting observed during the year 2003

Table 3. Spathe emergence/opening and fruit characters of date palm germplasm under hot arid conditions (2004)

Cultivar Genotype	Spathe		Bunch per palm			No. of (cm) Stand/ bunch	No. of berry/ strand	Weight of fruit (g)	Fruit size		Fruit yield (kg/plant)	Stone weight (g)
	Date of Emergence	Date of opening	No.	Length (cm.)	Av. bunch weight(g)				Length	Width		
Halawy	23.2.2004	8.32004	4.0	75.0	5.02	50.0	18.0	7.84	3.43	2.10	20.1	1.30
Khadrawy	23.2.2004	10.3. 2004	4.1	53.0	4.25	37.6	16.3	6.90	3.00	2.10	17.5	1.35
Shamran	25.2. 2004	6.3. 2004	3.2	77.0	3.25	35.0	17.0	7.31	3.30	2.00	9.80	1.23
Zahidi	23.2.2004	6.3.2004	7.1	60.0	2.50	31.0	21.0	4.36	2.30	1.80	18.0	0.90
Braim	-	-	-	-	-	-	-	-	-	-	-	-
Chip chap	-	-	-	-	-	-	-	-	-	-	-	-
Sewi	-	-	-	-	-	-	-	-	-	-	-	-
Khuneizi	26.2.2004	9.3.2004	2.0	63.5	1.00	17.0	9.0	8.33	2.93	2.00	2.3	1.00
Medjool	20.2.2004	3.3.2004	2.1	50.0	1.00	14.0	10.0	9.95	3.40	2.40	2.2	1.09
Sabiah	23.3.2004	1.3. 2004	8.2	90.3	4.00	26.0	18.0	5.71	2.80	1.90	32.5	0.96
Dayari	20.2.2004	1.3. 2004	8.0	50.5	.60	38.0	13.0	7.45	3.63	2.22	20.8	1.52
Muscat	29.1.2004	10.2.2004	5.0	75.0	1.75	42.0	11.0	4.96	2.90	1.70	8.75	1.08
Tayer	29.1.2004	16.2. 2004	5.0	48.0	2.0	30.0	9.0	4.81	3.06	.80	10.0	0.67
Umashok	20.2. 2004	3.3. 2004	3.0	32.5	1.50	23.0	6.0	7.33	3.10	1.76	4.50	1.34
Hayani	15.2. 2004	1.3. 2004	2.0	52.5	2.25	30.0	10.0	7.07	3.30	2.00	4.50	1.25
Hamara	20.2.2004	3.3. 2004	1.0	37.0	0.50	39.0	10.0	4.50	3.00	1.70	0.50	0.85
Sedami	25.2. 2004	3.3. 2004	3.0	70.6	0.60	24.0	6.0	5.10	2.51	1.70	2.00	1.17
Medini	23.2. 2004	1.3. 2004	7.0	47.0	2.75	34.0	10.0	6.55	3.26	2.00	19.30	1.23
Sayer	29.1. 2004	16.2. 2004	3.0	21.0	1.00	22.0	5.0	7.0	3.30	2.20	3.00	1.18
Bikaner	6.2.2004	10.3. 2004	4.0	88.6	1.70	27.0	13.0	4.15	2.40	1.80	6.80	1.05
Local												
* Nagal	29.1.2004	14.2. 2004	3.1	39.0	0.70	16.0	9.0	5.11	2.90	1.85	2.20	0.65
* Suria	22.2. 2004	1.3. 2004	3.0	45.0	0.50	20.0	8.0	7.31	3.20	2.00	1.60	1.11
C.D. at 5% -	-	-	1.38	3.22	0.40	1.73	2.06	0.59	0.32	0.24	2.02	0.21

* No flowering/fruitletting observed during the year 2004.

of spathe/flowering was recorded according to emergence. The period required for opening of spathe ranged from 11-21 days in the above germplasm.

Bunch Characters

The bunch characters viz. Size, compactness, weight, number of strand are an important factors in date palm. Bunch formation is governed by age of palm, genetic make up of the variety and environmental factors. The fruit yield directly depends upon size of bunch and berry, number of bunches/palm and number of fruits per strand. Both loose and compact bunches were observed in date palm genotype. Variation in number of bunches was 01 to 09 per tree (Table 2 and 3). Variation in number of bunches, size and berry number might be due to genotype, age of trees and management practices employed. The bunch weights also vary from 1.0 to 5.0 kg depending on size of berries and number of strands per bunch. The variation in number of berries per strand depends upon length of strand and per cent fruit set. In date palm, pollination also hampered the

fruit set. The significant variation in fruit yield per plant was also observed during the year of evaluation, though, the yield was low in all genotypes due to young age of plants. Variation in number of bunches and fruit yield in date palm is also reported by Pareek and Sodagar (1986). At initial stage dropping of immature berries was also observed in Muscat, Tayer, Hamara, Sedami, Sayer, which may possibly be due to improper pollination, moisture stress, high wind velocity besides physiological activities. It is one of most important factor related to the fruit yield. The compact type bunch were observed in Zahidi, Halawy, Braim, Chip chap, Sabiah, Khadrawy and Khuneizi. The significantly higher number of berry per strand was in Zahidi (21.0) during both the years of study. However, fruit production in date palm vary according to the variety, age of tree and growing conditions (Zaid, 1999).

Fruit Characters

The variations in shape and colour of fruits were observed at *doka* stage, which is very useful for accepting date

fruits for fresh consumption, though, the colour of berry is a varietal character. Fruit characters viz. size, shape, pulp, taste, etc. vary tremendously depending on variety and environmental conditions. However, the palm bearing dark red and yellow colour big size, sweet fruits were considered promising. Early *doka* stage was recorded in Halawy and Muscat during both the years of evaluation. Similar results have been reported by Chandra *et al.* (1990). The taste and quality of *doka* fruits varied greatly because of maturity, ripening and genetic characters of the variety. For fresh consumption of *doka* fruits, astringency should be less. At *doka* stage, the colour of berry was attractive in Halawy, Zahidi, Khuneizi, Braim, Chip chap, Sewi, Nagal and Bikaner local while the appearance was poor in Muscat and Tayer.

Maximum size of berry was observed in cultivar Medjool (4.90 x 3.30 and 3.40 x 2.40 cm) during 2003 and 2004, respectively (Table 2 and 3). Variation in fruit size, colour, berry yield have also been described by Chandra and Choudhary (1990), Chandra and Pareek (1992). As far as fruit weight is concerned cultivar Medjool produced biggest size during both the years. These findings are in concurrence with the results reported by Thatai (1997); Chandra and Choudhary (1990). The size of stone also differed significantly within the genotypes. It may possibly be due to genetic characters. The small size of stone was observed in varieties of Hayani, Sabiah and Khuneizi during 2003,

while in Nagal, Tayer, Hamara and Sabiah during 2004. Pareek and Sodagar (1986) expressed that better date selection can improved the production and quality of fruits.

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Evaluation of Pear (*Pyrus* spp.) Germplasm under Temperate Region of Himachal Pradesh

VD Verma*, K Pradheep, SK Yadav¹, JC Rana and Ram Chander

National Bureau of Plant Genetic Resources, Regional Station (NBPGR), Shimla-171 004 (Himachal Pradesh)

¹ Germplasm Evaluation Division, NBPGR, New Delhi-110 012

Fifteen pear accessions (European, Asiatic and hybrid types) were evaluated for important qualitative and quantitative characters with two checks namely EC 027810 (Flemish Beauty) and EC 126286 (Kieffer) under Shimla conditions. Coefficient of variation was highest for fruit weight (58.37%) followed by fruit length (38.25%) and width (33.99%) indicating considerable variability to exploit in breeding programme. Only one accession EC 038739, belonging to Asiatic types showed high productivity with agreeable quality characters also. Though low yielding, accessions viz. EC 552668, EC 027809, EC 552667 and EC 552676 showed their distinction for most of the fruit quality characters, hence may be used as breeding material for genetic improvement.

Key words: Pear, *Pyrus*, Evaluation, Germplasm

Pear occupies second position in area, production and popularity next to apple among the temperate fruits of the world and India as well (FAOSTAT, 2005). European pears (involving mostly one species *Pyrus communis* L.) are the main pear of commerce in Europe, North America, Africa and Australia. They possess a buttery juicy texture with delicate flavour and aroma. On the other hand, Oriental or Asiatic pears includes many species such as *P. pashia* Buch.-Ham, *P. pyrifolia* (Burm. f.) Nakai, *P. ussuriensis* Maxim, and *P. bretschneideri* Rehd. that are preferred for crisp-textured and sweet flavored fruits. European pears are considered the most delicious, while Oriental pears vary a good deal in quality and none of them can compare with the European types, but have an advantage of growing in sub-mountain region whereas the European ones can be grown only in the hills (Singh and Sharma, 1973). The sand pear (*P. pyrifolia*) is the main cultivated species in central-southern China and Japan. In India, pear is cultivated sporadically in hills at 1700-2400 m msl in entire Himalaya and Kodaikanal and Nilgiri hills of Tamil Nadu. Low chilling pears have adapted to sub-tropical regions also. Being a hardy crop, it can be grown even on marginal lands where other crops are outright failure; also they are free from serious pests and diseases. Choice of the cultivar is of paramount importance for successful cultivation in particular area/ niche. Evaluation studies in mid hills and sub-tropics were done by few workers (Sharma *et al.*, 1999; Dhillon and Sandhu, 2005; Aulakh *et al.*, 2005). In high hills like Shimla, pear genetic resources management was

started 40 years back but evaluation was done during 1982 (Rathore, 1982). Afterwards, many new accessions were added in pear germplasm procured through exotic and indigenous sources. Hence, the present study is an endeavor for the characterization and evaluation of pear genetic resources, thereby utilization either directly or for pear improvement work.

Materials and Methods

The study was carried out at field gene bank of NBPGR Regional Station, Phagli, Shimla, Himachal Pradesh (31°05'924" N latitude, 77°09'580" E longitude; 1924 m msl). Fifteen genetically diverse pear accessions comprising of 11 exotic (from four countries) and four indigenous accessions were taken for present study. Out of 15 accessions studied, eight belong to Asiatic type, four to European type, one hybrid and two of unknown origin (Table 1). The plants were grafted on wild pear *Pyrus pashia* (kainth) rootstock. All the plants of the accessions were of 12-15 years age. Experimental trees were grown under similar soil and cultural conditions. EC 027810 (Flemish Beauty) and EC 126286 (Kieffer) were used as checks. Observations were recorded on date of full bloom (when 80% flowers open) and fruit harvest (eating-ripe stage), days to fruit harvest (from date of full bloom), fruit length (cm), fruit width (cm), fruit weight (g), fruit shape, fruit ground color, fruit over colour, fruit surface texture, pulp texture, grittiness, pulp color pulp juiciness, pulp taste, total soluble solids (TSS) (using Digital Hand-held 'Pocket' Refractometer PAL-1) and productivity status. Descriptor states for qualitative characters were followed from the descriptors

* Author for Correspondence

Table 1. Important qualitative characters in pear accessions

Accession	Alternate Identity	Fruit shape	Fruit ground colour	Fruit over colour	Fruit surface texture	Pulp texture	Grittiness	Pulp colour	Pulp juiciness	Pulp taste	Productivity status*
EC552667	Battira Giffard ^d	Ovate pyriform	Green	Greenish yellow	Smooth	Medium	Medium	Creamy	Medium	Medium sweet	Low
EC552669	Chugeryony Shik ^d	Globose	Yellow	Dark brown	Medium rough	Melting	Medium	White	High	Medium sweet	Low
EC280768	Whangkeum ba ^b	Round	Green-yellow	Yellow with brown russet	Medium rough	Medium	Medium	Creamy	Very high	Highly sweet	Medium
EC168557	Hood ^c	Oblong-ovate	Green	Yellowish-Green	Smooth	Hard	High	Creamy	High	Sub-acidic	Low
EC038740	Nijiseiki ^b	Globose	Yellow	Greenish-Yellow	Smooth	Medium	Medium	White	Medium	Sub-acidic	Low
EC038739	Shinsui ^b	Globose	Yellow	Yellow with Brown russet	Medium rough	Medium	High	Creamy	Medium	Medium	High
EC552675	Doynee-du-Comice	Pyriform with narrow neck	Green-yellow	Yellow with brown russet	Medium rough	Melting	Low	Creamy	High	Highly sweet	Low
EC552668	Max red Bartlett ^a	Ovate pyriform	Yellow	Yellow with pink tinge	Smooth	Melting	Low	Creamy	Very high	Sweet	Low
EC027809	Manning Elizabeth ^a	Pyriform	Green-yellow	Yellow with pink tinge	Smooth	Soft	Low	Creamy	Less	Highly sweet	Low
EC552676	Chinese Sandy Pear ^b	Ovate pyriform	Green-yellow	Greenish yellow	Medium rough	Medium	Medium	Creamy	High	Sweet	Low
EC126287	Moonglow ^a	Ovate Pyriform	Green-yellow	Yellow with brown russet	Smooth	Melting	Low	White	Medium	Medium seet	Low
EC020821	BDJ233 ^b	Globose	Green	Greenish-Yellow	Smooth	Hard	Medium	White	Medium	Sub-acidic	Medium
IC020804	BDJ 179 ^b	Globose	Green	Greenish-Yellow	Medium rough	Hard	Medium	White	Medium	Medium sweet	Medium
IC020814	BDJ 208 ^b	Globose	Green	Greenish-Yellow	Medium	Hard	High	White	High	Sub-acidic	Medium
IC020808	BDJ 189 ^b	Globose	Green	Brownish	Rough	Hard	High	Creamy	High	Medium Sweet	Medium
Flemish Beauty (check 1)		Pyriform	Green-yellow	Brownish	Smooth	Melting	Low	White	Medium	Sweet	High
Kieffer (check 2)		Oblong-	Green-yellow	Bright-yellow	Medium rough	Hard	Medium	White	Medium	Sub-acidic	High

* Low: <25kg/plant; Medium: 25-50kg/plant; High: >50kg/plant

developed by National Bureau of Plant Genetic Resources (Mahajan *et al.*, 2002). Fruit data were recorded by randomly selected ten fruits from each accession. Mean values of three years (2002-2004) data were taken to draw the conclusion. Variability parameters were also worked out.

Results and Discussion

Data relating to various qualitative characters on 15 accessions along with their alternate identity (Table 1) showed their diverse nature represented by most of the descriptor states as mentioned by Mahajan *et al.* (2002). Out of 15 accessions studied, seven exhibited globose fruit shape and seven had smooth-surfaced fruits. Desirable white pulp color was displayed by six accessions whereas high productivity (>40kg/plant) was recorded by only one accession (EC 038739) and medium productivity (20-40kg/plant) by five accessions. Three years pooled mean values were calculated for date of full bloom and harvest, days to harvest, fruit length, fruit width, fruit weight and TSS (Table 2). Date of full bloom ranged from 25th February to 7th April while a large difference of 91 days between the early (EC 027809) and late maturing (IC 020804) accessions was noticed. Earliest maturing accessions i.e. EC 027809 and EC 552667 bore matured fruits 96 and 92 days respectively after full bloom, while earliest maturing check (EC 027810) took

105 days for fruit maturity. Earliest maturing nature of EC 027809 (Manning Elizabeth) was also reported by Rathore (1982). A vast range of variation of 32.47-240.83g was exhibited by fruit weight. Coefficient of variation was highest for fruit weight (58.37%) followed by fruit length (38.25%) and fruit width (33.99%) indicating that there is enough potential to exploit the variability present in these characters (Table 2). Existing variability in the studied pear accessions for morpho-phenological and fruit characters might be due to involvement of both intra- and inter-specific level of diversity.

In European pears, the characters like butter flesh, fine texture, juiciness and flavour are of fruit quality consideration. Apart from this, pyriform shaped fruits with 5-10 cm diameter, bright yellow color with red blush and high productivity are also desirable. In this context, all the European type of pears (4 nos.) exhibited soft/melting pulp texture and low grittiness. Of them EC 552668 (Max Red Bartlett) and EC 027809 (Manning Elizabeth) had russet-free yellow skin color with pink tinge while the former also possessed high-juicy fruits. In spite of that, none of the European pears other than the check EC 027810 (Flemish Beauty) had high productivity of above 40kg/plant. Rathore (1991) reported that it is a self-fertile as well as a good pollinizing cultivar.

Table 2. Pooled mean values of quantitative characters in 15 pear accessions

Accession	Date of full bloom	Date of fruit harvest	Days to fruit harvest	Fruit length (cm)	Fruit width (cm)	Fruit weight (g)	TSS (%)
EC552667	7/4	8/7	92	6.42	6.17	104.70	10.93
EC552669	12/3	14/7	124	6.77	7.13	139.56	8.77
EC280768	25/3	23/7	120	5.01	5.51	91.85	10.90
EC168557	12/3	21/7	131	6.59	6.57	147.77	11.73
EC038740	28/3	25/7	119	3.86	3.42	49.43	9.97
EC038739	22/3	24/7	124	4.34	5.01	49.23	13.80
EC552675	27/3	23/7	118	7.50	6.54	197.40	13.67
EC552668	2/4	1/8	121	8.22	7.94	240.83	11.10
EC027809	2/4	7/7	96	5.98	6.26	85.00	11.37
EC552676	24/3	4/8	133	7.89	5.77	91.74	14.07
EC126287	4/4	1/8	119	6.85	6.17	132.41	11.27
IC020821	1/3	9/8	189	1.94	2.42	32.47	9.00
IC020804	1/3	6/10	188	1.94	2.26	33.37	8.80
IC020814	27/2	4/9	189	2.78	2.57	49.56	9.77
IC020808	25/2	19/8	175	4.99	5.12	170.67	12.07
Flemish Beauty (check1)	6.4	20/7	105	7.23	6.66	165.80	11.40
Kieffer (check 2)	17/3	1/8	137	7.28	6.30	125.00	11.30
Mean			135.87	5.41	5.26	107.73	11.15
Maximum Value			189	8.22	7.94	240.83	14.07
Minimum Value			92	1.94	2.26	32.47	8.77
S.E			8.47	0.53	0.46	16.24	0.45
CV (%)			24.16	38.25	33.99	58.37	15.60

In Asiatic pears, high yielding regular bearing cultivars with good fruit size, fruits with light yellow or light green skin colour, firm, juicy, fine-texture with relatively free from grit cells and sweet flavour are desirable for commerce. None of the accessions studied had all the above traits which warrant the need for introduction of more germplasm of good fruit quality along with high productivity. Nevertheless, EC0 38739 (Shinsui) can be of worth-mentioning due to its high productivity status (which is the prime requirement) and agreeable fruit quality characteristics namely medium pulp texture, medium juciness and medium sweet pulp taste (Table 1). Even though low yielding, EC 027809 (Manning Elizabeth), EC 552667 (Batirra Giffard), EC 552676 (Chinese Sandy Pear) and EC 552668 (Max Red Bartlett) showed their distinction for most of the fruit quality characters studied. Former two also adjudged as early maturing accessions under the present study. Hence, they can be used as breeding material for genetic improvement within or between the Asiatic and European types.

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Seed Source Variability in *Terminalia arjuna* (Roxb.) W.&A. and *Terminalia tomentosa* W.&A.

R Kumar Gargi, MC Joshi, I Hembrom, SN Singhdeo and N Suryanarayana

Central Tasar Research and Training Institute (CTR&TI), Nagri, Ranchi-835303 (Jharkhand)

Terminalia arjuna and *T. tomentosa* are perennial and hard wood trees and are of tremendous economic importance besides primary food plants of tasar silkworm *Antheraea mylitta* D. Seeds are the principal source of natural regeneration and propagation in these species. A wide variation for twelve seed traits was observed in different seed sources of diverse origin in both the species collected from various locations. A positive and significant correlation was found between seed germination and seed weight, total biomass production and vigour index. On the other hand, a negative and significant correlation was recorded for days taken for initial germination and complete germination with width of wings. Present study will help in identification of genotypes that can be propagated at mass scale through seedlings.

Key words: *Terminalia* (Roxb.) species, Seed variability, Germination, Vigour index

Terminalia arjuna (Roxb) W&A and *T. tomentosa* are perennial, hard wood tree species of family Combretaceae. The trees are of immense economic importance in various industries like, pharmaceutical, timber, paper, fuel, fodder and lastly the foliage of these trees is primary food for tasar silkworm *Antheraea mylitta* D. Despite its great importance, the information available on the genetic variability of these species is insufficient. *T. arjuna* and *T. tomentosa* are widely distributed throughout the humid and semi-humid tropical forests in India up to an elevation of 1200 m. This variability within a population of tree species has been exploited during the selection of superior provenance for a given site to evolve strategies for the conservation of genetic diversity within population of tree species. It is well established that seeds are principal means of propagation and contain a lot of variation depending upon the source of origin with regard to morphological and physiological characters (Mathur *et al.*, 1984 and Vakshasya *et al.*, 1992.). Seed weight and size give an idea about the supply of potential energy available for seedling during its initial growth. It also indicates the amount of reserves available to the embryo for its growth and development and total biomass production in seedling stage (Shukla *et al.*, 2000). Knowledge of genetic variability is also required to evaluate the composition of group variation and to see evolutionary potentialities of the group (Luna *et al.*, 2006). The significance of these studies and seed source/provenance testing in forest tree improvement is well recognized. Therefore, it was thought it is prudent to study variation in seed traits and germination characteristics which could be used as index for the evaluation

of provenance in *T. arjuna* and *T. tomentosa* for improvement.

Material and Methods

Fully matured seeds were collected in March-April 2002 from five best trees among each identified seed source following the method for selection of candidate plus trees. Table 1 shows the details of the site of collection of seeds. The selected trees were mature but of different ages as it is not possible to get trees of the same age. It is prudent that seeds of mature trees will not differ much in their physiological characters. After harvest, seeds were sun dried for three days and stored in cloth bags under ambient condition in laboratory. For variability studies, seed weight, length, diameter and width of wings were recorded with the help of vernier calipers. Germination test were conducted using four replicates of 25 seeds from each genotype. The seeds were subjected to pretreatment of soaking in ordinary water for 48 for *T. tomentosa* and 96 hours for *T. arjuna* (Anonymous, 1985). Presoaked seeds were sown in polybags of 10 x 40 cm size filled with sterile river sand. Each bag contained one seed. Though germination started a week after sowing final number of germinated seedlings were counted after 45 days of sowing. Time taken for commencement and complete germination was recorded in each replication. The length of root and shoot of the seedlings were measured after 45 days after complete germination when there was no further improvement in per cent germination. Fresh and dry weight of the seedlings was also recorded for calculating the total biomass production. Vigour index was calculated as per the method of Abdul Baki and Anderson (1973). All the data were analyzed statistically.

Table 1. Places of seed collection and variation in respect to seed characters

Species	Place of collection	State	Single Seed Weight (g)	Seed Diameter (cm)	Seed Length (cm)	Width of wing (cm)
<i>T. arjuna</i>	Nawegaon	Maharashtra	4.95	10.63	3.65	1.29
<i>T. arjuna</i>	Arjuni	Maharashtra	1.90	6.58	3.63	.51
<i>T. arjuna</i>	Pahela	Maharashtra	2.06	6.66	3.63	0.46
<i>T. arjuna</i>	Laxmapur	Andhra Pradesh	2.10	6.72	3.47	0.54
<i>T. arjuna</i>	Mudimyal	Andhra Pradesh	4.30	6.71	3.29	0.53
<i>T. arjuna</i>	Narsapur	Andhra Pradesh	2.80	2.82	4.05	1.05
<i>T. arjuna</i>	Harrawala	Uttaranchal	4.30	6.48	4.57	1.32
<i>T. arjuna</i>	U.S.Nagar	Uttaranchal	3.20	8.51	5.10	1.25
<i>T. arjuna</i>	Laldhang	Uttaranchal	2.06	6.42	3.17	1.22
<i>T. arjuna</i>	Baharagoda	Jharkhand	2.65	13.17	6.22	1.33
<i>T. arjuna</i>	Chakradharapur	Jharkhand	3.52	8.07	6.30	1.18
<i>T. arjuna</i>	Pakhandeeh	Jharkhand	2.55	6.23	2.97	1.17
<i>T. tomentosa</i>	Khapa	Maharashtra	1.59	8.08	3.47	1.45
<i>T. tomentosa</i>	Nishti	Maharashtra	1.64	11.95	3.57	1.55
<i>T. tomentosa</i>	Vitoli	Maharashtra	1.52	11.45	3.49	1.53
<i>T. tomentosa</i>	Jawahar forest	Andhra Pradesh	1.63	10.60	3.63	1.45
<i>T. tomentosa</i>	Garopally	Andhra Pradesh	1.49	12.19	3.49	1.76
<i>T. tomentosa</i>	Kothapally	Andhra Pradesh	3.14	9.18	4.29	1.26
<i>T. tomentosa</i>	Rudraprayag	Uttaranchal	1.24	13.40	6.53	1.32
<i>T. tomentosa</i>	Harbartpur	Uttaranchal	3.09	14.35	6.73	2.12
<i>T. tomentosa</i>	Amauta	Uttaranchal	2.05	8.28	3.60	1.90
<i>T. tomentosa</i>	Bahata	Jharkhand	3.31	14.08	6.90	2.02
<i>T. tomentosa</i>	Kuchai	Jharkhand	1.93	13.60	6.67	1.98
<i>T. tomentosa</i>	Ranka	Jharkhand	2.63	13.40	6.00	2.17
Mean			2.57	9.56	4.52	1.35
Range			1.24-4.95	2.82-14.35	2.97-6.90	0.46-2.17
SEm±			0.96	0.97	0.07	0.06
CD at 5%			1.60	1.62	0.12	0.10

Results and Discussion

The mean, range and variance of 24 genotypes of two species for 12 characters are presented in Tables 1 and 2. Range of seed weight varied between 1.9 to 4.95 g in *T. arjuna* and 1.24 to 3.31 g in *T. tomentosa*; seed length (2.97 to 6.3 cm in *T. arjuna* and 3.47 to 6.9 cm in *T. tomentosa*); width of wings (0.46 to 1.33 cm in *T. arjuna* and 1.26 to 2.17 cm. in *T. tomentosa*) and seed diameter 2.82 to 13.17 cm in *T. arjuna* and 8.08 to 14.35 cm in *T. tomentosa*.

Days taken for complete germination were 8.33 to 40.33 in *T. arjuna* and 9.0 to 22.33 days in *T. tomentosa*. Seed germination ranged between 6 to 76 % in *T. arjuna* as compared to 15.67 to 81 % in *T. tomentosa*. A wide range for root length in *T. arjuna* (25.10 to 33.14 cm) and *T. tomentosa* (25.68 to 32.67 cm) was observed. Similarly, variation in shoot length was also recorded in both species. There was not much difference in the range for total biomass production on dry and fresh weight basis in all the genotypes in both species. However, vigour index varied greatly and it was 68.23 to 1068.04 % in *T. arjuna* and 172.57 to 1136.03 % in *T. tomentosa*.

Data indicate that significantly maximum values for seed weight (4.95 g), days taken for initial germination (38.67), days taken for complete germination (40.33) and root length (33.14 cm) were recorded for *T. arjuna*. Whereas, seed diameter (14.35 cm), seed length (6.90 cm), width of wings (2.17cm), seed germination (81.0 %), shoots length (18.70 cm), total biomass on fresh (3.80g) and dry weight basis (0.92 g) and vigour index (1136.03) were higher for *T. tomentosa*.

In character association analysis (Table 3) some of the important combinations showed positive and significant relationship such as seed weight with seed germination; seed diameter with seed length, width of wings and total biomass production; width of the wings with seed germination; dry biomass production and vigour index; seed germination with total biomass production and vigour index with biomass production. On the other hand, a negative and significant correlation was recorded for days taken for initial germination and complete germination with width of wings.

Similar results have been reported by Bhagat *et al.*, (1993) and Kumar and Gargi, (1998) in *Aesculus indica* and *Heteropanax fragrans*, respectively, wherein it was

Table 2. Mean values of various seed traits in *T. arjuna* and *T. tomentosa*

Species collection	Place of	State	DASIG	DASCG	SG (%)	SL (cm)	RL (cm)	BMFW (g)	BMDW (g)	VGI (%)
<i>T. arjuna</i>	Nawegaon	Maharashtra	19.33	21.33	76.00	16.82	32.92	3.60	0.87	1068.04
<i>T. arjuna</i>	Arjuni	Maharashtra	25.67	32.33	6.00	16.53	31.00	2.59	0.55	68.23
<i>T. arjuna</i>	Pahela	Maharashtra	38.67	40.33	23.00	13.61	33.14	2.19	0.45	325.42
<i>T. arjuna</i>	Laxmapur	Andhra Pradesh	34.67	35.33	16.33	12.90	28.23	1.96	0.46	198.63
<i>T. arjuna</i>	Mudimyal	Andhra Pradesh	18.67	20.33	25.33	12.91	32.84	1.81	0.48	356.67
<i>T. arjuna</i>	Narsapur	Andhra Pradesh	11.67	14.33	33.00	14.57	25.40	2.11	0.44	429.57
<i>T. arjuna</i>	Harrawala	Uttaranchal	6.33	8.67	70.67	9.33	30.68	2.70	0.60	497.74
<i>T. arjuna</i>	U.S.Nagar	Uttaranchal	11.67	15.33	41.33	14.23	25.10	2.14	0.46	1059.28
<i>T. arjuna</i>	Laldhang	Uttaranchal	6.67	8.33	20.67	16.67	31.83	2.84	0.54	493.84
<i>T. arjuna</i>	Baharagoda	Jharkhand	6.67	14.00	30.67	10.03	25.83	2.75	0.73	753.16
<i>T. arjuna</i>	Chakradharpur	Jharkhand	10.00	12.67	65.33	15.40	25.75	2.39	0.52	849.74
<i>T. arjuna</i>	Pakhandeoh	Jharkhand	11.33	13.00	58.00	15.60	28.73	3.09	0.65	726.53
<i>T. tomentosa</i>	Khapa	Maharashtra	10.67	15.67	46.00	9.97	25.93	2.67	0.63	509.77
<i>T. tomentosa</i>	Nishti	Maharashtra	11.33	15.67	41.33	9.50	30.83	2.76	0.64	414.38
<i>T. tomentosa</i>	Vitoli	Maharashtra	13.00	15.67	15.67	8.50	32.67	2.57	0.63	172.57
<i>T. tomentosa</i>	Jawahar forest	Andhra Pradesh	14.00	16.67	42.33	9.62	32.42	3.04	0.58	596.00
<i>T. tomentosa</i>	Garopally	Andhra Pradesh	12.33	15.00	32.33	8.53	25.68	2.65	0.58	1048.23
<i>T. tomentosa</i>	Kothapally	Andhra Pradesh	16.33	22.33	81.00	17.83	31.23	3.57	0.90	1136.03
<i>T. tomentosa</i>	Rudraprayag	Uttaranchal	6.67	9.00	40.00	17.18	32.67	3.67	0.93	270.84
<i>T. tomentosa</i>	Harbartpur	Uttaranchal	8.67	12.00	50.00	12.50	32.33	1.87	0.52	564.19
<i>T. tomentosa</i>	Amauta	Uttaranchal	11.33	12.33	60.67	13.00	27.83	2.12	0.47	338.48
<i>T. tomentosa</i>	Bahata	Jharkhand	11.00	14.00	65.33	18.70	32.43	3.79	0.97	842.81
<i>T. tomentosa</i>	Kuchai	Jharkhand	10.33	12.33	45.33	16.83	31.00	2.96	0.82	918.24
<i>T. tomentosa</i>	Ranka	Jharkhand	11.33	14.67	60.00	17.67	31.83	3.80	0.92	964.63
Mean			14.10	17.14	43.60	13.69	29.93	2.73	0.64	608.46
Range			6.33–	8.33–	6.00–	8.50–	25.10–	1.81–	0.44–	68.23–
			38.67	40.33	81.00	18.70	33.14	3.80	0.97	1136.03
S Em			0.46	0.67	1.13	0.33	0.45	0.10	0.02	3.66
CD at 5 %			0.79	1.11	1.88	0.54	0.75	0.16	0.03	6.11

DASIG days taken for initial germination; DASCG days taken for complete germination; SG seed germination; SL shoot length; RL root length; BMFW biomass on fresh weight basis; BMDW biomass on dry weight basis; VGI vigour index.

Table 3. Correlation coefficient for twelve characters of *T. arjuna* and *T. tomentosa*

	SSW(g)	SD(cm)	SEL(cm)	WW(cm)	DASIG	DASCG	SG (%)	SL(cm)	RL(cm)	BMFW(g)	BMDW(g)
SD(cm)	-0.1666										
SEL(cm)	0.1444	0.638**									
WW(cm)	-0.1049	0.722**	0.510*								
DASIG	-0.0370	-0.356	-0.406	-0.667							
DASCG	-0.0542	-0.316	-0.370	-0.672	0.978**						
SG (%)	0.5279*	0.218	0.325	0.491*	-0.386	-0.397					
SL(cm)	0.2544	0.003	0.355	-0.006	0.069	0.056	0.295				
RL(cm)	0.0860	0.287	0.025	0.023	0.204	0.164	0.020	0.263			
BMFW(g)	0.0047	0.473*	0.281	0.393	-0.287	-0.251	0.495*	0.467*	0.360		
BMDW(g)	0.0835	0.643**	0.482*	0.468*	-0.304	-0.255	0.504*	0.472*	0.383	0.923**	
VGI (%)	0.3895	0.354	0.344	0.453*	-0.319	-0.291	0.649**	0.281	-0.216	0.452*	0.460*

SSW (g) Single seed weight in gram; SD (cm) seed diameter in cm; SEL (cm) seed length in cm; WW (cm) width of wings in cm; DASIG days taken for initial germination; DASCG days taken for complete germination; SG (%) seed germination; SL (cm) Shoot length in cm; RL (cm) root length in cm; BMFW (g) biomass on fresh weight basis in g; BMDW (g) biomass on dry weight basis in g; VGI (%) vigour index.

concluded that heavier seed weight classes performed significantly better in terms of germination, survival, seedling weight and dry biomass than lighter seed weight classes. Relationship between seed weight with seed germination and vigour index has also been reported in mulberry (Dandin *et al.*, 1991), mango (Giri and Chaudhary, 1996) and in Ber (Srivastava *et al.*, 2001).

Mange and Sen (1995) also observed that germination percentage in *Prosopis cineraria* can be improved by selecting large and heavy seeds. Our findings are also in consonance with the above.

It is concluded from the present study that a significant amount of genetic variability for various seed traits (seed weight, diameter, germination per cent, vigour

index) is present in *T. arjuna* and *T. tomentosa* and heavy and large seeds have to be chosen for raising healthy seedlings. The identified genotypes have been established in the field gene bank at CTR. and TI., Nagri, Ranchi for utilization in large scale planting/tree improvement/ future breeding programme.

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Evaluation of Mungbean Germplasm for Genetic Variability

G Roopa Lavanya*

Department of Genetics and Plant Breeding, Allahabad Agricultural Institute–Deemed University, Allahabad (Uttar Pradesh)

In a study conducted during kharif, 2003 and 2004 comprising 132 mungbean genotypes to assess the genetic variability present among the genotypes. Genotypic coefficient of variation was observed high for seed yield per plant⁻¹, number of clusters per plant⁻¹, number of pods per plant⁻¹ and number of pods per cluster⁻¹. High estimates of heritability coupled with high genetic advance as per cent of mean was registered for plant height, seed yield per plant⁻¹ and number of pods per plant⁻¹, indicating that the genetic variances for these traits are probably owing to their high additive gene effects and thus there is better scope for improvement of these traits through direct selection.

Key words: Genetic variability, Heritability, Genetic advance, Additive gene effect

Pulses are rich sources of protein with two to three times more protein than that in cereals. Mungbean is one of the most important legume crop and ranks third in total production amongst the pulses grown in the country after chickpea and pigeonpea. The genetic reconstruction of a plant type is required for developing high yielding varieties by incorporating and improving the yield component characters. Therefore, evaluation of germplasm for genetic variability is essential for the present as well as future crop improvement programmes. Moreover, proper utilization of germplasm requires testing of genetic potential under local conditions or the target environment for which the breeding programme is aimed. In the view of the above perspectives, the present study was taken up to assess genetic variability in mungbean germplasm to identify genetically diverse and agronomically superior genotypes.

Materials and Methods

The experimental material comprised 132 genotypes of mungbean collected from different geographical regions of India and abroad and grown during *kharif*, 2003 and 2004 at Crop Research Farm of Department of Genetics and Plant Breeding, Allahabad Agricultural Institute–Deemed University, Allahabad. The mungbean germplasm included improved varieties, obsolete varieties, local land races, exotic collections and other species of genus *Vigna*. The experiment was laid out in randomized complete block design replicated thrice in crop geometry of 1 x 1 m² with 30 cm and 10 cm inter and intra row spacing, respectively. Recommended cultural practices and plant protection measures were

followed to raise a healthy crop. Five plants were selected at random from each block to record observations on 10 characters viz., plant height (cm), number of primary branches, number of clusters plant⁻¹, number of pods cluster⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹, pod length (cm), 100 seed weight (g), days to maturity and seed yield plant⁻¹ (g). The pooled mean values over seasons were subjected to analysis of variance. Genotypic and Phenotypic coefficient of variation (GCV and PCV) were calculated by following the method given Burton (1952). Heritability (broad sense) and expected genetic advance (as per cent of mean) were estimated as per Johnson *et al.* (1955).

Results and Discussion

Analysis of variance revealed significant differences for all 10 characters under study, indicating the presence of substantial genetic variability in the mungbean germplasm (Table 1). The variability among the genotypes, suggested ample scope for improvement through selection. Knowledge of genetic system controlling yield and its components is useful in understanding the prepotency of the parents and thus help to select parents possessing in-built genetic potential. The genotypes like IPRM-90, was identified as a desirable genotype for multiple characters like medium plant height, more number of primary branches plant⁻¹, more number of pods cluster⁻¹, number of pods plant⁻¹ and seed yield plant⁻¹. LM-1119 was identified for number of clusters plant⁻¹, number of pods cluster⁻¹ and number of pods plant⁻¹. Exotic collections viz., EC 393407, EC 398888, EC 398889, MSO-9 were characterized for long pods with more number of seeds

*Corresponding Author: Assistant Professor, Allahabad Agricultural Institute–Deemed University, Allahabad–211007

Table 1. Analysis of variance for 10 characters in 132 mungbean genotypes

Characters	Mean sum of squares		
	Replication	Treatment	Error
Degree of Freedom	2.00	131.00	262.00
Plant height (cm.)	594.47	361.73**	35.18
No. of primary branches/ plant	2.25	1.91**	0.86
No. of clusters / plant	16.52	72.59**	15.12
No. of pods/ cluster	0.17	2.86**	0.67
No. of pods/ plant	45.47	438.26**	65.37
No. of seeds/ pod	6.86	7.81**	1.17
Pod length (cm.)	2.92	4.26**	0.30
Days to maturity	85.63	177.16**	50.51
100-seed weight (g.)	3.60	15.96**	13.45
Seed yield / plant (g.)	36.88	39.74**	4.07

** Significant at 0.01 level of significance

pod⁻¹. Genotypes like HUM-1, T-44, PDM-54, PS-10, Pusa-9072 and ML-406 were identified as early maturing genotypes. Jyoti, LGG-499, PIMS-11/99, PDM-84-143, LGG-420 and IPRM-90 were recognized for high seed yield plant⁻¹ (Table 2).

Higher magnitude of GCV were recorded for seed yield plant⁻¹ (31.24%) followed by number of clusters

plant⁻¹ (28.39%), number of pods plant⁻¹ (27.48%) and number of pods cluster⁻¹ (25.96%), while plant height (21.99%) and pod length (17.48%) showed moderate GCV values, indicating substantial amount of genetic variability. However, Das *et al.* (1998) recorded high genotypic coefficient of variation for plant height, number of branches plant⁻¹, number of pods plant⁻¹, pod length and seed yield plant⁻¹. A wide range of phenotypic coefficient of variation was observed and ranged from 12.44% for days to maturity to 37.98% for number of clusters plant⁻¹. Seed yield plant⁻¹ (36.19%), number of pods cluster⁻¹ (35.98 %) and number of pods plant⁻¹ (33.95%) registered higher magnitude of PCV values, suggested favourable effect of environment in the expression of these characters (Table 3). However, high magnitudinal differences between PCV and GCV were observed for number of primary branches plant⁻¹ followed by number of pods cluster⁻¹ and number of clusters plant⁻¹, indicated greater influence of environment, whereas relatively low magnitudinal differences were observed for pod length and plant height. Highest

Table 2. Potential genotypes identified for different attributes in mungbean germplasm

S.No	Characters	Potential genotypes identified
1.	Plant height (55-65 cm)	IPRM-90, LM-497, V-557, ML-287, ML-588, K-1084, JYOTI, ML-131, PS-16, PANT MUNG-1, T-1, EC-398888, LGG-478, LGG-477, VC-3944, MSO-9, PUSA BOLD -2, LGG-491, LGG-476, NM-1
2.	No. of Primary branches plant ⁻¹	V-3561, IPRM-90, KM-2197, OBG-40, LAM-M2, K-2192, LGG-476, LLR-4
3.	No. of clusters plant ⁻¹	PUSA-9871, K-1084, WGG-2, PUSA-108, V-4589, PDM-139, LGG-491, LM-1119
4.	No. of pods cluster ⁻¹	PUSA BAIKAKHI, PS-10, SONAMUNG, UPM-83-1, T1, IPRM-90, OUM-11-5, LM-1119, ML-5, PANT MUNG -1, LGG-478,
5.	No. of pods plant ⁻¹	ML-287, V-3561, PS-16, LGG-499, SONAMUNG, PDM-84-143, LM-1119, ML-131, K-1284, IPRM-90
6.	No. of seeds pod ⁻¹	EC-393407, K-1310, K-92-200, EC-398888, LGG-477
7.	Pod length (cm)	EC-398888, MSO-8, EC-398889, MSO-9
8.	Days to maturity	EC-398889, PDM-54, PUSA BAIKAKHI, HUM-10, ML-406, T-44, HUM-1, PUSA-9072, HUM-14, HUM-7, DPM-60-1, PDM-1, PS-10, PUSA-102
9.	100 - seed weight (g)	EC-398889, K-1282, EC-398888, PUSA BOLD-2, MSO-9, WGG-2, HUM-14
10.	Seed yield plant ⁻¹ (g)	JYOTI, LGG-499, PIMS-11/ 99, IPRM-90, PDM-84-143, PDM-89-226, LGG-491, LGG-420, PANTMUNG-1

Table 3. Estimates of genetic parameters for 10 characters in 132 mungbean genotypes

Characters	Coefficient of variation (%)		Heritability (%) (broad sense)	Genetic advance	Genetic advance (as percent of mean)
	GCV	PCV			
Plant height (cm.)	21.99	25.29	75.64	18.68	39.36
No. of primary branches/plant	16.18	30.12	28.81	0.65	17.76
No. of clusters/plant	28.39	37.98	55.93	6.74	43.74
No. of pods/cluster	25.96	35.98	52.15	1.27	38.60
No. of pods/plant	27.48	33.95	65.54	18.59	45.82
No. of seeds/pod	15.58	19.27	65.43	2.48	25.97
Pod length (cm.)	17.48	19.36	81.53	2.14	32.57
Days to maturity	8.40	12.44	45.51	9.03	11.67
100-seed weight (g.)	23.96	28.96	35.94	0.46	12.04
Seed yield/plant (g.)	31.24	36.19	74.55	6.13	55.53

genotypic and phenotypic coefficient of variation for seed yield plant⁻¹, number of branches plant⁻¹ and number of pods plant⁻¹ (Reddy, 1997; Loganathan *et al.*, 2001) and 100-seed weight (Samad and Lavanya, 2005) were reported.

The perusal of the Table 3 revealed the estimates of heritability (%) in broad sense for 10 characters studied, which ranged from 28.81% for number of primary branches plant⁻¹ to 81.53% for pod length. Plant height (75.64%), seed yield plant⁻¹ (74.55%), number of pods plant⁻¹ (65.54%) and number of seeds pod⁻¹ (65.43%) recorded high heritability. Burton (1952) suggested that genetic variation along with the heritability estimates would give a better idea about the expected efficiency of selection. Thus, a character possessing high GCV along with the high heritability will be valuable in a selection programme. Seed yield plant⁻¹ and number of pods plant⁻¹ recorded high estimates of GCV coupled with high heritability.

Maximum genetic advance was recorded for plant height (18.68) followed by number of pods plant⁻¹ (18.59). However, high estimates of genetic advance as per cent of mean was registered for seed yield plant⁻¹ (55.53%), number of pods plant⁻¹ (45.82%), number of clusters plant⁻¹ (43.74%) and plant height (39.36%), suggesting that these characters are governed by additive genes and selection will be rewarding for improvement of such traits. Low genetic advance as per cent of mean was observed for days to maturity (11.67%), indicating the involvement of non additive gene action in controlling this trait and heterosis breeding may be useful for further generation of variability for this character.

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 indicates the mode of gene action in choosing an appropriate breeding methodology. High genetic advance as per cent of mean coupled with high heritability recorded for plant height, seed yield plant⁻¹ and number of pods plant⁻¹. This situation indicates that

the genetic variances for these traits are probably owing to their high additive gene effects (Johnson *et al.*, 1955) and thus there is better scope for improvement of these traits through direct selection.

High estimates of genetic advance as per cent of mean coupled with high estimates of heritability for number of pods plant⁻¹, seed yield plant⁻¹, plant height, number of seeds pod⁻¹ and number of clusters plant⁻¹ (Byregowda *et al.*, 1997; Ram *et al.*, 1997; Loganathan *et al.*, 2001; Samad and Lavanya, 2005) were also reported. These characters are likely to provide very high to high selection response, owing to their high transmissibility (Saxena and Singh, 2001). High estimates of genotypic coefficient of variation and 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.

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Studies on Variability, Heritability and Genetic Advance in Chilli (*Capsicum annuum* L.)

Shivkumar and RM Hosamani

AICRP (Vegetables), Department of Horticulture, University of Agricultural Sciences, Dharwad-580 005 (Karnataka)

Genetic variability, heritability and genetic advance for 20 different quantitative characters were studied in 69 genotypes of chillies. The study indicated that the moderate to high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for all the characters, high heritability (broad sense) with high genetic advance as percent mean was observed for most of the characters except plant height.

Key words: Variability, Heritability, Genetic advance, Chilli

Chilli (*Capsicum annuum* L.) is an important vegetable as well as spice crop widely grown throughout India. India being the secondary centre of origin, a lot of variability exists in this crop. A critical estimate and study of genetic variability is pre-requisite for initiating appropriate breeding procedure for effective selection of superior genotypes. The partitioning of total variability into heritable and non-heritable components by using suitable design will enable the progenies. Natural genetic variation for most of the yield attributes is considerable high in chillies. Therefore, there is an urgent need of information on the nature and magnitude of variation available in the material and part played by environment in expression of different characters. Keeping this in view,

the present investigation was undertaken to estimate the magnitude of heritable and non-heritable component of variation and genetic parameters such as genotypic coefficient of variation, heritability and genetic advance in 69 genotypes of chillies.

Material and Method

The present investigation was carried out at the AICRP (Vegetable), Department of Horticulture, University of Agricultural Sciences, Dharwad during the *khari*f 2004-05. Sixty-nine germplasm consisting some local collections of Byadagi and Dyavanur and some collections from Kashmir were taken for the study (Table 1). The mean performance of growth, yield and

Table 1. Source and place of collection of chilli genotypes used in the study

Sl. No.	Genotype code	Source/place of collection	Sl. No.	Genotype code	Source / Place of collection	Sl. No.	Genotype code	Source /place of collection
1	'101'	Hubli	25	'177'	Srinagar	49	'142'	Sherewad
2	'95'	Bilehal	26	'178'	Srinagar	50	'160'	Sherewad
3	'91/3'	Bilehal	27	'176'	Srinagar	51	'147'	Bilehal
4	'73/2'	Sherewad	28	'173'	Srinagar	52	'148'	Sherewad
5	'73/1'	Sherewad	29	'171'	Srinagar	53	'34/2'	Kubihal
6	'64'	Sherewad	30	'150'	Kubihal	54	'12'	Kundgol
7	'29/1'	Bilehal	31	'153'	Annigeri	55	'8/3'	Kundgol
8	'27'	Kundgol	32	'154'	Sherewad	56	'7'	Kubihal
9	'21'	Sherewad	33	'168'	Srinagar	57	'79'	Sherewad
10	'15'	Annigeri	34	'174'	Srinagar	58	'17/2'	Kundgol
11	'17'	Kundagol	35	'172'	Srinagar	59	'97'	Hubli
12	'13/1'	Kubihal	36	'169'	Srinagar	60	'25'	Annigeri
13	'13/4'	Kubihal	37	'166'	Srinagar	61	'167'	Srinagar
14	'80'	Sherewad	38	'170'	Srinagar	62	'117/3'	Dyavanur
15	'102'	Hubli	39	'175'	Srinagar	63	'89/2'	Kundgol
16	'29/6'	Bilehal	40	'117/2'	Dyavanur	64	'89/3'	Kundgol
17	'86'	Kundgol	41	'136'	Dyavanur	65	'106'	Hubli
18	'29/5'	Bilehal	42	'117/1'	Dyavanur	66	'115/1'	Hubli
19	'34/3'	Kubihal	43	'139'	Hubli	67	'91/4'	Bilehal
20	'6/1'	Bilehal	44	'137'	Hubli	68	'23'	Sherewad
21	'6/2'	Bilehal	45	'140'	Sherewad	69	'29/4'	Bilehal
22	'13/2'	Kubihal	46	'159'	Sherewad	70	'Byadagi Kaddi'	UAS Dharwad
23	'13/3'	Kubihal	47	'138'	Hubli	71	'Dyavanur Dabbi'	UAS Dharwad
24	'117/4'	Dyavanur	48	'146'	Sherewad			

disease components were presented (Table 2a, 2b and 2c). Experiment was laid out in randomized block design with two replications. Five weeks old seedlings were transplanted in 60x45 cm spacing and all the recommended agronomic package of practices were followed. The observations were recorded on five

randomly selected plants per replication for each germplasm on 20 important characters. The parameters of variability like grand mean, range, phenotypic and genotypic coefficient of variation (Burton and Dewane, 1953), broad sense heritability (Hanson *et al.*, 1956) and genetic advance (Johanson *et al.*, 1955) were calculated.

Table 2a. The mean performance of chilli genotypes for different growth parameters

S.No.	Genotype code	Plant height (cm)	No. of branches per plant	Plant spread (cm) (north-south)	Plant spread (cm) (east-west)	Stem length (cm)	Days to first flowering	Days to 50 per cent flowering
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
1	101	50.62	5.20	33.50	31.50	5.60	77.50	79.50
2	95	39.92	4.50	34.50	29.30	5.70	73.50	79.00
3	91/3	51.80	5.97	34.50	30.00	5.60	69.00	70.00
4	73/2	46.70	3.30	36.30	31.50	5.70	68.50	37.00
5	73/1	51.62	5.05	37.60	31.30	6.20	76.50	39.00
6	64	49.55	5.50	42.20	42.30	4.50	66.50	74.50
7	29/1	47.70	3.55	36.50	32.10	5.50	69.50	76.00
8	27	59.78	5.90	45.20	36.10	5.60	70.50	76.00
9	21	59.85	4.00	41.90	34.30	5.40	64.50	74.50
10	15	45.89	5.00	34.30	27.60	6.30	64.00	80.50
11	17	53.00	5.53	35.40	24.70	6.80	65.00	68.00
12	13/1	36.05	3.03	31.50	23.50	6.10	64.00	38.50
13	13/4	54.50	4.40	39.30	30.10	6.10	62.00	38.50
14	80	50.00	4.90	42.80	36.00	6.40	66.50	79.00
15	102	40.33	6.41	39.60	30.10	5.30	68.50	70.00
16	29/6	58.07	5.30	46.30	36.50	5.80	69.00	76.00
17	86	58.97	5.40	44.30	40.00	6.30	76.00	43.50
18	29/5	61.20	2.05	45.40	41.40	5.60	75.50	83.50
19	34/3	53.97	4.62	49.80	37.20	5.80	71.00	75.50
20	6/1	57.20	5.50	52.50	45.10	4.80	69.00	83.00
21	6/2	53.78	3.20	40.40	32.10	5.40	72.00	36.00
22	13/2	59.10	5.45	43.10	35.50	5.20	73.50	66.00
23	13/3	61.40	4.00	47.10	38.30	6.80	75.00	79.00
24	117/4	47.40	11.75	37.50	31.10	6.30	72.00	87.00
25	177	31.60	5.50	33.50	19.20	6.10	33.50	67.00
26	178	38.70	6.48	33.30	28.60	5.20	35.50	69.00
27	176	40.80	6.10	31.10	27.60	6.20	38.50	74.50
28	173	38.70	4.75	40.40	31.30	5.60	35.00	89.00
29	171	38.22	4.05	35.60	27.50	5.80	35.50	80.50
30	150	41.00	6.00	31.20	24.50	6.00	78.50	70.00
31	153	36.30	4.15	31.30	26.90	5.60	75.00	76.00
32	154	34.12	11.50	32.20	27.40	5.10	82.00	90.00
33	168	36.70	6.05	33.20	24.30	7.40	32.50	79.50
34	174	36.10	6.00	37.40	30.50	5.40	33.50	72.50
35	172	40.20	5.90	40.20	33.80	6.15	34.50	78.50
36	169	42.10	3.88	29.20	28.40	5.80	35.50	84.00
37	166	50.00	4.80	51.50	35.60	6.70	36.50	83.00
38	170	39.70	6.35	31.70	25.20	5.60	35.00	80.00
39	175	35.95	4.12	40.50	27.40	5.10	33.50	73.00
40	117/2	40.65	9.00	32.40	26.10	5.60	74.00	78.00
41	136	50.25	5.82	32.50	26.80	6.50	80.50	78.50
42	117/1	36.33	4.50	35.70	23.20	5.30	72.50	73.00
43	139	44.47	3.62	27.15	22.30	7.00	79.50	75.00
44	137	45.00	2.38	33.40	26.70	5.70	43.00	34.00
45	140	43.90	3.00	39.40	27.60	5.60	75.50	75.00
46	159	48.63	5.40	39.70	36.20	5.00	73.00	65.50
47	138	48.60	5.85	36.20	30.20	5.00	77.00	75.00
48	146	47.88	7.50	40.50	28.50	5.10	45.00	75.00
49	142	46.25	4.90	31.70	25.60	6.30	44.00	76.00
50	160	40.10	6.10	33.10	31.50	4.60	77.50	71.00

Contd.

Table 2a Contd.

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
51	147	40.73	2.50	37.50	32.60	4.40	40.50	36.50
52	148	41.62	3.50	37.80	29.10	5.30	39.50	36.00
53	34/2	57.65	5.40	43.30	31.20	5.00	68.00	82.00
54	12	51.20	5.90	38.40	32.20	5.50	72.50	65.00
55	8/3	43.40	4.90	38.50	30.40	5.25	73.50	73.00
56	7	47.30	4.05	33.30	29.40	6.50	66.50	70.00
57	79	56.00	6.43	42.30	29.50	5.90	76.50	73.00
58	17/2	39.70	5.00	44.40	41.70	5.70	74.50	71.50
59	97	41.60	4.60	40.70	32.20	5.90	72.00	38.00
60	25	53.75	4.30	46.20	38.70	5.20	71.50	36.50
61	167	42.35	3.75	50.10	41.50	6.60	71.00	66.50
62	117/3	44.00	8.35	43.00	40.20	4.45	68.00	70.00
63	89/2	54.10	4.75	30.50	30.20	4.00	70.50	79.00
64	89/3	40.55	3.69	40.50	33.30	3.70	75.50	67.00
65	106	42.05	6.50	41.30	37.50	2.90	75.00	73.00
66	115/1	32.00	5.70	35.20	25.20	4.50	82.00	77.00
67	91/4	45.50	4.40	64.50	42.50	7.45	86.50	40.50
68	23	59.00	5.60	61.50	65.40	4.55	75.00	38.50
69	29/4	41.00	4.80	29.20	38.20	5.15	73.50	80.00
70	Byadgi Kaddi	70.25	4.95	31.20	37.80	5.80	61.50	74.00
71	Dyavanur Dabbi	57.10	6.60	37.90	33.50	5.60	60.50	90.00
S.E.m±		6.23	0.60	—	—	—	2.35	3.55
CD (1%)		16.57	1.59	—	—	—	6.25	9.44
CD (5%)		12.46	1.20	—	—	—	5.10	4.70

Table 2b. The mean performance of chilli genotypes for different yield components

S.No.	Genotype	No. of fruits per plant	Fruit length (cm)	Fruit diameter (cm)	Fruit stalk length (cm)	Pericarp weight (g)	Weight of seeds per fruit (g)	Fruit stalk weight (g)	Fruit weight (g)	Number of seeds per fruit (g)	Fruit yield per plant (g)	Fruit yield per ha (kg)
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)
1	101	2.50	7.20	2.23	323	0.34	0.14	007	0.54	26.00	1.00	3703
2	95	7.50	8.15	4.15	3.20	0.33	0.33	0.09	0.75	4720	440	16296
3	91/3	450	560	2.78	3.16	0.31	0.01	0.05	0.38	200	1.45	53.71
4	73/2	5 75	6.80	283	3 15	0.26	0.12	004	0.42	22.30	2.00	74.07
5	73/1	12 50	7.36	3.05	3 15	0.28	0.13	003	0.45	15.15	3.70	137 04
6	64	6.00	388	401	4 26	0.29	0.65	0.02	0.96	4040	3.90	14445
7	29/1	5 80	653	606	3.67	0.57	0.43	0.05	1 04	51 80	5.30	19629
8	27	7.25	7.66	4.62	355	0.45	0.30	006	0.81	47.70	5.09	188.33
9	21	18.50	7.05	5.10	3.40	0.37	0.55	004	0.95	64.00	6.80	251. 85j
10	15	2.50	499	3.12	2.49	0.23	0.11	0.03	0 37	21 25	3.92	145 37
11	17	3.75	5.94	4.09	3.17	0.39	0.20	0.04	0.63	25.14	1 85	6852
12	13/1	5.50	7.00	4.05	3.59	0.34	0.35	0.02	0.71	50.40	3.80	140.74.1
13	13/4	8.65	7.46	389	3.46	0.24	0.30	002	0.56	49.35	3.81	141 11
14	-30	965	9.03	3.93	3.20	0 52	0.32	002	0.36	3430	5.50	20370
15	102	4.15	6.76	3.16	343	0.39	0.16	0.04	0.60	25.05	2.39	88.51
16	29/6	6.80	792	351	3.12	0.42	0.31	0.04	0.76	57.06	3.85	142.40
17	86	6.65	606	297	3.32	0.23	0.14	0.05	0.42	24 10	2.34	8649
18	29/5	600	5.84	428	3.28	0.38	0.26	004	0.67	41 28	3.88	143 52
19	34/3	12.90	8.09	3 15	3.36	0.29	0.27	005	0.62	38.93	5.80	214.82
20	6/1	10.00	790	407	3.32	0.53	0 30	0.06	0.88	61.65	8.38	310.18
21	6/2	4.35	622	3.19	3.25	0.29	0.25	0.07	0.61	38 50	1570	581.48
22	13/2	8 50	6.75	3 17	340	0.20	0.25	007	0.50	42.96	3.39	125.56
23	13/3	9 15	6.99	294	3.46	0.24	0.25	0.05	0.55	36.00	3.85	14260
24	117/4	5.85	7.12	437	3.06	0.33	0.26	009	0.68	39.82	4.10	151 85
25	177	685	5.68	350	3 15	0.25	0.05	005	0.36	8.76	2.26	83.70
26	178	15.85	6.77	3.22	3.25	0.22	0 23	008	0.53	50.18	6.15	227.78
27	176	11.25	6 11	3.28	3.05	0.32	0.06	0.03	0.41	2.85	3.55	131.48
28	173	300	6.66	3.60	3.15	0.20	0 14	006	0.40	19.15	1.20	44.44
29	171	11.25	5.09	2.97	300	0.23	0 19	001	0.44	34.70	362	134.26
30	150	3.50	9.62	538	3.18	0.39	0.25	0.04	0.67	4370	1 95	7222
31	153	1.75	6.88	2.75	3.00	0.24	0.18	0.09	0.50	27.85	0.65	24.08

Cont.

Table 2b Contd.

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)
32	154	475	4.12	6.39	263	0.31	032	0.08	0.71	52.15	3.68	136.11
33	168	4.10	5 77	3.22	305	0 17	021	0.04	042	41.32	1.73	64.07
34	174	5.50	7.10	4 15	3.10	037	0.41	0.07	0.85	74.70	4.10	151.85
35	172	6.75	9.40	4.57	3.64	050	0.36	0.07	0.92	5683	4.12	152.78
36	169	17.25	5.85	3.95	3.28	030	027	003	0.65	45.55	6.88	254.63
37	166	13.50	6.43	356	3.08	0.23	0 19	0.01	043	19.55	4.98	18463
38	170	5.90	6.53	341	3.32	0.28	0.32	0.07	067	57 18	3.61	13370
39	175	4.50	5.30	4.80	3.38	022	0 28	0.06	0.56	52 50	2.25	8334
40	117/2	200	8 12	500	3 33	0.41	0.81	009	1.30	79.00	265	98 15
41	136	3.75	9 15	3.06	3.45	0.36	028	0.08	0.72	38.67	3.00	111.11
42	117/1	7.50	6.65	3.35	5.85	0.19	0.11	006	0.37	2385	3.50	129.63
43	139	475	5.78	3 12	3.37	036	0.13	0.07	0.54	19 58	2.75	101.85
44	137	5.00	845	3.95	2.79	0.22	0.28	009	0 58	37.22	3.53	130.56
45	140	6.35	680	3 33	3.12	0 31	0.17	003	0.51	24.25	2.34	86.66
46	159	4.50	8.25	303	3.18	0.36	020	0.02	0.59	30.72	2.90	107.41
47	138	2.25	902	3.10	2.13	0.32	0.42	0.06	080	7000	1 65	61.11
48	146	4 50	6.51	3.13	3 15	0.29	0.16	004	0.49	31 81	1.74	64.44
49	142	7.00	6.30	3.80	4.10	029	049	0.08	0.86	58.40	3.15	116.66
50	160	8.65	622	379	299	0.06	0.39	0.01	0.46	5900	476	176 11
51	147	725	644	4.75	3.13	0.54	0.16	006	0.77	21.67	3.30	122.40
52	148	7.25	9.05	4.15	3.04	0 34	0.28	004	067	58.25	420	155.55
53	34/2	1565	7 56	2 55	347	0 31	030	0.03	0.64	49 18	6.95	257.41
54	12	3.25	5.64	3.24	3.19	0.38	0.16	0.04	0.58	2395	2.03	7500
55	8/3	2.50	6.65	322	2.78	0.26	009	008	0.43	9.12	1.12	41 67
56	7	2.00	483	3.50	3.33	0.50	0.13	0.08	0.72	17 30	1 35	5000
57	79	350	4.89	3.21	3.38	0.28	0 14	005	0.47	20.19	1.60	59.26
58	17/2	6.50	7.68	4.43	3.18	0 52	0.39	0.01	0.93	59.68	5.62	208.33!
59	97	3.00	7.88	3.50	338	0.41	0.19	0.06	066	3045	2.20	81.48
60	25	14 75	8.18	3.71	3.36	0.17	0.56	006	0.79	59.45	7.75	287.04
61	167	9.75	8.99	3 14	3.65	0.59	0.16	006	0.81	37.08	7.03	260.18
62	117/3	6 00	7.75	5 10	330	0.31	0.38	0 09	0.78	4990	4.40	16296
63	89/2	1.00	11.75	5.15	3.60	065	0.70	009	1.45	82.50	1.45	53.71
64	89/3	1.50	1062	3.75	338	037	045	008	090	51 00	1 20	44.44
65	106	5.00	8 10	4 25	4.70	029	0.36	0.07	0.72	62 15	325	120.37!
66	115/1	26 50	7.20	3 30	3 10	024	0 18	0.05	0.47	27,10	1075	398,15
67	91/4	3.00	743	3.28	3 10	0 34	0.11	0.05	0.51	2300	1.55	5741
68	23	400	728	2.67	3.10	0.14	0.63	002	0.78	4888	2.90	10740
69	29/4	10.00	6.75	330	3.45	0.16	0.47	0.02	064	68.01	5.75	212.96
70	Byaclagi Kaddi	8.00	10.97	3.37	288	0.56	025	0.09	0.94	24.10	5.65	209.26
71	Dyavanur Dabbi	2.50	728	5 10	3.20	0 53	0.20	0.08	0.85	19.20	6.40	237.04
S.Em ±		080	0.65	0.29	0.28	006	0.05	0.01	5.11	0.03	0.66	24.78
CD<1%t		2.12	1.72	0.77	0.74	0 17	0.13	002	1359	0.09	1.75	65.91
CD (5%)		1.60	1.30	0.58	056	0 13	0 10	0 12	1022	0.07	8 32	4956

Angular transformed values were used disease and pest incidence parameters.

Results and Discussion

The analysis of variance indicated highly significant differences among genotypes for all the characters studied, providing ample of scope for selection for majority of the traits in the progenies. The mean, range, genotypic variance, phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance and genetic advance as per cent mean for 20 characters studied were

presented in Table 3. Number of fruits per plant varied from 1.00 in (89/2) to 26.50 (115/1), dry fruit yield per plant from 0.65 g (6/2) to 15.70 g (117/3), powdery mildew disease incidence from 32.36 in genotype 27 to 71.79 (13/1), Nandadevi and Hosamani (2003), Munshi and Behera (2000), Acharyya *et al.* (2002) and Prabhudeva (2003) also reported wide range of variation for most of the characters studied in this crop. The GCV, which gives a picture of extent of genetic variability in the population ranged from 12.63 per cent (fruit stalk length) to 64.60 percent (number of fruits per plant).

Table 2c. The mean performance of chilli genotypes for different pest and disease components (Transformed values)

S.No.	Genotype	Powdery mildew incidence	Fruit borer incidence	Fruit rot incidence	Leaf curl complex incidence	RHHC incidence
(1)	(2)	(3)	(4)	(5)	(6)	(7)
1	101	62.45	18.15	32.58	58.46	39.11
2	95	54.90	20.42	40.38	54.85	17.92
3	91/3	38.60	16.80	20.25	48.62	14.64
4	73/2	66.30	16.50	26.75	52.86	16.06
5	73/1	59.10	20.79	31.62	43.32	7.90
6	64	64.69	20.74	35.67	44 18	18.85
7	29/1	66.13	15.70	26 80	50.30	20.63
8	27	32.36	9.43	30.98	36.30	17.92
9	2V	59.12	14.60	18.42	41.58	16.42
10	15	53 52	18.09	45.58	54.06	25 83
11	17	54.73	19.76	39 53	51.88	10.20
12	13/r	71.79	21 70	20.25	47 67	34.60
13	13/4	57.55	17 31	21.53	41.89	20.26
14	80	53.40	15.05	38.35	34.24	13.00
15	102	47 26	18.15	25.10	43 51	30.65
16	29/6	60.49	17.26	38.94	51.44	19.42
17	86	44.43	13.85	22.00	51.42	10.00
18	29/5	42.18	16.85	40 10	50.07	20.13
19	-34/3	46.67	17.85	14.13	47.35	37.79
20	6/1	48.22	7.55	39.52	51.12	22.90
21	6/2	44.65	16 53	31.11	43.67	17 25
22	13/2	60.82	20.85	35.55	49.18	16.48
23	13/3	59.68	15.92	29.99	32.26	18.04
24	117/4	60.43	20.20	31.62	49.17	20.17
25	177	57.03	17.85	18 38	33.56	16.32
26	178	58.57	19.59	13.55	47.04	8.66
27	176	53 74	16.10	36.26	52.17	21.96
28	173	64.30	15.10	32 89	43.34	30.06
29	171	55.89	16.69	20 67	45.57	33.08
30	150	55.00	23 34	20.25	34.85	19.77
31	-153	40 63	21.09	25.10	43.65	36.03
32	154	47.12	17.60	18.57	44.08	30.05
33	-168	52.87	24.53	13.66	40.90	35.90
34	174	58.20	25.33	8.86	33.82	43.62
35	172	60.94	18.46	6.95	34.91	45.45
36	169	58.70	22.05	15.89	44.43	19.58
37	166	59.44	21.25	28 14	51.86	27.83
38	170	55.00	17.15	34.44	40.61	32.32
39	175	40.72	12.58	17.42	48.97	42.39
40	117/2	45.97	15.18	10.46	32.14	15.49
41	136	56.76	23.36	22.74	49.11	16.55
42	117/1	59.47	25.62	30.99	47.12	19.15
43	139	46.09	16.73	34.75	39 70	22.53
44	137	52 19	20.96	37.47	39 43	39.53
45	140	49.90	23.97	39.53	47.50	18.24
46	159	45.00	20.55	32.89	32 01	24.23
47	138	44.17	23.76	35 56	40.60	15.23
48	146	50.19	24.15	30.31	46.64	12.52
49	142	58.39	11.86	23.97	49.67	11.27
50	160	58.66	7.56	34.90	36.27	28.07
51	147	55.25	18.67	29.14	48.28	12.84
52	148	61.49	22.21	28.56	45.35	13.63
53	34/2	59 44	18.94	18.36	38.26	28.82
54	12	65.05	22.17	38.64	35.94	24.17
55	8/3	64.86	16.69	35.05	51.85	24.61
56	T	51.79	14.43	31.31	50.85	11.46
57	79	34.85	23.40	29.81	46.52	44.47
58	17/2	63.85	20.19	26.90	41.93	27.25
59	97	60.77	21.68	33 83	43.34	31.85

Contd.

Table 2c Cont.

(1)	(2)	(3)	(4)	(5)	(6)	(7)
60	25	54.72	23.69	20.20	45.03	17.05
61	167	65.01	17.20	27.61	46.26	14.81
62	117/3	59.78	19.66	34.44	46.55	30.36
63	89/2	44.53	15.04	13.51	34.63	34.73
64	89/3	63.13	14.71	17.95	50.25	38.44
65	106	59.26	21.80	26 53	52.36	10.40
66	115/1	65.01	24.46	13.16	37.08	38.99
67	91/4	68 27	26 74	35.03	47.67	27.28
68	23	50.01	24.90	23.05	39.92	37.79
69	29/4	55.58	19.73	31.62	52.57	17.20
70	Byadagi Kaddi	53.06	23.77	29.66	56.95	27.17
71	Dyavanur Dabbi	63.65	18.99	26.56	48.78	34.50
S.Em±		2.30	0 81	1.37	1.13	0.57
CD(1%)		6.11	2 15	3.64	3.00	1.52
CD (5%)		4.60	1.62	2.74	2.66	1.14

The GCV values were considerable high for most of characters except for fruit stalk length, powdery mildew disease incidence and leaf curl complex incidence. These high GCV values bearing characters having higher range of variation have a better scope for improvement through selection. Table 2 showed narrow difference between GCV and PCV values for most of the characters indicated that these characters were less influenced by environment. These findings are in agreement with those reported by Munshi and Behera (2000), Acharyya *et al.* (2002) and Prabhudeva (2003). Heritability estimates were high for all the characters under study except plant height (56.40). The highest being observed in red headed hairy caterpillar incidence (99.70). High genetic advance with high heritability was reported in most of the characters except plant height. High heritability coupled with high genetic advance is indicative of greater proportion of additive genetic variance and consequently a high genetic gain is expected from selection under such a situation (Singh and Rai, 1981). The characters, which exhibited high variability with moderate or low genetic advance, can be improved by intermating the superior genotypes in the segregating population developed from multiple crosses and the desirable genes can be accumulated in lines (Bhagyalakshmi *et al.*, 1990).

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Table 3. Different genetic parameters for twenty quantitative traits in chilli germplasm

Character	Mean	Range	Genotypic variance (σ_g)	Phenotypic variance (σ_p)	Genotypic coefficient of variance (GCV%)	Phenotypic coefficient of variance (PCV%)	Heritability (h^2_{lm} %)	Genetic advance (GA)	Genetic advance as percent mean (GAM%)
Plant height	46.78 cm	31.60-61.40 cm	50.16	56.39	15.14	20.16	56.40	10.95	23.40
Number of branches per plant	5.19	2.05-11.50	2.65	3.25	31.35	33.45	87.80	3.14	60.50
Days to first flowering	63.78	32.50-86.50	250.39	255.89	24.81	25.08	97.80	32.25	50.56
Days to 50% flowering	68.85	34.00-90.00	242.33	254.94	22.61	23.19	95.10	31.27	45.41
Number of fruits per plant	7.00	1.00-26.50	20.47	21.37	64.6	65.62	96.90	9.19	131.14
Fruit length	7.20 cm	4.12-11.75 cm	1.87	2.52	18.99	21.07	81.20	2.54	35.27
Fruit diameter	3.73 cm	2.23-6.39 cm	1.12	1.60	20.06	23.85	70.80	1.30	34.85
Fruit stalk length	3.29 cm	2.13-5.85 cm	0.017	0.45	12.63	15.37	67.50	0.70	21.12
Fruit weight	0.66 g	0.36-1.45 g	0.043	0.10	31.35	32.93	90.60	0.41	62.12
Pericarp weight	0.33 g	0.06-0.65 g	0.013	0.06	33.99	37.37	87.20	0.21	63.63
Fruit stalk weight	0.05	0.01-0.90	0.00045	0.01	40.59	45.61	79.20	0.04	80.00
Number of seeds per fruit	39.49	2.00-82.50	323.04	328.15	45.50	47.31	92.50	35.61	90.17
Weight of seeds per fruit	0.27 g	0.01-0.81 g	0.24	0.06	55.95	57.64	94.20	0.31	114.81
Dry fruit yield per plant	3.87 g	0.85-15.70 g	5.69	6.35	61.50	63.88	92.70	175.20	121.98
Dry fruit yield per hectare	143.62 kg	24.08-581.44 kg	7802.5	7827.28	61.50	63.88	92.70	175.20	121.98
Powdery mildew disease incidence	55.12	32.36-71.79	66.10	68.40	14.75	15.33	92.60	16.11	29.22
Fruit borer incidence	18.89	7.55-26.74	16.28	17.30	21.36	22.03	94.00	8.06	42.66
Fruit rot incidence	27.49	6.95-45.58	17.33	78.70	31.98	32.37	97.60	17.90	65.51
Leaf curl complex incidence	44.92	32.01-58.46	42.00	43.13	14.43	14.65	97.00	13.15	29.27
Red headed hairy caterpillar incidence	23.94	7.90-45.45	98.50	98.82	41.13	41.52	99.70	24.41	101.96

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Genetic Variability in Aghani Group of Indian Cauliflower (*Brassica oleracea* var. *botrytis*)

B Singh, Ajay Kumar Pandey, Ajay Verma and Mathura Rai

Indian Institute of Vegetable Research, Banaras Hindu University, Varanasi-221005 (Uttar Pradesh)

Highest variability was observed in leaf size, curd weight without guard leaves and curd weight with guard leaves. Phenotypic coefficient of variance was invariably higher than corresponding genotypic coefficient of variance for all the morphological traits. More than 80% heritability was recorded for curd weight with guard leaves, curd weight without guard leaves and leaf size. Leaf size, curd weight with guard leaves and curd weight without guard leaves exhibited high genetic advance along with high heritability. Yield was significant and positive correlated with curd width and curd weight with guard leaves. Leaf size had positive correlation with curd weight with guard leaves. Head compactness exhibited negative significant correlation with curd width. The highest positive direct effect was exerted by curd weight with guard leaves and curd width whereas negative effect observed for leaf size. Multivariate Cluster Analysis based on Ward's method showed that the genotypes were mainly divided at the first node into 2 clusters with 7 and 23 genotypes in different groups.

Key words: Aghani cauliflower, PCV, GCV, h^2 , Genetic advance, Multivariate clustering

Introduction

Cauliflower (*Brassica oleracea* L. var. *botrytis*) commonly known as 'Phool gobhi', is most popular vegetable in India among the cole crops. Indian cauliflower are characteristically different from European type, as tolerant to high temperature and humid conditions. Most of the Indian cultivars are named after the month of maturity like Aghani (25th September) etc. The mid group cultivars are of short plant type, bluish green leaves with waxy bloom and with very small to medium curd size. Cauliflower was introduced to India in 1822 when Dr. Jemson, a botanist Kew, took charge of the Company Bagh (United Provinces, Saharanpur in the Northern plains) to carry out some horticulture experiments during the period of the East India Company (Swarup and Chatterjee, 1972). The original introductions were cornish type which originated in England followed by temperate type, originated in Germany and Netherlands in 18th Century (Swarup and Chatterjee, 1972). Presently, tropical Indian cauliflower is a result of intercrossing between European and Cornish type, which is more adopted and resistant to high temperature and high rainfall.

Materials and Methods

The present investigation was carried out at the research farm of Indian Institute of Vegetable Research; Varanasi during 2004-05. The experiment was laid out in Randomized Block Design with three replication and recommended agronomical practices were followed to raise good crop. Data were recorded on 12 morphological

characters viz. plant height, number of leaves/ plants, leaf length, leaf width, curd length, curd width, stalk length, curd weight with guard leaves, leaf area, leaf size, head compactness, and curd weight without guard leaves or yield of thirty Aghani genotypes of cauliflower collected all over the country. Recorded values were subjected to statistical analysis of variance and co-variance as prescribed by Burton (1952). Correlation coefficients were carried out according to the method suggested by Panse and Sukhatme (1967) and path coefficient analysis was followed as explained by Dewey and Lu (1959), while heritability (%) and expected genetic advance were worked out as suggested by Johnson *et al.*, (1955), respectively. Multivariate clustering analysis has been carried out to choose the parents for hybridization. This approach help in reducing the large amount of data about the parents to manageable proportions (Peter and Martinalli, 1989).

Results and Discussion

Variability Analysis

The analysis of variance (ANOVA) revealed that all genotypes expressed highly significant differences for twelve quantitative characters under study, indicating adequate scope for selection of superior and diverse genotypes (Table 1). The maximum genotypes showed wide range of variability for leaf size (620-1341), curd weight without guard leaves (603-1043), curd weight with guard leaves (830-1412) plant height (54-63) and leaf width (14-25). The genotypes with high mean value can

Table 1. Variability, heritability and expected genetic advance for Aghani cauliflowers

Character	Range	Grand Mean	Variability		Heritability %	Genetic advance	Genetic advance as % of mean
			GCV	PCV			
Plant height (cm)	54.67-63.00	58.06	3.39	4.69	52.2	2.39	2429.3
No of Leaves per Plant	25.00-35.33	30.71	7.59	9.17	68.5	3.97	773.6
Leaf Length (cm)	43.33-56.00	50.59	5.61	6.62	71.7	4.95	1022.0
Leaf width (cm)	14.00-25.00	18.83	13.38	15.70	72.6	4.42	426.0
Curd length (cm)	13.00-18.00	15.61	10.20	14.30	50.9	2.34	667.1
Curd width (cm)	15.67-20.00	17.31	4.95	8.80	31.6	0.99	1748.5
Stalk Length (cm)	6.00-11.33	8.84	15.00	24.31	38.1	1.69	523.1
Curd weight with Gourd leaves (gm)	830.00-1411.67	1006.81	12.33	12.65	95.1	249.37	403.7
Leaf Size (cm)	620.00-1341.33	954.18	17.16	18.28	88.1	316.55	301.4
Leaf area (cm ²)	1.85-3.32	2.742	9.22	15.11	37.2	0.32	856.9
Head Compactness (%)	10.39-2059	14.93	14.80	19.95	55.0	3.38	441.7
Yield (Curd weight without gourd leaves) (gm)	603.33-1043.33	764.92	13.28	13.84	92.1	200.85	380.8

PCV & GCV – Phenotypic coefficient of variation and genotypic coefficient of variation

be directly used for adaptation or can be used as parents in hybridization. This indicates that the indigenous materials have sufficient amount of variation for most of the traits and selection will be very effective. The phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the traits, being highest for stalk length (24.3 -15) followed by curd length (14.3-10.2), which indicate that the genotypic expression was super-imposed by the environmental influences.

More than 80% heritability was recorded for curd weight with guard leaves, curd weight without guard leaves and leaf size. The characters which exhibited high heritability suggested that selection will be more effective for as the characters. High genetic advance was observed in leaf size (316.55), curd weight with guard leaves (249.37) and curd weight without guard leaves (200.85). High genetic advance as percentage of mean was observed for plant height (2429), curd width (1022) and leaf length (1022). High heritability estimate in combination with high genetic advance is more useful than heritability alone in selecting the best individuals. Leaf size (88, 316), curd weight with guard leaves (95, 249) and curd weight without guard leaves (92, 201) exhibited high values. Kanwar and Korla (2002) observed that phenotypic and genotypic coefficient of variance in late maturing cauliflower was moderate for stalk length and net curd weight and high heritability with moderate genetic gain for stalk length and leaves per plant. Singh *et al.* (1976) reported considerable amount of genetic variability for leaf curd growth in late cauliflower. Net curd yield per plant exhibited high genotypic and phenotypic variation, heritability and genetic advance whereas gross weight

per plant, curd size index and leaves per plant exhibited moderate values in late cauliflower as reported by Kumar *et al.* (2001), Khar *et al.* (1997), and Kanwar and Korla (2003).

Correlation Calculations

Leaf length, curd width, curd weight with guard leaves and leaf size had positive significant correlation with curd weight without guard leaves (Table 2). Curd width had significant correlation with curd length (0.46). Significant positive correlation was observed for curd weight with guard leaves with leaf length and curd width. Leaf size had significant positive correlation with leaf length, leaf width and curd weight with guard leaves. Leaf width had significant negative correlation with number of leaves per plant. Highly significant negative correlation was observed for head compactness with curd width and curd length. Highly significant negative correlation was found between leaf area and leaf size. Kanwar and Korla (2002) observed that net curd weight was significantly and positively correlated with stalk length, gross plant weight and harvest index in late cauliflower. Aditya *et al.* (1989), reported that gross weight was positively and significantly correlated with stalk length, leaves per plants, curd diameter and curd depth whereas day to curd initiation showed negative association with net curd weight and harvest index.

Direct and Indirect Analysis

The highest positive direct effect was exerted by curd weight with guard leaves (0.621), followed by curd with (0.535), head compactness (0.468), leaf length (0.343), leaf width (0.338), leaf plant height (0.037) and curd length (0.026), while highest negative direct effect was

Table 2. Phenotypic (rp) and genotypic (rg) correlation analysis

Plant height (cm)	No. of leaves per plant	Leaf length (cm)	Leaf width (cm)	Curd length (cm)	Curd width (cm)	Stalk length (cm)	Curd weight with gourd leaves (gm)	Leaf size (cm)	Leaf area (cm ²)	Head Compactness (%)	Correlation with yield
(rp)	0.228	0.203	-0.126	-0.068	0.110	-0.115	-0.098	-0.043	0.084	-0.073	0.018
(rg)	0.200	0.314	-0.231	-0.013	0.147	-0.186	-0.141	-0.079	0.339*	-0.137	0.018
	(rp)	0.023	-0.318*	-0.207	-0.190	0.032	-0.143	-0.262	0.227	0.128	-0.229
	(rg)	0.057	-0.485*	-0.261	-0.408*	0.049	-0.177	-0.357*	0.634*	0.102	-0.272
		(rp)	0.234	0.046	0.315*	0.194	0.468*	0.573*	0.027	-0.016	0.499*
		(rg)	0.573*	0.137	0.539*	0.443*	0.563*	0.871**	-0.287	0.073	0.569*
			(rp)	0.161	0.119	0.161	0.378*	0.926**	-0.761**	0.052	0.215
			(rg)	0.131	0.239	0.333*	0.429*	0.958**	-0.037	0.023	0.261
				(rp)	0.458*	-0.087	0.211	0.170	-0.077	-0.321*	0.249
				(rg)	0.582*	-0.014	0.228	0.157	-0.107	-0.356*	0.271
					(rp)	0.058	0.445*	0.231	-0.069	-0.721**	0.519*
					(rg)	0.446*	0.624*	0.378*	0.034	-0.597*	0.639*
						(rp)	0.187	0.214	0.018	-0.070	0.520*
						(rg)	0.341*	0.404*	-0.158	-0.279	0.148
							(rp)	0.502*	-0.129	0.048	0.867**
							(rg)	0.523*	-0.207	0.160	0.893**
								(rp)	-0.629**	0.026	0.371*
								(rg)	-0.892**	0.037	0.392*
									(rp)	-0.033	-0.047
									(rg)	-0.063	-0.046
										(rp)	0.079
										(rg)	0.270

* and ** - significant at 5% and 1 % level of significance, respectively

exerted by leaf size (-0.650) followed number of leaves (-0.162) on curd weight without guard leaves. Head compactness had negative indirect effect by curd width (-0.34), leaf size by leaf width (-0.60) and curd width by head compactness (-0.39) on curd weight without guard leaves.

Leaf width exerted positive indirect effect by leaf size (0.31), curd width by leaf length (0.25) and curd weight with guard leaves (0.24), curd weight with guard leaves by leaf length (0.29), curd length (0.28) and leaf size (0.31) on curd weight without guard leaves. Similarly leaf size contributed indirect effect by leaf area on important trait positively. Bhutia *et al.* (1980) reported

that curd depth and leaves per plant with gross weight and gross weight and harvest index with net curd weight showed positive direct effect in tropical cauliflower. Lui *et al.* (2004) found the significant direct effects of plant mass and curd diameter on curd mass, and indirect effects of leaf mass, leaf area, and diameter of curd stem on curd mass through plant mass and curd diameter. Jamwal *et al.* (1992) observed that curd yield/plant was strongly associated with curd size index and gross weight/plant. Curd size index and leaf size are seen as promising characters for use in selection programmes. Kanwar and Korla (2003) reported that the number of leaves per plant had the greatest direct and positive effect on net curd

Table 3. Direct (diagonal) and Indirect effect of yield contributing traits

Plant height (cm)	No. of leaves per plant	Leaf length (cm)	Leaf width (cm)	Curd length (cm)	Curd width (cm)	Stalk length (cm)	Curd weight with gourd leaves (gm)	Leaf size (cm)	Leaf area (cm ²)	Head compactness (%)	Correlation with yield
0.037	-0.037	0.070	-0.043	-0.002	0.059	0.004	-0.061	0.028	-0.003	-0.034	0.018
0.009	-0.162	0.008	-0.107	-0.005	-0.102	-0.001	-0.089	0.170	-0.009	0.060	-0.229
0.008	-0.004	0.343	0.079	0.001	0.169	-0.006	0.290	-0.373	-0.001	-0.008	0.499**
-0.005	0.051	0.080	0.338	0.004	0.063	-0.005	0.235	-0.602	0.031	0.024	0.215
-0.003	0.033	0.016	0.054	0.026	0.245	0.003	0.131	-0.110	0.003	-0.150	0.249
0.004	0.031	0.108	0.040	0.012	0.535	-0.002	0.276	-0.150	0.003	-0.337	0.519**
-0.004	-0.005	0.067	0.054	-0.002	0.031	-0.032	0.116	-0.139	-0.001	-0.033	0.052
-0.004	0.023	0.161	0.128	0.005	0.238	-0.006	0.621	-0.327	0.005	0.023	0.867**
-0.002	0.042	0.197	0.313	0.004	0.124	-0.007	0.312	-0.650	0.025	0.012	0.371*
0.003	0.03	0.009	-0.257	-0.002	-0.037	-0.001	-0.080	0.409	-0.040	-0.015	0.047
-0.003	-0.021	-0.006	0.018	-0.008	-0.386	0.002	0.030	-0.017	-0.001	0.468	0.079

weight. Based on correlation and path analyses, the number of leaves per plant, gross plant weight may be considered for selection of promising genotypes.

Hierarchical Cluster Analysis

Multivariate hierarchical clustering was carried for twelve different morphological characters (Fig. 1). Distance between all pairs of genotypes was calculated using squared Euclidean distance method and genotypes were clustered based on Ward's method. Cluster analysis showed mainly 2 clusters. From the dendrogram, it can be concluded that the genotypes were mainly divided at the first node into 2 clusters with 7 and 23 genotypes in different groups. Cluster with 23 genotypes was again divided into 2 groups at the second node with 20 and 3 genotypes. Similarly, 20 genotypes further divided into 2 groups at the third node with 18 and 2 genotypes, respectively.

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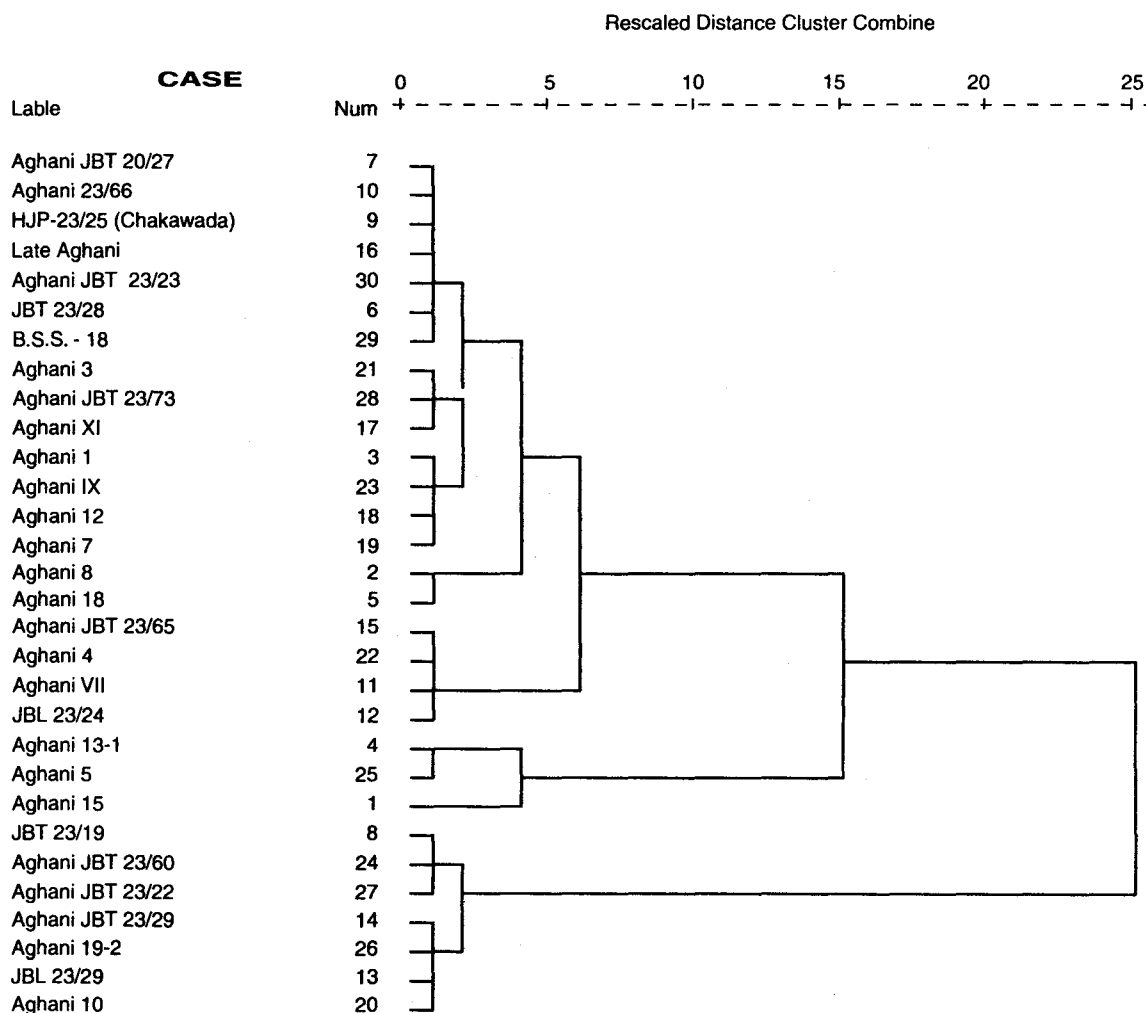


Fig. 1: Multivariate cluster analysis of 30 genotypes using Ward's Method

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Genetic Variability of Ber (*Ziziphus mauritiana* Lamk.) and its Prospects for Crop Improvement

Arun K Shukla, Dhurendra Singh, Anil K Shukla* and DG Dhandar

Central Institute for Arid Horticulture, Bikaner-334 006 (Rajasthan)

Diverse germplasm of ber assembled at Central Institute for Arid Horticulture, Bikaner, Rajasthan repository consisting of 338 genotypes/strains from different parts of the country were evaluated with respect to morphometric characters, yield and yield attributes for further utilization in improvement programme so as to meet the future demand of growing population. Out of the genotypes collected through explorations AKS/NRCAH-15 was observed to be a precocious and prolific bearer. IC322120 and IC322121 from Gujarat were found promising with respect to yield and yield attributing traits. The local variety Illaichi was found prolific bearing in clusters that could be potentially used as parental line in systematic hybridization programme. Variety Rashmi was found superior over Umran – a leading variety, in terms of fruit taste, flavour and palatable attributes. Many collections, viz. IC322120, IC322121, AKS/NRCAH-15 and Illaichi seems to be utilized in processing, through drying with excellent quality. This paper discusses the performance of promising ber genotypes and status of the conservation of ber genotypes in the field repository being maintained and evaluated under hot arid ecosystem of Thar desert.

Key words: Conservation, Germplasm, Variability, *Ziziphus mauritiana*

Introduction

Indian ber (*Ziziphus mauritiana* L.) (family Rhamnaceae) is said to be indigenous fruit crop while *Ziziphus jujuba* Mill. is native to China Indo-Malaysia region is the centre of both evolution and distribution of the genus *Ziziphus* (Liu and Cheng, 1995). However, De Candolle (1886) stated that Myanmar (Burma) and India are the home of ber. Its cultivation is more common in Uttar Pradesh, Haryana, Rajasthan, Gujarat and Maharashtra. This fruit crop has vast scope of growing in wasteland like salt affected marginal forest soil (Shukla, 1996). Ber being cross pollinated and heterozygous crop, growing of plants through seed may results in maximum variability in seedlings. A wide range of variability exists in ber in India (Sharma and Kore, 1990). The variation has been observed for all the characters suggesting substantial scope for improvement (Pathak and Pathak, 1993). Sometime, specific genotype(s) may be obtained from the seedling population, that may arise due to natural outcrossing or spontaneous mutation. Identification and selection of desired ideotypes may results in improvement of fruit crops. Moreover, some rare types of variability are extinct from the nature (due to deforestation or natural disaster) which may be the potential source for resistant to biotic and abiotic stresses. In India a number of ber cultivars have been developed largely by the growers through selection in different regions. Maximum variability of ber is observed in Rajasthan, Gujarat, Haryana, Punjab, Madhya Pradesh and Uttar Pradesh. In

Gujarat, Mehsana, Anand, Panchmahal, Patan and Sabarkata districts have rich diversity in ber (Shukla *et al.*, 2004a). It is also reported that the smaller fruits of Umran is known as Chameli in Gujarat (Shukla *et al.*, 2003b). There are many unexplored area of ber variability from where promising types need to be collected for further characterization and evaluation. Historically central part of the country is supposed to be the richest area in the wild ber germplasm (Shukla *et al.*, 2004a). Therefore, it is highly desirable to identify the elite germplasm, collect them and maintain for their utilization in crop improvement programme of either through conventional and or biotechnological approaches.

Materials and Methods

There were two approaches adopted for the collection of the ber germplasm. In the first approach commercial varieties and genotypes were collected in the form of bud stick for *in situ* budding or direct planting of budded plants through survey at farmers field and forest area and also those maintained by different institutes. In second approach, survey for the identification of elite type germplasms were conducted by the institute. Selective sampling method was adopted for the identification of elite genotypes. While identifying the plant about 30 fruits were collected from each elite plants of ber for development of progeny line and analysis of physico-chemical attributes. The plant height and spread was recorded with the help of scale and long bamboo stick or ranging rod and average fruit weight was recorded.

*Corresponding author: Deptt of Horticulture, MPUAT, Udaipur; E-mail: anilciah@yahoo.com

Vernier Callipers was used for taking observation on fruit size. TSS was recorded with the help of hand refractometer. The bud wood of identified plants were collected and budded *in situ*. Further, *in situ* budding is recommended technology for establishment of the new genotypes under hot-arid ecosystem (Shukla *et al.*, 2004b). For this purpose rootstock were planted at the recommended distance (6.0 x 6.0 m) and after its establishment in the field *in-situ* budding was performed.

Results and Discussion

A total of 338 genotype/strains of ber have been collected and maintained in the national repository of CIAH, Bikaner. Out of that 89 genotypes/strains were collected through survey from Rajasthan (Chirana, Jobner, Bhusawar, Udaipurvati, Banar and Sirohi) Gujarat (Patan, Mehsana, Anand, Panchmahal and Sabarkata), Andaman, Uttarakhand (Udham Singh Nagar, Nainital, Haridwar, Dehradun and Pauri) and Uttar Pradesh (Raibareli, Pratapgarh, Allahabad, Mirzapur, Varanasi, Deoria, Gorakhpur and Faizabad) and remaining 244 cultivars/genotypes and five exotic species/cultivars of ber were collected and maintained from different institutes. Among the genotypes collected through survey IC322117 was found cluster bearer and partly tolerant to infestation by fruit fly. Further, in two genotypes (IC322120 and IC322121) there were two types of fruits (Table 1) – the fruits of early setting type having bigger size (4.35x3.45 cm and 5.23 x 4.14 cm, respectively) and the fruits of late setting type locally known as Chameli were smaller (2.47x2.23 cm and 3.13x2.54 cm, respectively (Shukla *et al.*, 2003b). The average fruit weight of bigger size fruit was 27.71g in IC322120 and 39.97g in IC322121. However, the average fruit weight of Chameli type fruit varied from 5.42g (IC 322120) to 9.22g (IC 322121). However, the genotype AKS/NRCAH-15 was found promising under hot arid ecosystem which is precocious and prolific bearer. The average fruit weight was about 27g, TSS 23%, total sugar 4.29% and ascorbic acid content was 60mg/100 g fruit. Average stone weight was 1.3g, dry matter content was 19.87% (Annual Report, 2002; Shukla *et al.*, 2003; Dhandar *et al.*, 2003). In most of the genotypes flowering period were observed between first week of September to first week of November (Table 2). Number of flowers per cluster varied from 08 to 25. Likewise the colour of the petiole varied from the light green to green and its length varied from 0.5 cm to 2.00 cm. However, the information with respect to growth characteristics of the important genotypes of ber,

Table 1. Yield attributes of ber genotypes

IC/ Collector No	Average fruit weight (g)	Fruit size (cm)		TSS(%)
		Length	Width	
IC322112	13.00	3.83	2.54	18
IC322113	1.40	4.23	2.44	16
IC322114	15.80	4.68	3.14	16
IC322115	17.16	3.99	2.34	16
IC322116	2.09	1.54	1.67	19
IC322117	2.67	3.12	2.73	17
IC322118	11.47	2.65	2.48	16
IC322119	15.08	3.00	2.50	17
IC322120	(i) 27.71	(i) 4.35	(i) 3.45	(i)19
	(ii) 5.42	(ii) 2.47	(ii) 2.23	(ii)18
IC322121	(i) 39.97	(i) 5.23	(i) 4.14	(i) 14.4
	(ii) 9.22	(ii) 3.13	(ii) 2.54	(ii) 15.4
IC322122	4.92	1.73	1.73	18
IC322123	4.31	1.82	2.14	20
IC322124	6.42	2.34	2.22	19
IC322125	4.27	1.82	1.84	18
IC322126	5.00	3.15	2.54	17
AKS/NRCAH 15	27.00	4.60	3.00	23

presented in the Table 2. In ber maturity behaviour of fruit is one of the most important traits which determines the economics of the crops and better adaptation to arid environment. This aspects was studied crucially and some of the genotypes like AKS/NRCAH-15 and CIAH Hybrid 1 were found very promising having characteristics of early ripening. Variability within the clone was noticed under this investigation. A clear variability was observed in different strains of Gola collected from various region like Haryana, Gujarat and Rajasthan. Remarkable variability was exhibited in strains of Mundia. Characteristics of dwarfism were also very important morphological character of plants and played important role in orcharding under different agro-ecological conditions. Under drought condition and storms and speedy wind weather vagaries, dwarf cultivar/genotypes performed well. Some of the genotypes such as AKS/NRCAH-15, Illaichi, found physiologically dwarf having short internodes, poor apical dominance and slow growth and development of the branches. This morphological variability will be useful in molecular characterization of the germplasm for development of linkage map and quantitative traits loci (QTL) and isolation of desired genes. Moreover, the biodiversity of ber collected at the CIAH, will be useful in the improvement programme for the development of new varieties to meet out the challenges of future competitive market and consumer demands.

Table 2. Characteristics of important genotypes of ber

IC/ Collector No	Source	District	State	Plant Height (m)	Plant (m) E-W	Spread N-S	Leaf size (cm)	Petiole length (cm)	Foliage colour	Petiole colour	Flowering Period			Number of flower per cluster
											Initiation	Peak	End	
IC322112	Farmers field	Sirohi	Rajasthan	2.50	4.00	4.00	9.1x6.1	2.00	Green	Light green	10.9	4.10	15.11	19
IC322113	Farmers field	Sirohi	Rajasthan	2.75	2.50	2.00	8.1x3.2	1.70	Dark Green	Green	19.9	4.10	18.11	13
IC322114	Farmers field	Sirohi	Rajasthan	2.10	3.00	2.00	7.9x6.1	1.90	Green	Light green	12.9	4.10	16.11	19
IC322115	Farmers field	Sirohi	Rajasthan	2.50	4.00	3.00	9.2x6.4	2.00	Green	Green with purple tinge	11.9	4.10	14.11	24
IC322116	Farmers field	Patan	Gujarat	2.75	3.00	3.00	2.1x2	1.00	Light green	Light green	9.9	4.10	17.11	22
IC322117	Farmers field	Patan	Gujarat	3.50	3.00	3.00	3.7x2.1	1.60	Light green	Light green	19.9	13.10	25.11	12
IC322118	Farmers field	Patan	Gujarat	2.75	3.00	2.50	7.1x3.6	2.00	Green	Light green	19.9	4.10	15.11	12
IC322119	Farmers field	Mehsana	Gujarat	3.00	4.00	4.00	5.1x3.2	1.20	Green	Light green	28.9	27.10	22.11	14
IC322120	Orchard	Mehsana	Gujarat	2.75	4.00	4.00	6.3x3.7	1.30	Dark green	Green	19.9	4.10	12.11	17
IC322121	Orchard	Mehsana	Gujarat	3.00	5.50	5.00	8.7x6.1	2.10	Dark green	Green	19.9	4.10	19.11	14
IC322122	Farmers field	Anand	Gujarat	2.50	3.00	4.00	3.7x2.6	1.30	Green	Light green	28.9	27.10	19.11	08
IC322123	PWD guest house	Anand	Gujarat	3.50	4.00	4.00	4.2x2.8	1.00	Green	Light green	20.9	26.10	22.11	13
IC322124	Farmers field	Panch- mahal	Gujarat	2.00	4.00	2.00	5x3.2	1.20	Light green	Light green	20.9	5.10	12.11	14
IC322125	Farmers field	Panch- mahal	Gujarat	3.75	3.00	3.00	4.4x3.6	0.50	Green	Light green	5.10	25.10	22.11	08
IC322126	Orchard	Sabar- kata	Gujarat	3.00	4.00	3.75	5.5x2.8	1.20	Green	Light green	15.9	5.10	17.11	12
AKS/ NRCAH 15	Farmers field	Bharat- pur	Rajasthan	3.30	4.75	3.60	8.37x4.3	1.67	Green	Light green	05.9	15.9	10.11	25

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Screening of American Cotton (*Gossypium hirsutum* L.) and Desi Cotton (*G. arboreum*) for Fibre Quality Traits, Seed Cotton Yield and Important Yield Components

RA Meena, D Monga, Rajiv Kumar and Hamid Hasan

Central Institute for Cotton Research, Regional Station, Sirsa-125 055 (Haryana)

In *G. hirsutum* 1199 geographically and phenotypically diverse lines and in *G. arboreum* 540 lines maintained at CICR, Regional Station Sirsa were evaluated for fibre quality traits for three years from 2001-02 to 2003-04. In *G. hirsutum*, 10 superior accession with long fibre (29.0 mm and above) were identified. The fibre fineness in these accession ranged between 3.5 to 4.6 micronaire. Except accession DP 45 A(y) and AC 130 in which the fibre fineness was 3.5 and 3.7 micronaire respectively, the fibre fineness in remaining accessions was as per accepted fibre quality norms. Among these 10 lines, five accessions namely SCC 113, NA 1375, DP 45A (y), Cotton 5 and AC-130 showed high fibre strength ranging from 25.1 g/tex to 27.1 g/tex. Accessions SCC 113, Cotton 5 and Cotton 17 showed good uniformity (more than 50%). Some accessions like MC 86, JKCL 702 and Cotton 5 Showed good ginning outturn (more than 34.7%). In *G. arboreum* also the superior ten accession for fibre length more than 25.4 mm were identified. The fibre fineness in these cultivars ranged from 4.1 to 6.0 micronaire and was below 5.0 micronaire in accessions AC 3196, DCB 5, AKA 60-2, AC 3535, 1789, CISA 12 and DCB 11. Accessions AC 3722 and AKA 60-2 showed good fibre strength (above 22 g/tex) and Accessions DCB 11 and DCB 5 showed good ginning outturn (35 percent or above). Accession SCC 113 and Cotton 5 of *G. Hirsutum* and DCB 11 and AC 3196 of *G. arboreum* exhibited a combination of superior fibre quality traits and higher yield.

Key words: *Gossypium hirsutum*, *G. arboreum*, Fibre property, Germplasm

Cotton is a major fibre crop of global importance and has high commercial value. The recent technological advancement in textile industry demand that the cotton research should lay emphasis on improvement of fibre quality i.e. fibre length, fineness, strength and maturity. The quality of raw material plays a vital role on yarn quality. The appearance and durability of the yarn and fabric is also dependent on fibre properties. Presently cultivated American cotton (*Gossypium hirsutum*) cultivars in north zone belong to medium staple category and have low strength. On the contrary, high speed rotor spinning used by textile mills require cotton with high fibre strength. Similarly desi cottons (*G. arboreum* L.) cultivated in this zone possess short fibre length (around 16-18 mm) with coarse nature (micronaire around 7-8) and low strength (16-18 g/tex). These are the major drawbacks and are the main reasons for poor demand of desi cottons grown in north zone in textile industry. Although, in addition to inherent resistance against insect pests, diseases and moisture stress, the yield potential of desi cotton in north zone is much higher than American cotton cultivars but due to poor demand and low market price the area under this cotton has stagnated at around 25% of total cotton area of the zone. The improvement in fibre quality is a serious constraint in both the American and desi cottons cultivated in north zone and need immediate attention. Plant genetic resources are the foundation of any crop improvement programme. The improvement in

the status of cotton of this zone can be possible by screening of available genetic resources of both the species to identify superior fibre quality lines and their utilization in breeding programme (Meena *et al.*, 2001). Several reports on variability for economic traits in *G. hirsutum* and *G. arboreum* cotton are available (Anon. 1989, Singh and Narayanan, 1987 and Siwach *et al.*, 1988) but the information on sources of superior fibre properties is meager. Keeping in mind the future need, an attempt has been made to screen germplasm available at CICR, Regional Station, Sirsa for fibre quality traits as well as for seed cotton yield and important yield components.

Material and Methods

Eleven hundred and ninety nine *G. hirsutum* and 540 *G. arboreum* geographically and phenotypically diverse lines from the gene pool of cotton maintained at CICR, Regional Station Sirsa, were evaluated for fibre quality traits, yield and important yield components for three years from 2001-02 to 2003-04. Each accession was sown in 20 dibbles at 67.5 cm x 30 cm spacing. Recommended agronomic and plant protection practices were followed. Observations on yield/plant, boll weight, bolls/plant, ginning outturn, seed index, lint index were recorded. The data on fibre length, fibre strength, uniformity ratio and fibre fineness were recorded through Central Institute for Research on Cotton Technology (RIRCOT), Sirsa.

Mean data for 3 years for each parameter were considered for analysis.

Results and Discussion

To improve the fibre length in north zone, 10 superior accessions of *G. hirsutum* which have fibre length of 29.0 mm or more are identified from gene pool and are given in Table 1. The maximum fibre length was observed in accession SSC 113 (31.6 mm) followed by JKCL 702 (30.2 mm) and NA 1375 (30.2 mm). The fibre fineness which is also important fibre property trait ranged between 3.5 to 4.6 micronaire in the above selected ten superior accessions for fibre length. In all the accessions the fibre fineness was between 3.8 to 4.6 micronaire which is in accepted norms of the textile industry except accession DP 45 A(y) and AC 130 in which it was 3.5 and 3.7 micronaire respectively. A large quantity of the long staple cotton (28mm to 32mm) would be required in future which is presently being imported from China, Australia etc. (Sreenivasan, 2004). Some other North Zone cultures such as P 56-2, P 56-6, C 4-9-2-1-1, C4-9-2-1-1-2 and P 4515-1 showing good micronaire were earlier reported by Singh *et al.* (2004).

Among 10 superior lines for fibre length, the accessions AC 130, Cotton 5, NA 1375, DP 45A(y) and SCC 113 possess fibre strength more than 25 g/tex which is a most desired fibre property trait for modern textile industry. Maximum fibre strength was noticed in accession AC 130 (27.1 g/tex) followed by Cotton 5 (26.4 g/tex) and NA 1375 (25.9 g/tex). The minimum 48% uniformity ratio as per the CIRCOT norms is considered good. In these selected accessions the uniformity ratio was more than 50 % in Cotton 5 (51%). Uniformity ratio

was 50% in SCC 113 and Cotton 17. The ginning outturn more than 34.7% was observed in Cotton 5 (37.1%) followed by JKCL 702 (36.2%) and MC 86 (34.7%).

Among the superior accessions for fibre length, the accession DP 45A (y), AC 130, Cotton 5, Cotton 17 and SCC 113 showed high yield (more than 100 g per plant); Accessions DP 45 A(y), SA 733 and SCC 113 showed good boll weight of more than 3 gm; Accessions AC 130, Cotton 17, SCC 113 and Cotton 5 showed high boll number (more than 36.8); Accessions MC 86, SCC 113, JKCL 702 and Cotton 5 showed high seed index (more than 10 g). The accession SCC 113 was found to have superior fibre length, fibre fineness, uniformity ratio, fibre strength, boll weight and yield. Similarly accession Cotton 5 showed superiority for fibre length, fibre fineness, uniformity ratio, fibre strength, ginning outturn and yield. The superior accession for both fibre quality as well as yield contributing traits can be utilized for improvement of desired traits.

The fibre length in desi cotton is most important fibre quality trait. In general the fibre length of cultivars of desi cotton in north zone is below 20 mm. In genetic stock of *G. arboreum* evaluated at this station, a wide range of variability for fibre length was noticed. In addition to already known source of fibre length in *G. arboreum* cultivars of central and south zone, i.e. DLSA 17, PA 255, PA 204 and MDL 2463 (Rajendran and Jain 2004, Meena *et al.*, 2005), ten superior accessions, which have fibre length more than 25.4 mm under north zone conditions were identified and are presented in Table 2. The maximum fibre length was observed in accession AC 3535 (28.8 mm) followed by CISA 12 (27.5 mm)

Table 1. Superior accessions for fibre properties in *G. hirsutum* cotton (mean of 3 years)

S. No.	Accession name	2.5% Span length (mm)	Fineness micronaire (10 ⁻⁶ g/in)	Fibre strength (g/tex)	Uniformity (gm) ratio (%)	Ginning out-turn (%)	Yield plant (gm)	Boll weight (gm)	Boll number (gm)	Seed index
1	SCC 113	31.6	3.9	25.1	50	32.8	161.9	3.8	42.5	10.3
2	JKCL 702	30.2	4.0	23.1	43	36.2	37.5	2.8	13.5	10.8
3	NA 1375	30.2	3.8	25.9	45	32.8	96.0	2.9	33.0	9.0
4	Cotton 5	29.6	4.6	26.4	51	37.1	120.1	2.6	45.5	12.1
5	AC 130	29.3	3.7	27.1	47	30.9	100.9	2.8	36.8	8.0
6	DP 45 A (y)	29.3	3.5	25.9	43	31.5	100.1	3.0	32.5	9.0
7	SA 733	29.2	4.1	23.4	48	31.9	68.0	3.4	26.0	9.9
8	MC 86	29.1	4.5	21.6	46	34.7	60.3	2.9	20.5	10.4
9	SA 881	29.1	4.5	23.4	47	31.1	63.4	2.9	22.0	9.6
10	Cotton 17	29.0	4.5	22.1	50	31.0	130.0	2.9	40.1	9.1
	CD at 5%	1.1	0.9	2.6	2.3	3.4	12.2	0.18	3.6	0.8

Table 2. Superior accessions for fibre properties in *G. arboreum* cotton (mean of 3 years)

S. No.	Accession name	2.5% Span length (mm)	Fineness micronaire (10 ⁻⁶ g/in)	Fibre strength (g/tex)	Uniformity (gm) ratio (%)	Ginning outturn (%)	Yield plant (gm)	Boll weight (gm)	Boll number	Seed index (gm)
1	AC 3535	28.8	4.9	20.8	50	27.0	53.7	2.90	18.5	6.7
2	CISA 12	27.5	5.0	18.4	40	31.0	54.6	2.25	24.3	8.0
3	DCB 11	27.3	5.0	21.0	46	36.3	89.1	2.70	33.0	7.2
4	1789	26.4	4.9	19.5	48	32.6	70.6	2.60	27.2	7.2
5	AC 3196	26.3	4.1	21.3	51	32.5	77.6	2.20	35.3	6.4
6	AC 3722	26.2	4.5	22.9	46	31.0	41.1	2.35	17.5	6.8
7	6637	26.1	6.0	21.1	52	31.9	49.7	2.20	22.6	6.8
8	AKA 60-2	26.0	4.8	22.6	52	30.8	43.6	2.32	18.8	6.3
9	DCB 5	25.7	4.6	18.3	47	35.1	86.5	2.60	33.8	5.6
10	CISA 21	25.4	5.1	17.3	49	30.8	75.2	2.60	29.5	7.5
	CD at 5%	1.3	0.4	1.5	4.3	2.4	5.2	0.12	2.8	0.5

and DC B 11 (27.3 mm). Some of desi cotton cultures of this zone with fibre length up to 23.6 mm were earlier reported by Gumber *et al.* (2004). The coarse nature of fibre in desi cotton is a major problem. Among these ten accessions, the micronaire value ranged from 4.1 to 6.0. in Accessions AC 3535, CISA 12, DCB 11, 1789 AC 3196, AC 3722, AKA 60-2 and DCB 5, the micronaire was below 5.0 micronaire and as per accepted norms of the industry. The superior accessions for fibre fineness were AC 3196 (4.1) followed by AC 3722 (4.5) and DCB 5, the micronaire was below 5.0 micronaire and as per accepted norms of the industry. The superior accessions for fibre fineness were AC 3196 (4.1) followed by AC 3722 (4.5) and DCB 5 (4.6). These can be utilized for improvement in ginning outturn in addition to fibre length.

Along with more fibre length the superior accessions for yield per plant were DCB 11 (89.1 gm) followed by DCB 5 (86.5 gm) and AC 3196 (77.6 gm); for boll number per plant AC 3196 (35.3) followed by DCB 5 (33.8) and DCB 11; for boll weight AC 3535 (2.9 gm) followed by DCB 11 (2.70 gm), 1789 (7.2 gm) were found superior. Accessions DCB 11, AC 3196 exhibited a combination of higher yield, superior fibre properties and high ginning outturn. These are the useful source for fibre length as well yield and can be used for improvement in desired traits.

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Studies on Conservation of Some Genetic Resources of Plum in Punjab Sub-tropics

JS Bal and SS Sandhawalia

Department of Horticulture, Khalsa College, Amritsar, Punjab

The root propensity of the four elite varieties identified plum genotypes viz., Kalanoki, Manaka, Dhariwala and Alu Bokhara Peshawari from Punjab sub-tropics was assessed with the use of varying levels of IBA. The different genotypes showed a varying response to the different levels of IBA in respect to the sprouting and survival success, root count and shoot growth. Highest success was achieved through the use of IBA 200 ppm in all the four varieties. The representative plants propagated through this studies have been conserved in the departmental plum collection block for the future evaluation.

Key words: Elite varieties, Plum, Punjab Subtropics, Rooting IBA

Plum is a temperate fruit and in India, it is primarily grown in the north-west Himalayan region comprising the states of Jammu and Kashmir, Himachal Pradesh and Uttarakhand. Some low chilling types of plum are also successfully growing in the northern plains of India particularly the states of Punjab, Haryana and Uttar Pradesh where some local cultivars are of quite prominence like Kala Amritsari in Punjab and Titron in Uttar Pradesh. The plum produced in sub-tropics comes in the market much earlier than the temperate plum and thereby find a ready market. However, the fruits produced in the plains are of small size and seriously confronted with the problem of sourness, which necessitates a viable breeding programme for the development of acceptable plum cultivars. In Punjab the major plum production centres are Gurdaspur, Amritsar and Ferozpur, where a wide range of variability had been reported (Bal and Sandhawalia, 2000; Bal, 2003). Enormous varietal wealth of plum is facing serious threat of extinction, due to shrinkage of natural habitat and fast urbanization of the production centres particularly around big cities like Amritsar. The present study is an endeavour to take up the *ex-situ* for conservation of some promising genetic resources known for their particular desirable traits, through cuttings treated with varying levels of IBA. These resources can be of great help as donor parents for launching a viable plum breeding programme in the sub-tropics.

Materials and Methods

The experiment was conducted in the fruit nursery of Khalsa College, Amritsar during 1995-96 to examine the rooting behaviour of four elite selections of plum locally named as Kala Noki, Manaka, Dhariwala and Alu Bokhara Peshawari in relation to varying levels of IBA. The cuttings of all the four genotypes were

taken from the dormant season's wood in first week of December. Uniform cuttings (20 cm length) with 3 buds were made from middle portions of shoots. The cuttings taken from four genotypes were treated with varying levels of IBA (0, 100, 500, 2000, 3000 and 4000ppm). The treated cuttings were labeled properly and kept for callusing in wet sand for 20 days and planted thereafter in the well prepared nursery beds. The trial was laid out by using RBD factorial design. The observation in respect of rooting propensity and shoot growth were recorded after 90 days of planting.

Results and Discussion

The data predicted a highly variable trend in different genotypes under observations, in respect of sprouting and survival success (Table 1 and 2). The highest sprouting success was noticed in Alu Bokhara Peshawari and lowest in Manaka when the cuttings were treated with IBA. The differences in rooting behaviour of different genotypes can be attributed to the difference in the anatomy of different genotypes (Rana and Sharma, 1999; Bal and Sandhawalia, 2000; Bal 2003). The IBA treatments exerted a significant effect on sprouting and survival success in all the four genotypes. An overall examination of data showed that a fast rise in rooting success with the increasing level of IBA from 100 ppm to 2000 ppm and registered a negative trend with the further increase in the level of IBA. The IBA treatment 2000 ppm proved to be most efficacious in improving the rooting success. The increased survival rate of cuttings with the use of IBA at 2000 ppm may be attributed to fast regulation of cell division and differentiation of root initials by the catalysing effect of IBA (Hartman, 1982). The different genotypes responded differently to the varying levels of IBA. In the genotype Kala Noki (Selection 1) a fast upsurge

Table 1. Effect of different concentrations of IBA on sprouting percentage of different varieties of plum

Varieties	Concentration of IBA						Mean
	Control	100 ppm	500 ppm	2000 ppm	3000 ppm	4000 ppm	
Kalanoki (Section 1)	34.66	86.66	80.33	92.00	85.33	64.00	73.83
Manaka (Section 2)	40.00	51.66	49.33	85.33	61.33	60.00	58.44
Dhariwala (Section 3)	16.00	36.00	93.33	90.66	84.00	78.66	64.44
Alu Bokhara Peshwari (Section 4)	60.00	64.00	84.00	98.66	80.00	61.33	74.66
Mean	37.50	60.33	76.74	91.86	77.66	65.99	

CD at 5% level of significance

Varieties : 2.35

Concentrations : 3.40

Interaction (V x C) : 2.01

Table 2. Effect of different concentrations of IBA on survival percentage of different plum varieties

Varieties	Concentration of IBA						Mean
	Control	100 ppm	500 ppm	2000 ppm	3000 ppm	4000 ppm	
Kalanoki (Section 1)	30.00	62.66	70.66	76.33	72.00	37.66	58.21
Manaka (Section 2)	28.00	46.66	45.33	73.33	50.66	22.66	44.44
Dhariwala (Section 3)	16.00	32.00	74.66	81.33	64.00	50.66	52.99
Alu Bokhara Peshwari (Section 4)	52.00	61.33	80.00	94.66	73.33	54.66	69.33
Mean	33.33	50.66	67.66	81.33	64.99	41.41	

CD at 5% level of significance

Varieties : 8.41

Concentrations : 10.50

Interaction (V x C) : 3.53

of rooting success was achieved with the lowest concentration of IBA 100 ppm which continued with the increases in IBA concentration upto 2000 ppm but the magnitude of increase was very low. Genotype Manaka registered a significant increase in rooting success with 100 ppm. IBA, remained almost static in 500 ppm and registered a fast increase with 2000 ppm. Dhariwala plum experienced a high success percentage with the IBA 500 ppm and remained statistically as such with the 2000 ppm, whereas Alu Bokhara Peshawari registered much high sprouting success (60.00 %) as compared to the other genotypes without the aid of IBA. It experienced a rise in sprouting with IBA 100 ppm. The sprouting was fastly increased to (84.00 %) with IBA 500 ppm. The highest sprouting (98.99 %) was achieved with IBA 2000 ppm but declined sharply with the further increasing levels of IBA. The decline

in rooting success with the higher levels of IBA 3000 and 4000 ppm in all the four genotypes could be attributed to inhibiting effect of IBA after threshold level. The results of present studies are in conformity with the earlier findings (Sharma *et al.*, 1988; Rana and Sharma, 1999. Bal and Sandhawalia, 2000) have reported a variable trend of different genotypes towards varying concentration of the auxins.

The data presented that the root number and root weight was significantly variable in different genotypes (Table 3 and 4). The maximum number of roots (55.00) and root weight (630.00 mg) was recorded in Kala Noki cuttings when treated with IBA 2000 ppm, which was significantly highest as compared to other varieties of plum. The number of roots and root weight per cutting experienced the increase with the increased level of IBA upto 2000 ppm. The higher level of IBA 3000

Table 3. Effect of different concentrations of IBA on number of roots of different varieties of plum

Varieties	Concentrations of IBA						Mean
	Control	100 ppm	500 ppm	2000 ppm	3000 ppm	4000 ppm	
Kaianoki (Section 1)	10.33	9.00	22.34	55.00	31.00	42.16	28.47
Manaka (Section 2)	11.00	7.33	18.00	27.33	25.67	18.66	18.00
Dhariwala (Section 3)	6.33	13.34	18.66	20.00	30.33	16.00	17.44
Alu Bokhara Peshwari (Section 4)	9.34	11.00	15.00	41.34	31.67	25.00	22.22
Mean	9.25	10.16	18.50	35.91	29.67	25.45	

CD at 5% level of significance

Varieties : 0.61

Concentrations : 0.74

Interaction (V x C) : 1.49

Table 4. Effect of different concentrations of IBA on root weight (mg) of different varieties of plum

Varieties	Concentrations of IBA						Mean
	Control	100 ppm	500 ppm	2000 ppm	3000 ppm	4000 ppm	
Kaianoki (Section 1)	202	250	500	630	550	430	427.00
Manaka (Section 2)	200	218	411	450	430	311	333.66
Dhariwala (Section 3)	150	320	350	400	350	300	311.66
Alu Bokhara Peshwari (Section 4)	250	300	320	550	430	358	364.42
Mean	200.50	267.50	390.40	507.50	444.00	350.00	

CD at 5% level of significance

Varieties : 12.57

Concentrations : 14.35

Interaction (V x C) : 21.33

ppm and 4000 ppm showed decline in root number and root weight. The IBA significantly helped to boost the root growth in all the four genotypes. The results are in agreement with the previous findings that IBA at certain threshold levels trigger the rooting propensity of cuttings (Hartman, 1982). IBA 2000 ppm proved to be the best treatment to increase number of roots and root weight in plum genotypes except the genotype Dhariwala (Selection 3) where highest root number (30.33 %) was achieved in this genotypes with IBA 3000 ppm.

Maximum shoot length (7.07 cm) was observed in cuttings of Kala Noki followed by Alu Bokhara Peshawari (7.03 cm) which was significantly higher than the shoot length recorded in Manaka (Selection 2) to be 5.96 cm and 5.25 cm Dhariwala (Selection 3) (Table 5). The shoot length of the different plum selections responded variably to the different level of IBA 100 ppm. The shoot length experienced a significant increase with the IBA 500 ppm. The higher level of IBA could not exert significant influence on shoot length and followed a decrease in shoot length with the highest level of IBA 4000 ppm. The selections

Table 5. Effect of different concentrations of IBA on shoot length (cm) of different plum varieties.

Varieties	Concentrations of IBA						Mean
	Control	100 ppm	500 ppm	2000 ppm	3000 ppm	4000 ppm	
Kalanoki (Section 1)	5.28	5.94	7.78	7.84	8.50	7.05	7.07
Manaka (Section 2)	5.77	5.42	6.02	6.05	6.60	5.87	5.96
Dhariwala (Section 3)	5.86	5.45	5.35	5.68	5.53	3.60	5.25
Alu Bokhara Peshwari (Section 4)	4.96	5.29	6.57	8.85	7.13	7.00	7.03
Mean	5.47	5.53	6.43	7.10	6.95	6.48	

CD at 5% level of significance

Varieties	: 0.89
Concentrations	: 1.09
Interaction (V x C)	: NS

Manaka and Dhariwala responded non significantly to different levels of IBA. The plum selection Alu Bokhara Peshawari experienced increased shoot length significantly in the IBA treatment 500 ppm, their after with the further increasing level of IBA 2000 ppm, the shoot length was recorded the highest (8.85 cm). Shoot length was noticed to be significantly low with the further increasing level of IBA. The variable response of different genotype to the different level of IBA can be attributed to the genetic make up of the different cultivars. The promotion of shoot length in variety Kala Noki might be the resultant of more number of roots and root length produced by its cuttings. The meagre root growth in plum genotypes Manaka and Dhariwala plum may be responsible for lesser shoot growth. The increased number of roots per cuttings under the treatments IBA 2000 ppm might have enhanced the uptake of water and nutrients resulting in higher growth of rooted cuttings.

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SHORT COMMUNICATION

Addition to the Rare and Economically Useful Plant Germplasm *Allium clarkei* Hook f. from Uttarakhand

KS Negi, SS Rathoure, AK Sharma¹, VK Pant and KC Muneem

National Bureau of Plant Genetic Resources, Regional Station, Bhowali-263 132, Niglat, Nainital, Uttarakhand

¹ Department of Horticulture, Janta Vedic P.G. College, Baraut, Bagpat, Uttar Pradesh

Key words: *Allium clarkei*, Collection, Germplasm

Genus *Allium* L. (Alliaceae) has 700-1000 species of herbaceous nature and is distributed in the Northern temperate and alpine zones of the world (Buijsen, 1990; Hanelt *et al.*, 1992). Indian Gene Centre is considered fairly rich distribution and occurrence of about 30-35 species including 4-5 cultivated species (Hooker, 1892; Stearn, 1947; Negi, 2006; Negi and Gaur, 1991; Negi and Pant, 1992; Negi *et al.*, 1991, 1993).

During multi crop/region specific/crop specific and ethnobotanical explorations undertaken in Western Himalaya of Uttarakhand (1999-2005), authors came across a less-known, economically useful *Allium* species. This was an addition to the germplasm of Uttarakhand. The species was gathered/collected from the protected habitats i.e. kitchen garden/backyards/ dooryards of Darma Valley of Munsiyari, 29° 9' - 30° 49' N latitude and 79° 45' - 89° 3' E longitude, district Pithoragarh, Uttarakhand situated at an altitude of 1500 m asl.

After critical morphological studies and comparison with the herbarium material preserved in Northern Circle, Botanical Survey of India, Dehradun (BSD) and Indian Council of Forest Research and Education (erstwhile Forest Research Institute) Dehradun (DD), species was confirmed as *Allium clarkei* Hook. f.

No relevant account of this *Allium* species has been made in recent compilations (Polutin and Stainton, 1984; Naithani, 1984; Chandel and Pandey, 1992; Sharma *et al.*, 1996; Gaur, 1999; Pandey and Pandey, 2005). Hooker (1892) has reported it from Kashmir at Skardo (North-West Himalaya). Singh and Singh (1992) have reported its wild population from Valley of Flowers, Chamoli, Uttarakhand. This species is endemic to north-west Himalaya at 1500-3800 m. altitude (Negi, 2006).

A detailed taxonomic description, distribution, habitat, uses etc., along with figure (Fig. 1) of the specimen are provided here to facilitate further collection and easy identification. Seeds/bulbs and plant specimens

have been rejuvenated, multiplied and maintained at Field Gene Bank of NBPGR, Regional Station Bhowali, Nainital, Uttarakhand. This species is an addition, rare and economically useful plant germplasm from Uttarakhand.

Description

Allium clarkei Hook. f. Fl. Brit India 6: 344 (1892).

Annual herb, 50-55 cm high; bulbs small, single, ovoid 2.5 cm long, outer scales closed and finely reticulated pale; leaves 4-8 (sometimes 10-32), 25.0 -35.0 X 0.6

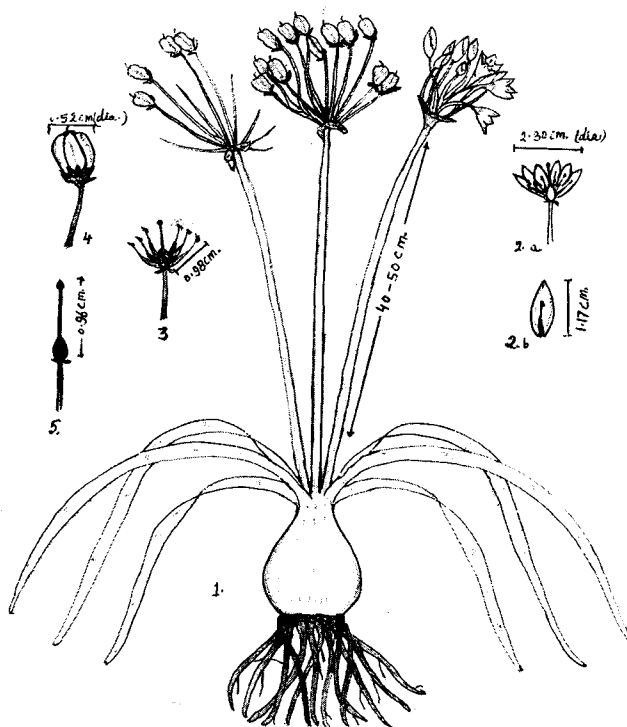


Fig. 1: *Allium clarkei* Hook f.
1) Annual herb with bulb, leaves and flower spikes;
2 a. Flower with pedicel; 2 b. Sepal;
3. Stamens with ovary; 4. Capsule; 5. Ovary

-1.1 cm, obtuse, flat, sub-basal, shorter than the slender scape; scape 40 - 50 cm long, terete; head 4.5 - 5.5 cm dia., lax fid; pedicels 16-22 nos., 2.2 - 3.5 cm long; flowers stellate, white, perianth 0.90 cm long, acuminate; stamens shorter than perianth, filaments inserted near their bases, anthers large; ovary sub-globose; style included; capsule broadly obcordate, 0.40 - 0.52 cm dia., 10-20 seeds in each capsule; seeds black and smooth. Smell of crushed leaves pungent like onion.

Specimens examined: Valley of Flowers, Chamoli, Uttarakhand, BSD 29571; Hoshiarpur, Punjab, BSD 41521; Mulekh, Ladakh, BSD 58841.

Distribution reported: Mapwabad- Munsyari-Madkot-Daranti Kanta, Pithoragarh, Uttarakhand; October 22, 2002; Voucher specimen: AKS-126/IC383446, 1500-2000 m; Field Gene Bank of NBPGR, R/S Bhowali, Nainital, Uttarakhand.

Ecology: Semi-domesticated in kitchen gardens/dooryards/backyards of natives.

Phenology: Flowering and Fruiting: April-June.

Uses: In district Pithoragarh, *Allium clarkei* Hook. f., locally called as 'Pharan'. Young leaves are cooked as pot herb or aromatic vegetable mixed with potato. Dried leaves are used as condiments. Bulbs are eaten raw or cooked. Dried leaves and floral spikes are being sold @ Rs. 10/- to Rs. 15/- per ten gms in the local market of Uttarakhand.

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SHORT COMMUNICATION

Flowering Behaviour of Wild Species of *Oryza*

LK Bose, SK Pradhan, S Singh, R Chandra and OH Singh

Crop Improvement Division, Central Rice Research Institute, Cuttack, Orissa

Key words: Wild species, *Oryza*, Anthesis, Flowering time

The plant breeders have, historically, utilized the variability in land races for selection and improvement of crop plants. The variability and germplasm resources available for many cultivated species are becoming extremely limited. Enrichment of genetic resources is therefore extremely important. Utilization of wild species is one of the technique to broaden the available germplasm (Stalker, 1980; Sahu *et al.*, 1994; Bose, 2005; Sen *et al.*, 2005). Broadening of gene pool of rice through utilization of wild species of rice for enriching the useful traits in the improved background is to be tapped more and more as the wild species are the reservoir of resistance source for many diseases and insect pests. However, it is observed that there is a wide variation in the flowering time and anthesis of wild species of *Oryza*. For successful hybridization programme; we need to know the exact flowering and anthesis time of the wild species our climatic conditions.

Nineteen wild species of *Oryza* were used as experimental materials and planted during wet season, 2004 at Central Rice Research Institute, Cuttack. First, the seeds of wild species were kept in oven at 50°C for seven days to break the seed dormancy. Then seeds were exposed to room temperature for 24 hours after which seeds were dehusked and placed in petri plates containing moist filter paper for germination. After a week, germinated seeds were transferred to earthen pots. After 25 days, seedlings were transferred to field. One row per species containing twenty plants were transplanted at 20cm plant-to-plant and 20cm row-to-row with two replications per entry. Observations on anthesis time and period of spikelet opening were recorded.

Anthesis time and period of spikelet opening are presented in Table 1. It is observed that the time of spikelet opening differed widely among the various *Oryza* species. In *Oryza latifolia*, *O. Alta* and *O. minuta* flowering started as early as 5.00 AM and continued upto 7.30 AM but in case of *O. australiensis* it was from 2.00 PM to 5.00 PM. The similar trend was observed for spikelet opening also. Normally, the period of opening ranged

between 1.00 to 1.30 hours in majority of the species except *O. australiensis* and *O. brachyantha* where it ranged from 2.00 to 2.30 hours. Wide variation was also observed in spikelet opening of *O. ridleyi* which ranged from 0.30 to 3.00 hours. Variation in anthesis time of *O. malampuzhaensis*, *O. grandiglumis*, *O. schwenifurthina*, *O. granulata*, *O. longiglumis* and *O. latifolia* was half an hour to as high as five hours in *Porteresia coarctata*. The flowering time of all the studied species of *Oryza* spreaded from 5.00 AM to 5.00 PM.

In *O. officinalis*, *O. Alta*, *O. minuta* and *O. granulata*, the flowering time of spikelet opening was between 5.00 AM to 5.30 AM while in *O. australiensis* it was between 2.00 PM to 4.30 PM and in others it was between these two extremes. The flowering behaviour and time of anthesis in some wild species of *Oryza* have been earlier reported by Butany and Gangadharan

Table 1. Anthesis time and period of spikelet opening in *Oryza* species

<i>Oryza</i> species	No. of collections Studied	Time of anthesis	Period of spikelet opening (hours)
<i>Oryza nivara</i>	3	9.00-10.00	1.0-1.5
<i>O. rufipogon</i>	6	9.30-12.00	1.0-1.5
<i>O. longistaminata</i>	5	11.00-14.30	1.0-2.0
<i>O. meridionalis</i>	2	9.30-10.00	1.0-1.5
<i>O. officinalis</i>	8	5.00-6.00	1.0-1.5
<i>O. eichingeri</i>	3	7.30-11.00	1.0-1.5
<i>O. punctata</i>	3	10.00-12.00	1.0-2.5
<i>O. rhizomatis</i>	3	5.00-6.00	1.0-1.5
<i>O. latifolia</i>	10	5.00-6.30	1.0-2.5
<i>O. grandiglumis</i>	3	7.00-7.30	1.0-1.5
<i>O. minuta</i>	2	5.30-7.30	1.0-2.0
<i>O. malampuzhaensis</i>	2	7.30-8.00	1.0-1.5
<i>O. sweinfurthiana</i>	2	9.00-9.30	1.0-1.5
<i>O. australiensis</i>	3	14.00-17.00	2.0-2.5
<i>O. brachyantha</i>	2	9.30-10.30	2.0-2.5
<i>O. ridleyi</i>	2	7.30-9.30	2.0-3.0
<i>O. longiglumis</i>	2	6.30-7.00	0.5-1.0
<i>O. granulata</i>	3	6.00-6.30	1.5-2.0
<i>Porteresia coarctata</i>	2	12.00-15.30	1.0-1.5

(1960) and Harlan (1976). The knowledge of flowering behaviour and anthesis time in wild species of *Oryza* would help in hybridization programme for successful alien gene introgression into improved varieties lacking the desirable gene(s).

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SHORT COMMUNICATION

Rice Donors Tolerant to Complete Submergence

BC Patra, SSC Patnaik and RK Sarkar

Central Rice Research Institute, Cuttack-753 006 (Orissa)

Key words: *Oryza sativa* L., Germplasm, Complete Submergence Tolerant

Rice is grown in varied ecological regions ranging from irrigated to upland, rainfed lowland, deep water and tidal wetland. About 29% of India's total rice area i.e. about 13 million ha is rainfed lowland, which contributes only 19% to national rice production. In a normal year about 4 million ha remains drought prone while 3 million ha is favourable. Another 3 million ha is medium deep waterlogged with water standing up to 50 cm for about a week or so. The remaining 3 million hectare of submergence or flood prone area. The rice crop in this area remains submerged for 1-2 weeks or so giving little or no return at all. Rainfed lowland constitutes a highly fragile ecosystem, which is always prone to flash floods and submergence with an average productivity of 1.2 tonnes/ha in normal years and hardly 0.5 tonnes/ha in case of submergence. Among the 42 biotic and abiotic stresses, submergence has been identified as the third most important constraint in the way of higher rice productivity in eastern India (Hossain and Laborte 1996), which sometimes results in near total yield loss. Besides India, flooding is widespread in other South and South-east Asian countries and affects approximately 22 million ha of rice lands. Therefore better varieties are needed to enhance the productivity of such areas.

The genetic pool of submergence tolerant rice cultivars is limited. Some submergence tolerant rice cultivars like FR 13A, FR 43B, 'Goda Heenati' etc. were identified long back and they are similar in the sense that all the cultivars possess the same submergence tolerant gene (*Sub 1*) in chromosome number 9 (Xu *et al.* 2004). Moreover, the existing tolerant cultivars have very poor combining ability and agronomic characters. Hence, development of high yielding submergence tolerant cultivars using these cultures as one of the parents was successful (Mallik 2000). Identification of new donors (gene resources) thus is highly desirable to achieve success in this field.

The germplasm were grown under normal condition with recommended package of practices to characterize and document the agro-morphological traits. For screening against submergence tolerance, the seeds were direct seeded in specially designed field cemented tanks

(40 x 8 m) with known submergence tolerant (cultivar FR 13A) and susceptible cultivar (cultivar IR 42) as checks. Twenty-one-day-old seedlings were submerged for 12 days under 80 cm of water. Survival count was taken visually on 10th day of de-submergence. The characteristics of the floodwater in terms of light transmission (%) were measured at 1200 h (LI COR, Lincoln, USA), and water temperature and oxygen concentration were determined at 0600 and 1630 h (Syland, Heppenheim, Germany). Light intensity at 60 cm water depth varied between 37.6 and 41.2 % of the incident irradiance above the floodwater. The oxygen concentration at the same water depth was 4.4-7.4 mg l⁻¹ at 0600 h and 6.2-11.6 mg l⁻¹ at 1630 h. The temperature did not vary greatly, being 29.1-33.3°C throughout the period of experiment.

Identification of diverse gene sources for desired traits and their incorporation into the promising cultivars are the most effective way to tackle the adverse situations. These two germplasm namely 'Kalaputia' and 'Kusuma' were screened for their valuable traits like submergence tolerance in the experimental fields of the institute. They withstood complete submergence even if their leaf tips remained below the water surface for more than 12 days (Table 1). The elongation ability of these two landraces was as good as the international submergence tolerant check 'FR 13A'. Accumulation of non-structural carbohydrate (NSC) content before submergence was found to be more in 'Kalaputia', followed by 'FR 13A' and 'Kusuma'. Tolerant cultivars accumulate greater quantities of NSC before submergence compared to the susceptible cultivar (Table 1). This is in conformity with earlier findings (Das *et al.* 2005, Sarkar 1998). Submergence reduced the chlorophyll content (Table 1). The percentage of decrease was maximum in susceptible cultivar 'IR 42' (70.8 %), followed by 'Kusuma' (40.7 %), 'FR 13A' (15.9 %) and 'Kalaputia' (13.6 %). Lower elongation and maintenance of higher quantities of chlorophyll content during submergence is associated with submergence tolerance (Sarkar and Bera 1997, Sarkar *et al.* 2001). Though the survival percentage of 'Kusuma'

Table 1. Total non-structural carbohydrate (NSC) content before submergence and elongation capacity, chlorophyll content and survival capacity due to complete submergence

Cultivar	NSC (%)	Plant Height (cm)			Chlorophyll (mg g ⁻¹ FW)		Survival (%)
		BS	AS	Elongation	BS	AS	
'Kalaputia'	11.5	27	50	23	2.80	2.42	88
'Kusuma'	10.1	34	66	32	2.95	1.77	75
'FR 13A' (T-check)	10.2	33	64	31	2.20	1.85	82
'IR 42' (S-check)	6.2	28	65	37	2.19	0.64	0

BS, AS = before and after submergence; Elongation = AS-BS; T= tolerant; S= susceptible; FW=fresh weight

Table 2. Agro-morphological traits of the landraces

Characteristics	Kalaputia (PCP-01)	Kusuma (PD-75)	FR 13A
Blade colour	Light green	Dark green	Light green
Apiculus & stigma colour	Purple	Straw white	Straw white
Ligule shape	2-cleft	2-cleft	2-cleft
Basal leaf sheath colour	Purple	Purple	Green
Culm angle & flag leaf angle	Erect	Erect	Erect
Culm strength & panicle type	Intermediate	Intermediate	Intermediate
Panicle exertion	Well exerted	Well exerted	Well exerted
Secondary branching	Absent	Absent	Absent
Leaf length (cm)	50.5	31.4	58.2
Leaf width (cm)	1.54	0.6	1.49
Plant Height (cm)	105.7	140	149.2
Number of EBT	10.6	9.5	13.6
Panicle length (cm)	21.7	17.9	23.6
Awning	Completely awned	Awn less	Completely awned
Husk colour	Black	Dark purple	Straw white
Kernel colour	Red	Red	Red
Grain length (mm)	8.3	8.0	9.0
Grain breadth (mm)	3.2	2.8	3.4
l/b ratio	2.59	2.86	2.6
Brown rice length (mm)	6.5	7.5	6.0
Brown rice breadth (mm)	2.25	2.75	2.0
l/b ratio	2.8	2.72	3.0
Brown rice shape	Long bold	Long bold	Long bold
Maturity duration (days)	155	165	160

was low compared to the 'FR 13A', yet the cultivar was better than FR 13A due to its awn less characteristics. Awning is undesirable in rice as it creates problems in post harvest handling of the produce. In general, submergence tolerant cultivars possess awn (Mallik 2000). 'Kalaputia' possesses black husk with reduced elongation under submergence and can be easily distinguished from 'FR 13A'. Identification of these two lines is given us hope and extended the scope for further research to develop high yielding submergence tolerant rice varieties.

All the submergence tolerant cultivars namely 'Kalaputia', 'Kusuma' and 'FR 13A' were characterized morpho-agronomically in accordance with IRRI-IPGRI descriptor (Table 2). They were different in respect of apiculus and stigma colour, leaf length and breadth, plant height, awning characteristics. The mean quantitative characters of both the genotypes also showed that they were different. These two newly identified, valued cultivars would be submitted to the Germplasm Registration Committee of NBPGR for registration.

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Evaluation of Apricot Genotypes for Yield and Quality Attributes under Kashmir Conditions

KK Srivastava, Biswajit Das and FA Panday

Division of Pomology, Sher-e-Kashmir University of Agricultural Sciences & Technology of Kashmir, Shalimar Campus, Srinagar-191 121 (Jammu & Kashmir)

Key words: Evaluation, Genotypes, Quality, Apricot, *Prunus armeniaca*, Kashmir valley

Introduction

Apricot (*Prunus armeniaca* L.) native of Armeniaca, belongs to family Rosaceae. The countries under north western Asia contribute major share in apricot production annually followed by Turkey, Italy, Spain, Greece, France and the USA. A wild form of apricot known as *Zardalu* appears to be indigenous to India. Jammu and Kashmir produces most of the fresh and dried apricot in India. North-western Himalayan region exhibit wide variability in respect of morpho-physico-chemical characters of apricots. Considering the vast spectrum of genotypic variability in terms of seedling as well as clonal origin in Kashmir valley, the present study was undertaken for survey, evaluation and conservation of superior apricot genotypes.

Materials and Methods

An extensive survey programme of five districts of the Kashmir comprising Srinagar, Baramulla, Kupwara, Anantnag and Budgam were carried out during 2002-2004. Genotypes possessing desirable horticultural traits were collected and analysed in the laboratory. The observations were recorded on physico-chemical quality of fruit and yield on spot. The standard methods were adopted for recording the observations like fruit weight, fruit length and fruit diameter. Fruit shape, symmetry along suture, skin colour, separation of stone and kernel taste were recorded as per descriptor of IPGR1 (1984). Total sugar contents of the fruits was estimated following the standard method described by AOAC (1984) and TSS by hand refractometer. Titratable acidity was determined by titrating against 0.1N NaOH. The data gathered were statistically analysed as per Panse and Sukthame (1967).

Result and Discussion

Different apricot genotypes exhibited varying fruit characters. Data on fruit yield, fruit weight, fruit length, diameter, shape, symmetry along suture, skin colour, TSS, total sugar, acidity, separation of stone, stone weight, stone kernel taste and time of maturity have been presented in

Table 1. Fruit yield/tree in different genotypes varied from 20 kg in APS 30 to 55 kg in APS 19. Maximum fruit yield recorded to APS 19, APS 8, APS 9 and APS 2 whereas minimum in APS 30. The fruit weight varied from 11.3 g (APS 26) to 91 g (APS 8). The minimum fruit length was recorded in APS 1, APS 26, APS 28 and APS 15. Whereas maximum in APS 8 APS 9. APS 4 and APS 2. Fruit diameter varied from 2.6 cm (APS 13), 5.2 cm (APS 8). The evaluated genotypes were round, oblong, flattened and round-flat in shape. APS 5, APS 8, APS 17, APS 27 and APS 30 bear fruits oblong in shape whereas APS 3, APS 18. APS 21 are flattened in shape and APS 1, APS 7, APS 13, APS 19 and APS 22 are round-flat shaped. Symmetry along the suture was recorded, all the genotypes were symmetrical along suture except APS 4, APS 5, APS 6, APS 7, APS 19, APS 22, APS 24 and APS 28 were orange whereas APS 18, APS 20, APS 21, APS 22, APS 23 and APS 25 were orange with red blush. Maximum total soluble solids were recorded in APS 7, APS 15, APS 16 and APS 17 whereas minimum in APS 29, APS 30, APS 26, APS 18 and APS 19. Total sugars varied from 0.4 per cent (APS 30) to 15.07 per cent in APS 6 genotypes. Minimum acidity 0.07 percent was noted in APS 25 whereas maximum 1.50 per cent in APS 28. Separation of stone was noted in all the genotypes under study. Clinging stone recorded in APS 6, APS 9, APS 11, APS 12 and APS 27, whereas semi-clinging was found in APS 1, APS 4, APS 7, APS 14, APS 17 and APS 25, rest all the genotypes were of free-stone separation type. Maximum kernel weight 4.5 g/kernel was recorded in APS 8, whereas minimum 1.3 g noted in APS 19, remaining genotypes having medium weight stone. APS 12, APS 14. APS 26 and APS 28 having bitter kernel rest all the genotypes were recorded sweet in taste. The fruit maturity in apricot genotypes ranged from 20th May (APS 18, APS 19 APS 20, APS 21, APS 22 and APS 23) to 7 July (APS 25, APS 26, APS 27, APS 28, APS 29 and APS 30). The maturity time differ at different topography and

Table 1. Fruit characters of different apricot genotypes collected from Kashmir valley

Name of genotypes	Approximate yield/tree (kg)	Fruit weight (g)	Fruit length (cm)	Fruit diameter (cm)	Fruit shape	Symmetry along suture	Skin colour	TSS (%)	Total sugar	Acidity (%)	Separation of stone	Stone weight (g)	Kernel taste	Time of maturity
APS 1	35.0	25.7	3.0	3.6	RF	Sy	Y	16.1	12.0	0.16	SC	3.0	S	25-30 June
APS 2	47.33	63.0	4.8	5.0	R	Sy	Y	14.5	11.0	0.31	F	2.2	S	25-30 July
APS 3	42.2	58.4	4.7	5.0	F	Sy	Y	15.5	12.8	0.20	F	3.0	S	25-30 July
APS 4	25.0	31.0	5.0	4.6	R	Sy	0	14.2	11.4	0.10	SC	2.6	S	-do-
APS 5	27.0	43.5	4.4	4.0	ob	Sy	0	9.8	10.1	0.10	SC	2.2	S	-
APS 6	32.7	53.0	4.5	4.6	R	Sy	0	13.5	15.7	0.15	C	2.0	S	-
APS 7	27.0	32.7	3.56	3.8	RF	As	Y	21.5	13.0	0.08	SC	3.2	S	28-30 June
APS 8	51.0	91.0	6.40	5.0	ob	Sy	Y	13.5	8.5	1.0	F	4.5	S	-do-
APS 9	47.7	76.5	5.40	5.2	R	Sy	Y	10.36	13.3	0.7	C	4.2	S	20-25 June
APS 10	32.3	22.0	3.7	3.4	R	Sy	0	14.1	10.5	1.2	C	1.36	S	-do-
APS 11	22.7	31.1	3.9	3.7	R	Sy	Y	14.0	10.0	0.61	C	1.50	S	-do-
APS 12	32.0	33.0	3.5	3.8	R	Sy	Y	13.13	10.7	0.69	C	2.3	B	-do-
APS 13	35.0	17.0	3.91	2.6	RF	Sy	V	16.6	10.2	0.68	F	3.1	B	-do-
APS 14	32.7	37.0	4.2	3.8	ob	Sy	Y	12.6	10.7	1.2	SC	3.1	B	28-1 July
APS 15	23.0	40.0	3.4	3.8	R	Sy	Y	18.8	8.9	0.9	F	2.8	S	-do-
APS 16	21.0	24.0	4.1	3.1	R	Sy	Y	18.2	9.2	0.3	F	2.2	S	-do-
APS 17	35.0	46.1	4.2	4.4	ob	Sy	Y	16.6	87	0.98	SC	3.2	S	-do-
APS 18	34.0	37.0	3.8	4.2	F	Sy	Orange with red bluish	10.0	12.5	0.36	F	2.6	S	20-30 May
APS 19	55.0	27.0	3.6	3.6	RF	As	0	9.6	12.3	0.30	F	1.3	S	-do-
APS 20	32.0	21.2	4.3	3.5	R	Sy	Orange with red bluish	13.2	10.5	0.09	F	2.0	S	-do-
APS 21	31.0	37.0	3.9	4.2	F	As	Orange bluish	12.0	9.8	0.11	F	1.5	S	-do-
APS 22	36.0	37.0	4.2	4.1	RF	As	Orange & red bluish	13.0	11.5	1.1	F	2.6	S	-do-
APS 23	43.0	33.8	4.5	4.0	R	Sy	Yellow & red bluish	11.6	10.0	0.9	F	3.1	S	-do-
APS 24	35.0	32.0	4.5	4.2	R	Sy	0	11.5	9.7	0.08	F	2.4	S	30 June
APS 25	31.0	31.3	4.2	3.7	R	Sy	Orange & red bluish	12.8	8.4	0.07	SC	1.3	S	5-7 July
APS 26	26.0	11.3	3.10	3.8	R	Sy	Y	11.7	8.8	0.97	F	2.3	B	-do-
APS 27	25.0	37.1	3.18	3.0	ob	Sy	Y	13.7	11.0	0.90	C	1.9	S	-do-
APS 28	24.0	25.9	3.10	2.8	P	Sy	0	13.7	9.5	1.50	F	1.5	B	-do-
APS 29	25.0	25.5	3.49	2.9	R	Sy	Y	11.5	8.8	0.80	F	1.8	S	-do-
APS 30	20.0	26.6	3.36	2.2	ob	Sy	Y	12.5	8.4	1.32	F	1.5	S	-do-
St. Dev.	10.49	17.18	0.72	0.74	-	-	-	2.8	1.8	0.039	-	0.83	-	-
CV (%)	4.0	4.4	6.9	7.2	-	-	-	6.06	4.52	129.0	-	13.64	-	-
SEM±	1.93	2.6	0.08	0.075	-	-	-	0.69	0.23	0.16	-	0.11	-	-
LSD(P=0.05)		3.87	5.22	0.17	0.15	-	-	-	1.4	0.46	0.33		0.23	-

Where R : Round, ob : oblong, AS : Asymmetrical, Sy : Symmetrical, F : Free stone, SC : Semi-clinging, C : clinging, S : sweet, B : Bitter

microclimatic conditions. The fruits from Uri region mature earliest whereas apricot from Srinagar and adjoining areas matured late, in Ladakh and Kargil region they started ripening from August onwards (Bhat *et al.*, 2002). The present investigator concluded that a wide range of variability existed in apricot population in Kashmir valley. *Prunus dasycarpa* Ehrh is said to be grown in Kashmir and is considered to possess considerable variability (Wealth of India, 1969). The reason for variation in yield and quality attributes may be due to the tree having variable genetic constitution and agro-climatic conditions. The wide range of variation with regard to quality attribute have also been reported in different regions of the apricot growing areas (Zaffar *et al.*, 2004); Bhatia *et al.*, 1977; Bhat *et al.*, 2002).

Promising genotypes, viz, APS 2, APS 6, APS 7, APS 8, APS 9, APS 19 have been planted along with other recommended and standard varieties of apricot for further study.

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SHORT COMMUNICATION

Sprouting, Growth and Seed Production in Amaranth (*Amaranthus* spp.) Germplasm after Frost

RS Rathi, HL Raiger, BS Phogat and RP Dua

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

Key words: Amaranth, Germplasm, Frost

Amaranth is a crop with multiple uses as food, fodder, medicine and oil. It is grown both in tropical and temperate regions from sea level upto an altitude of 3000 masl. *Amaranthus hypochondriacus*, *A. cruentus*, *A. caudatus* and *A. edulis* are the main grain species while *A. dubius*, *A. bilitum*, *A. viridis* and *A. tricolor* are largely grown for vegetable. *A. hybridus* is used both for vegetable and fodder production (Joshi and Rana, 1991).

Sixty six accessions of recently collected amaranth germplasm were grown for agro-morphological characterization and evaluation at the research farm of National Bureau of Plant Genetic Resources located in Indian Agricultural Research Institute, New Delhi. The crop was sown during October 2005 in Augmented Block Design (Federer, 1956) in seven unequal blocks alongwith three check varieties, namely, Annapurna,

GA-1 and GA-2. Each accession was sown in three rows of 3m length spaced 45 cm apart. Thinning was done 20 days after sowing and a plant to plant distance of 15 cm was maintained.

Three unprecedented spells of frost during the first fortnight of December 2005 (Fig. 1) at vegetative stage severely damaged the crop of amaranth. However, 12 accessions of amaranth showed sprouting 58 days after sowing. The performance of these 12 amaranth accessions with respect to 14 agro-morphological descriptors/descriptor states is discussed in this communication.

The variability observed for different traits is presented in table 1. Plant height was observed to range from 38 cm to 105 cm with the check variety GA-2 exhibiting maximum value (105 cm). Similarly, the number of branches per plant varied from 1.0 to 8.2 and none of the germplasm lines was observed to be more profusely

Table 1. Variability observed in amaranth germplasm for different descriptors/descriptor states

Accession No.	Plant height (cm)	Nos. of branches/plant	Leaf length (cm)	Leaf width (cm)	Days to taken for sprouting	Days to flower after sprouting	Days to 50% flowering	Petiole length (cm)	Panicle colour	Panicle length (cm)	Days to maturity	Seed yield/ plant (g)	Seed yield/ plot (g)
EC519522	64.50	4.50	7.60	4.40	58	31	41	4.80	Green	53.50	98	–	–
EC519526	67.20	3.60	8.20	4.80	58	32	41	3.60	Green	50.00	108	–	–
EC519558	68.00	5.00	12.10	6.70	58	57	73	7.30	Green	47.00	112	–	–
IC415224	58.00	2.80	3.80	1.80	58	51	62	2.40	Redish	30.80	95	–	–
IC415271	57.00	2.40	4.50	2.30	58	52	62	6.00	Yellowish green	25.00	106	–	–
IC423400	65.75	4.50	9.44	5.42	58	32	45	5.77	Greenish yellow	45.75	100	12.00	355.00
IC444190	42.80	3.00	5.30	2.70	58	52	62	3.00	Yellowish green	30.00	103	–	–
IC444193	38.00	4.00	4.20	2.40	58	53	63	1.60	Red	29.00	107	–	–
SM/BC-12	56.50	2.80	3.50	1.93	58	52	64	2.30	Redish	20.00	106	–	–
Annapurna (C)	42.00	1.00	4.40	2.20	58	54	62	2.20	Yellowish green	25.00	94	–	–
GA-1 (C)	65.00	1.00	9.40	3.60	58	54	62	5.00	Yellowish green	36.00	101	–	–
GA-2 (C)	105.00	8.20	11.40	5.46	58	52	65	8.06	Red	57.00	110	30.00	315.00
Minimum	38.00	1.00	3.50	1.80	58	32	45	1.60	–	20.00	94	–	–
Maximum	65.75	4.50	9.44	5.42	58	54	64	6.00	–	45.75	107	–	–
Mean	51.44	2.93	5.02	2.68	58.00	49.43	60.00	3.32	–	29.36	101.57	–	–

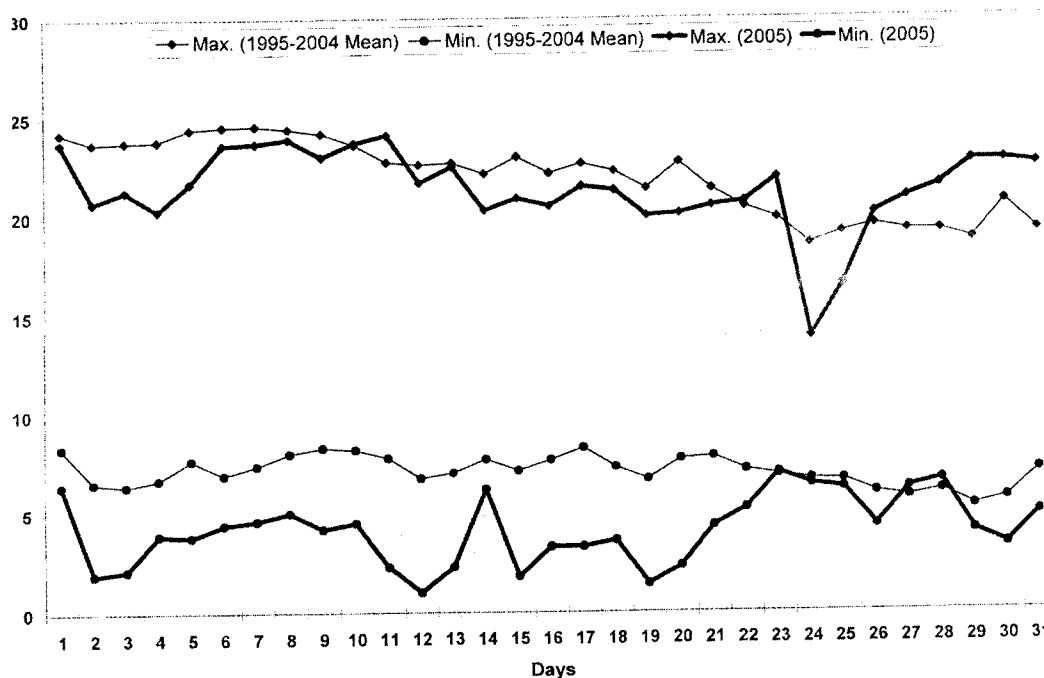


Fig. 1: Maximum and minimum temperature (°C) during December

branched than GA-2. Initiation of flowering was recorded between 31 days (EC519522) and 57 days (EC519558) after sprouting. The early flowering lines were EC519522, IC423400 and EC519526. The range for panicle length was 20-57 cm and genotypes GA-2 (57 cm) and EC519522 (53.5 cm) had more panicle length than the other germplasm lines. Seed production was observed in only two accessions i.e. IC423400 and GA-2. In GA-2 also, seed production was observed in only one block out of the seven blocks, which was probably due to the effect for a tall tree nearby. GA-2 was observed to produce more seed per plant (30 g/plant) as compared to IC423400 (12 g/plant) while on the other hand, IC423400 produced

more seed per plot (355 g) than GA-2 (315 g).

The accession IC423400 was *A. caudatus*, which has been reported to be resistant to chilling (Phogat and Sharma, 2000).

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BOOK REVIEW

Trees of Delhi – A Field Guide by Pradip Krishan

Publisher: Dorling Kindersley (India) Pvt. Limited, Delhi, 2006; Price: Rs. 799/-

'Trees of Delhi' is a well-illustrated book covering 252 tree species found in Delhi and surrounding areas, both native ones and those grown in gardens and as avenue trees. This book is definitely a field guide, with species arranged by the shape of leaves, a prominent feature by which trees can be identified whether they are in bloom or not by amateurs and professionals. The book, replete with well-reproduced photographs, with its compact binding and easy-to-carry size makes it ideal for field use.

The book has three chapters: an introduction, the tree guide, which constitutes the main body of the book and, a last part, titled the Back of the book. Introduction gives information on Delhi and its history and environs besides providing a guide to the use of the book for identification. The landscape views included in the text definitely brings to memory places seen during collection trips on the Ridge and while driving down Delhi roads lined with magnificent avenue trees. The maps of Delhi as it was, in particular those depicting the original Ridge and the gardens, bring to life the romance of historic Delhi. One finds good learning (and teaching) material in the diagrammatic depiction of the Ridge, photo of Mangarban forest and other items relating to the study and identification of the trees. The text echoes the feelings of frustration one faces when searching for the correct scientific name of plants: "Learning the scientific names is hard enough- keeping up with the changes can be teeth-gnashingly frustrating."

The chapter on Tree Guide is arranged according to common names of plants. This is probably easier for the amateur but frustrating for the professional who has to keep checking back to the index for the appropriate Latin name. However, the book ensures familiarity to the common names of trees, one aspect which needs to be encouraged among botanists. Shape of leaf is the major trait used to group the trees into ten sections. Moreover, the trees have been linked to the family they belong to by a commonly known tree of the family, viz. Amla/Castor for Family Euphorbiaceae, Ber for Family Rhamnaceae, Mehndi for Family Lythraceae and so on. It is a good scheme to ensure that the amateur uses the

book without getting intimidated by too many Latin names and taxonomic rules. The arrangement and layout of the information regarding each tree is also pleasing. Photographs are included that are appropriate for the identification of the tree that is being described. Also valuable information on related and similar trees is provided where required to ensure correct identification. A gold-mine of information is provided in the most useable manner in the portions dealing with How to distinguish between Delhi's fig trees, How to distinguish between Delhi's *Cassia* and *Senna* trees, A key to Delhi's spiny mimosas and others. Information on locations where one may find the tree makes this a valuable asset for the serious tree-hunter.

The final chapter provides twenty-one pages of enjoyable reading on various trees described in the book and related ones. Flowers of the fig and their pollination mechanisms are described in over two and a half pages. The scientific logic behind calling Krishna fig a variety of the Indian banyan tree, *Ficus benghalensis* is described. Details of the distinguishing characteristics of varieties of frangipani (*Plumeria*) are given here. The relief is enormous in knowing that *Maytenus senegalensis* continues to be called by the same name as when one studied it during botanizing trips to the Delhi Ridge. This part of the book also has the indices of the families and the scientific names of the trees written at their scientific best (along with author's names). Hence, all aspects of the trees of Delhi which are interesting and important for full appreciation of their diversity have been included in these pages, thereby keeping the Tree Guide clutter-free.

This book evokes pleasurable memories of walks in the Ridge during student days. It helps one to appreciate the trees of Delhi in general and those of the Ridge in particular. This book could be used to initiate a nature conservation movement on the Ridge, and other green areas of the Delhi region. Children and adults could be initiated into the botanical and nature lore of the region through walks in set tracks in place of the forbidding caution notices put up by the Delhi Forest Department along the protected areas of the Ridge.

Trees of Delhi and the author's comments have been widely publicized through major dailies following the release of the book. The initial demand for the book was high, so much so that one had to wait for a month to lay hands on a copy. This review, however, is from the point of a professional botanist. The precursor to this publication, *The Flora of Delhi* by Dr JK Maheshwari (published in two volumes between 1963 and 1966) was the outcome of a Ph D thesis from the Botany Department of the University of Delhi and has given a lot of satisfaction during botanizing trips. *Trees of Delhi* deal with a prominent part of the Flora of Delhi and serves

to satisfy both the layman and professional. Last but not the least, the author has requested feedback; I intend to do so to ensure that in the follow-up publication, probably of the trees of India the author again succeeds in deciphering botany and its jargon and present it in a more palatable and enjoyable manner.

E Roshini Nayar

*Division of Plant Exploration and Germplasm Collection
National Bureau of Plant Genetic Resources
New Delhi-110 012*

Forthcoming Publication

Lab Manual in Biochemistry, Immunology and Biotechnology by *Arti Nigam and Archana Ayyagari*
(Being published from Tata McGraw-Hill Publishing Company Limited, New Delhi, likely to out in 2007)

Although scattered literature is available that covers exercises in Biochemistry, Immunology and Biotechnology but there has been a conspicuous requirement for a book that imparts knowledge on principles, protocols, methodologies and applications of techniques accurately and in a user-friendly style.

Drs Arti Nigam (Reader, Institute of Home Economics) and Archana Ayyagari, (Reader, Swami Shraddhanand College) of University of Delhi ventured to produce to the point principles, clearly stated protocols, important precautions, lucid flow charts, authentic pictures in this reliable and user-friendly laboratory manual that will fit well to the requirements of the students, teachers and researchers in the field of biotechnology, biochemistry and immunology.

The book begins with basic and fundamental exercises in biochemistry such as the concept of buffers, pH, spectrophotometry etc. while it ends with the most

sophisticated protocols of cloning and expression of foreign genes, southern blotting, and PCR. Special attention has been paid in defining the fundamental concepts. The book has been structured in 10 sections. Section I to V deals with the main techniques of biochemistry and clinical biotechnology, cell biology and enzymology. Section VI presents all the important concepts and latest techniques of immunology. Section VII to X deals with some advanced exercises of biotechnology. It also contains aspects of isolation and cultivation of microbial and eukaryotic viruses, methods of direct gene transfer, mutagenesis and recombinant DNA technology.

This book will not only be beneficial to the students, teachers and researchers of biochemistry, microbiology, immunology, genetics, and biotechnology, but also to those belonging to other related disciplines.

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