REVIEW PAPER

New Seed Bill 2004 – Issues and Analysis

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This paper focuses on the new Indian Seeds Bill 2004 which aims to regulate the seed market and ensure seeds of quality. It discusses the proposed changes in this new bill, i.e., making the registration of cultivars obligatory, creating a National Register of seeds, regulating the import and export of seeds, accommodating new regulations on genetically modified crops, and improving market conditions for private seed companies, as well as its effects on both farmers and seed producers. Various issues related to the bill has been thoroughly discussed, discrepancies sorted out and changes suggested. In addition, the history of Indian seed regulation and seed laws in selected Asian countries are enumerated.

Key words: New Seed Bill, Seed Act, PPV & FR, WTO, IPR

The question arises as to what was the need for such a bill to come into existence. For this, it is essential that the history of Indian seed regulation be briefly looked into. Two decades after India's independence, during the 1960s, the formal seed sector in India was dominated by the Public sector. It was in 1961 that the National Seeds Corporation (NSC) was established under the Ministry of Agriculture and was at the centre of seed production of breeders, foundation and certified seeds and their quality control. In furtherance of their control in the seeds sector, the National Seeds Project (NSP) was undertaken by the Indian Government in 1967 with the assistance of the World Bank. The National Seeds Project set up seed processing plants in 17 states to provide 'certified' seeds of food crops, mainly self-pollinating crops, to farmers but they have not proved to be efficient. The private sector also has not proved much more efficient for the cultivator or for the consumer. This led to the National Seed Policy of 1988, which involved a US $ 150m loan from the World Bank to help privatize the Indian Seed Industry. At this time, the import of seeds was still restricted but this sector was gradually opened up, to allow more private participation. Further, after India signed the GATT agreement and joined the WTO, these agreements required that India should make some changes to its law, especially regarding Intellectual Property Rights. These requirements were met through the Protection for Plant Variety and Farmers' Rights Act, 2001. In 2002, a new National Seed Policy was released, and as mentioned above, to meet the goals of this policy the new Seed Bill was drafted and tabled in the Parliament in 2004. The objective of the new seed policy seems to be to reduce the direct involvement of government in seed production and marketing, and to actively encourage the private sector to engage in research and development of new varieties. One of the stated aims of the National Seed Policy, 2002 was to encourage more private participation in agriculture and seed production, specifically, to complement the existing structures and to replace them, when necessary. Liberalization has been targeted towards certain components of national seed policies, retaining regulation of some components to safeguard national interests. Public and private sectors need to complement each other, perhaps on the basis of a division between cash crops and essential food crops. It is a fact that neither the private nor the public sector can fulfill India's agricultural requirements by itself. Only effective cooperation and coordination will allow farmers to have access to quality seed and thus contribute to sustainable agriculture and food security. Based on the changes that have taken place in the seed sector since 1966, the existing Seeds Act, 1966 is proposed to be replaced by a suitable legislation. Over the years, the following deficiencies have been noted in the existing Seeds Act:

- registration of seed variety not compulsory
- non-notified varieties are not covered
- commercial crops and plantation crops are not covered
- certification only through State Seed Certification Agencies and
- no provision for regulation of transgenic materials.

The National Seed Policy, 2002 clearly identifies the twin aims of encouraging the seed industry, especially the domestic industry and of ensuring maximum prosperity

and security for farmers. A number of the National Seed Policy's recommendations have been addressed in the Protection of Plant Varieties and Farmers' Rights Act, 2002, including the establishment of a National Gene Fund and a Plant Varieties' authority to regulate the quality of seeds in the country. Meanwhile the World Bank continued to fund other seed projects intended to increase the production of green revolution varieties, to coordinate the efforts of the State Farms Corporation of India (SFCI) and emerging private companies and in addition to create and modify the infrastructure for seed testing, research and certification. At this time, there were relatively few private companies involved with seeds (mainly small enterprises confined to the production of some vegetable and ornamental flower seeds) and government policies focused on the public sector with limited private-sector participation. The further aims of the National Seed Policy that include building up infrastructure, ensuring good quality of seeds and facilitating international trade in seeds, are sought to be addressed through the proposed Seeds Bill, 2004.

The Seed Bill, 2004

The revision of existing Seeds Act is proposed to:

- overcome its present deficiencies,
- create facilitative climate for growth of seed industry,
- enhance seed replacement rates for various crops,
- boost the export of seeds and encourage import of useful germplasm, and
- create conducive atmosphere for application of frontier sciences in varietal development and for enhanced investment in research and development.

The preamble of the bill makes clear its intention. The Bill states that it is to "provide for regulating the quality of seeds for sale, import and export and to facilitate production and supply of seeds of quality and for matters connected therewith or incidental thereto". The New Seeds Bill makes an attempt to regulate the Indian seed trade in tune with current realities. This Bill is notable for the following major differences with the old Seed Act. The Bill stipulates compulsory registration of all seeds traded in India; this is not required under the old Act, which allows sale of Government notified and `truthfully labelled' varieties with voluntary seed certification. Truthfully labelled means the seed is guaranteed by the seller for the prescribed minimum standards. The Bill requires compulsory State level registration of seed producer, processing unit and trader; the old Act insists only on a license for trading. The Bill will introduce compulsory registration of nurseries selling horticultural plants. The duration of registration is 15 or 18 years, with provision to double this term. Under the old Act it is 15 years for notified varieties and open-ended for `truthfully labelled' varieties. Only the Central and State seed testing laboratories could offer seed certification under the old Act; accredited individuals or institutions will be allowed to under the new Bill. Seed certification is mandatory in the new Bill and it allows self-certification. It also introduces a National Register of Seeds and seeks to centralize registration by abrogating the authority of States to approve regional varieties. Enforcement is largely left to the old administrative set-up, which earned notoriety for inefficiency and corruption (Bala Ravi, 2005).

Rationale for the Seed Bill

The new seed bill is a tool to address the grievances and the concerns which the Seed Bill of 1966 does not cover. Even though a large majority of our population depends on agriculture for their livelihood, agriculture in India remains relatively unproductive. A need was felt for using new techniques and methods to increase the productivity of Indian agriculture. At the same time the Biotechnology sector came up with promises of extremely productive Genetically Modified (GM) Crops. These new scientifically manipulated crops caught the imagination of the Indian Government, and to some extent, that of farmers as well. It is believed that this new technology has the potential to improve living standards by the commercialization of such GM crops. The major rationale behind the policy is the hope that these developments would provide Indian farmers multiple choices and increased access to improved seeds. As such, the Seed Bill 2004 also seeks to address the concerns of the Seed Industry. The Seed Association of India and the Association of Seed Industries raised certain demands at the National Seeds seminar organized by them in 2005. They demanded a level playing field for the private sector, for subsidies and support to the private sector for R&D. Another major demand was that seeds be taken out from the purview of the Consumer Protection Act, 1986 and that a scientific system of scrutinizing claims, along with a system of crop insurance, should be developed to study the causes of crop failure. While the Seeds Bill, 2004 does take care of the infra-structural demands but it retained the right of the farmer to go to the Consumer Courts under the Consumer

Protection Act, 1986. One cannot be sure if, in the present situation in India, where a majority of farmers are not only small landholders, but they are also illiterate and/or uneducated, a system of crop insurance can work to their advantage. It was in this atmosphere that the National Seed Policy was formulated in 2002 with the National Seed Bill being drafted in 2004 (Saggi Naiyya, 2006).

Highlights of the Bill

Agricultural growth in India averaged just 2.8% per annum during the period of 1991-2005, much lower than the average annual GDP growth of 6.2% during this period. Given that about two-thirds of the country's population is dependent on farm related income, increasing agricultural growth rate will be beneficial not just for the country's food security but also for improving the livelihood of a large proportion of the population. Availability of good quality seeds to farmers is a necessary condition for boosting agricultural output. Currently, the seed sector is governed by the Seeds Act, 1966, the Seeds Control Order, 1983 (under the Essential Commodities Act, 1955), and the Protection of Plant Varieties and Farmers' Rights Act, 2001 (PPV & FR Act). The Seeds Act, 1966 regulates the quality of certified seeds; the Seeds Control Order, 1983 regulates and licenses the sale of seeds; and the PPV & FR Act protects the intellectual property rights of plant breeders (Madhavan and Sanyal, 2006). The highlights of the proposed Seeds Act are as under:

- The Seeds Bill, 2004 aims to regulate the quality of seeds sold, and replaces the Seeds Act, 1966.
- The Bill does not restrict the farmer's right to use or sell his farm seeds and planting material, provided he does not sell them under a brand name. All seeds and planting material sold by farmers will have to conform to the minimum standards applicable to registered seeds.
- If a registered variety of seed fails to perform to expected standards, the farmer can claim compensation from the producer or dealer under the Consumer Protection Act, 1986.
- Accreditation of ICAR centers, State Agricultural Universities and Private Organizations to conduct agronomic trials.
- Every seed producer and dealer, and horticulture nursery has to be registered with the state government. All varieties of seeds for sale have to be registered. The seeds are required to meet certain prescribed minimum standards.
- Maintenance of National Register of varieties.
- To regulate the export and import of seeds.
- Enhancement of penalty for major and minor infringement.
- Inclusion of provisions to regulate GM crops and ban on terminator seed.

Issues and Analysis

The Seeds Bill 2004 may be seen in the context of the Seeds Act, 1966 which it replaces, and the PPV & FR Act, 2001. The main objective of the Seeds Bill is to ensure availability of quality seeds to farmers. The proposed Bill seeks to update the existing Act in order to address changes in technology and the structure of the seeds sector. The PPV & FR Act sets up a framework to protect the intellectual property rights of breeders, while safeguarding the rights of farmers (Madhavan and Sanyal, 2006). Main changes in the Seeds Bill 2004 from the Seeds Act, 1966 are:

- Some provisions of the Seeds Bill, 2004 contradict and overlap with the Protection of Plant Varieties and Farmers' Rights Act, 2001 (PPV & FR Act).
- Although farmers are exempt from registering their seed varieties, the seeds have to conform to standards prescribed for commercial seeds. Farmers may find it difficult to adhere to the standards required of commercially sold seeds.
- Compensation for underperformance of seeds will be governed by consumer courts. This provision is unlike the PPV & FR Act, which allows compensation to be decided by the Authority established under that Act.
- Seed inspectors can take samples from anyone selling purchasing or transporting seed. They have the power of search and seizure without a warrant.
- It is not clear whether the Bill bans certain genetic engineering technologies such as 'genetic use restriction technology' and 'terminator technology.' These technologies preserve intellectual property rights by either requiring specific additives, or by making the next generation seeds sterile

A comparison between Seed Bill 2004 and Seed Act 1966 is given in Table 1 (Madhavan and Sanyal, 2006). There are several contradictions and overlaps occur between the PPV & FR Act and the Seeds Bill, 2004 (Table 2).

Protection of Farmers' Rights

This Bill exempts a farmer from compulsory registration of seed varieties in order to use, exchange, share or sell his farm seeds or planting material. However, it stipulates that he cannot sell any seed under a brand name. Also, any seed sold by a farmer has to conform to the minimum limits of germination, and physical and genetic purity as applicable to commercially sold seeds. This last proviso (minimum standards of germination and purity) could be difficult to implement. It is estimated that seeds saved and exchanged by farmers constitute above 80% of the seeds planted, and there would be a need to establish the physical infrastructure required to test these. Such testing would also lead to an increase in the cost of seeds (Madhavan and Sanyal, 2006).

- In contrast, the PPV & FR Act, 2001, only restricts the farmer from selling branded seed. There is no other requirement for a farmer to sell seeds. The exemption clause given in the PPV & FR Act is easier to implement.
- The farmer has to approach the Consumer Courts to claim compensation if the seeds do not perform to expected levels. There is a contradiction between this provision and the PPV & FR Act which permits farmers to claim compensation through the Authority set up under that Act. Given the number of factors (such as climate, fertilizer, water) that affect the performance of a crop, it may be difficult to prove that underperformance of a crop was on account of poor quality of seed. Indeed, there have been recent cases where the issue has not been fully resolved. Furthermore, it is not clear whether the compensation would include the value of the crop or only the cost of the seed.

Registration and Certification

- Only those varieties of seeds that are registered may be sold. The Bill does not clarify whether a seed producer may sell seed which is registered by a different producer. The absence of a non-exclusivity requirement could lead to a monopoly

Table 1. Comparison of Seed Bill 2004 and Seed Act 1966*

	Seed Bill 2004	Seed Act 1966
Definition	'Agriculture' includes horticulture, forestry, cultivation of plantation, medicinal and aromatic plants.	'Agriculture' includes horticulture.
	Definitions of "Seed" and "Variety" have been changed to make them more specific and technical.	
	Defines terms such as "Dealer", "Essentially Derived Variety", "Extant Variety", "Farmer", "Horticulture Nursery", "Misbranded", "Spurious Seed", and "Transgenic Variety".	Does not define these terms
Registration	All seeds for sale must be registered.	Only varieties notified by the government need to be registered.
Seed Committee	Constitutes Central and State Seed Committees. A Registration Sub-Committee would register seeds of all varieties.	Constitutes Central Seed Committee. The central government, after consulting with the CSC, may notify a seed in order to regulate the quality of seed.
Transgenic Varieties	Special provisions for registration of transgenic varieties of seeds.	No provision for transgenic varieties of seeds.
Compensation to Farmers	Provides for compensation to farmers under the Consumer Protection Act, 1986 in the event of under performance of seeds.	No specific provision for compensation mentioned in the Act.
Export and Import	All seed imports are regulated by the Plant Quarantine (Regulation of Import into India) Order, 2003 or any corresponding order of the Destructive Insects and Pests Act, 1914; shall conform to minimum limits of germination etc. Exports can be restricted if it adversely affects the food security of the country.	A person is restricted from exporting or importing notified variety of seed unless it conforms to minimum limits of germination etc.
Penalties	Any person who contravenes any provisions of the Act or imports, sells or stocks seeds deemed to be misbranded or not registered, can be punishable by a fine of Rs 5,000 to Rs 25,000. The penalty for giving false information is a imprisonment up to six months and/or a fine up to Rs 50,000.	Any person who contravenes any provisions of the Act, prevents a Seed Inspector from taking samples etc. shall shall be punished for the first offence with a fine which may extend to Rs 500. If the offence is repeated he may be imprisoned for a maximum term of six months and/or fined up to Rs 1,000.

* Madhavan and Sanyal (2006)

Table 2. Comparison of Seeds Bill, 2004 and PPV & FR Act, 2001*

	Seed Bill 2004	PPV & FR Act 2001
Definitions	"Farmer" means any person who cultivates crops either by cultivating the land himself or through any other person but does not include any individual, company, trader or dealer who engages in the procurement and sale of seeds on a commercial basis.	"Farmer" means any person who cultivates crops by cultivating the land himself or cultivates crops by directly supervising the cultivation or land through any other person; or conserves and preserves, severally or jointly, with any other person any wild species or traditional varieties or adds value to such wild species or traditional varieties through selection and identification of their useful properties.
Registration	Establishes a Registration Sub-Committee, which would maintain a National Register of Seeds. No specifications regarding parentage of variety. Registration is for 15 years for annual/biennial crops and 18 years for long duration perennials. On expiry, registration can be renewed for a similar period.	Establishes a Plant Varieties Registry, which would maintain a National Register of Plant Varieties. Specifies details under which a variety may be registered such as a complete passport data of the parental lines from which a variety has been derived. Registration is for 15 years for annual/biennial crops and 18 years for long duration perennials. Registration cannot be renewed.
Farmers' Rights	A farmer can save, use, exchange, share or sell his farm seeds and planting material. He cannot sell seeds under a brand name. Seeds sold have to conform to the minimum limit of germination, physical purity, genetic purity prescribed by the Act.	A farmer is entitled to save, use, sow, resow, exchange, share or sell his farm produce including seed of a variety protected under the Act in the same manner before this Act came into force. He cannot sell branded seed of a variety protected under the Act.
Compensation	The seed producer, distributor or vendor will have to disclose the expected performance of a particular variety of seed under certain given conditions. If the seed fails to perform to expected standards, the farmer can claim compensation from the dealer, distributor or vendor under the Consumer Protection Act, 1986.	If a breeder of a propagating material of a variety registered under the Act sells his product to a farmer, he has to disclose the expected performance under given conditions. If the propagating material fails to perform, the farmer can claim compensation in the prescribed manner before the Protection of Plant Varieties and Farmers' Rights Authority.
Penalties	Any person who contravenes any provisions of the Act, prevents a Seed Inspector from taking samples etc. shall be punished for the first offence with a fine up to Rs 500. If the offence is repeated he may be imprisoned up to six months and/or fined up to Rs 1,000.	Penalty for applying false denomination to a variety is imprisonment up to two years and/or a fine between rupees 50,000 and rupees five lakh. Penalty for falsely representing a variety as registered is imprisonment up to three years and/or a fine between rupees one lakh and rupees five lakh or both. Penalty for subsequent offence is imprisonment up to three years and/or a fine between rupees two lakh and rupees twenty lakh.

* Madhavan and Sanyal (2006)

on existing and common varieties by the first mover on any registration. Issues regarding intellectual property rights may be addressed through the provisions of the PPV & FR Act.

- The Bill leaves it to regulations to specify the information that an applicant has to furnish, such as data about the source and geographical origin, in order to register a seed variety. It might lead to a situation where seeds could be registered without disclosing the parentage or origin of the seed. Although the PPV & FR Act, 2001, makes it mandatory for the applicant to issue specific details about the parental lines of a variety, it is not clear which legislation would take precedence in case of conflict. In such a case, an applicant might be able to register a variety of seed which has traditionally been used by a farmer (i.e., farmers' variety). The Bill also does not have the provision of benefit-sharing as mentioned in the Convention on Biological Diversity and the PPV & FR Act, in which case any applicant can register and use a farmer's variety of seed without compensating the farmer.
- The Bill does not provide for a mechanism to trace back a packet of seed to the dealer, processor and producer. Also, there is no specification of quality assurance systems. This would make it difficult to trace back a defective lot, and rectify any deficiencies in the supply chain.
- The Bill forbids the use of any technology that may be harmful or potentially harmful, and includes 'genetic use restriction technology' and 'terminator technology' in the definition of 'technology'. It is

not clear whether both these technologies are explicitly banned in this Bill. A farmer planting seeds containing terminator technology cannot use the seed from his crop for the next generation, and has to purchase new seed every season. The PPV & FR Act, 2001 does not permit registration of any variety containing terminator technology.

- Seed producers would be permitted to self-certify the performance of their seeds under certain conditions. The seed companies need to provide the results of multi-locational trials before registration. This opens up the possibility of false declaration by seed companies. To prevent this, there could be a case for allowing only government agencies to conduct these trials and grant certification.

Horticulture Nurseries

- Every horticultural nursery has to be registered with the state government and has to maintain records of layout plan, source of every planting material etc. The argument is that performance of horticultural planting material (such as mango) is known only after a number of years, and these trees are harvested for a number of years. The investment and risk for the farmer is significantly higher than in the case of one-season grain, and this justifies stricter norms. That said, nurseries in the unorganized sector may find it difficult to adhere to these conditions.

Role of Seed Inspectors

- The Seed Inspector has the power to enter and search as well as break open container or break open doors, without a warrant. This is different from the provisions under the Code of Criminal Procedure, 1973 under which a warrant signed by the district magistrate, sub-divisional magistrate or first class magistrate is necessary for search and seizure.

Penalties

The penalty for selling substandard seeds is between Rs. 5,000 and Rs. 25,000. This may not prove to be a deterrent for a large seed company but which may be significant for a farmer or a small dealer.

Bill is Facing Controversy

The National Seeds Bill 2004 has provoked great controversy. It was referred to the Standing Parliamentary Committee on Agriculture, after being introduced in the Rajya Sabha in December 2004 which sought responses from all stakeholders. A modified version is expected to get back to the Rajya Sabha. The current draft describes the bill as one *"to provide for regulating the quality of seeds for sale, import and export and to facilitate production and supply of seeds of quality and for matters connected therewith or incidental thereto"*. The draft bill also appears to have an express objective of increasing private participation in the seed trade in the country and to liberalize imports of seed and other planting material into the country, ostensibly to meet WTO commitments. The bill then goes on to propose various mechanisms and modalities by which regulation of seed would happen – compulsory registration of all seed varieties; certification not just by State Seed Certification agencies but by accredited agencies outside the government too; inclusion of commercial crops and plantation crops too into the purview of the Bill; provisions for regulation of transgenic material; slight increase in penalties for contravening the law and so on.

Control from Farmers to Seed Companies

Indian agriculture is mainly run by seed saved from farmers' own fields, very often by women in farming communities who use their traditional knowledge and skills in selecting and saving seed. Nearly 75 per cent of the seed required for Indian farming is estimated to be created by farmers themselves in this manner. When it comes to seeds, Indian agriculture has seen and continues to witness a variety of roles that farmers perform. While some farmers and farming communities have been breeders of seed varieties, most farmers are seed producers in that they save seeds from their own crop to be re-used. Many farmers also engage in seed exchange and thereby meet their varied needs. Farmers are also consumers as they buy seeds from companies and traders. Activists have been fighting for the apriori rights for indigenous communities and their seed resources, especially outside an IPR framework. A few such rights were recognized in the Convention on Biological Diversity (CBD) and laws flowing from it. Farmers' rights as breeders in particular accrue from the CBD and the Indian legislation based on that - the Biological Diversity Act. These are also enshrined in the Protection of Plant Varieties and Farmers' Rights Act (PPV & FR), which was evolved using the *sui generis* clause of TRIPS, the WTO instrument. It is this legislation which also recognizes the rights of farmers as seed users and seed buyers. However, this is a scenario that is fast changing. Governments are urging farmers to increase seed replacement rates 'for higher productivity', with seed

corporations using technological, institutional and legal means to increase their markets. The objective seems to be to make farmers seed consumers wherein they depend on external sources for their seed. Within the formal seed sector, the role of the public sector in seed development, production and supply is rapidly decreasing with the private sector taking over (Sahai, 2002).

Why this Bill now?

- Seeds in Indian agriculture are governed by nearly thirty legislations – the Seeds Act 1966; the Essential Commodities Act, 1955; the Biological Diversity Act, 2002; Plant Varieties Protection and Farmers' Rights Act, 2001; Patents Amendment Act, 2005; Environment Protection Act, 1986; Consumer Protection Act, 1986; Geographical Indication of Goods Act, 1999; The Plants, Fruits and Seeds (Regulation of Import into India) Order, 1989 and so on. While some of these legislations are meant to regulate the formal seed sector and ensure that adequate and good quality of seed is supplied to farmers, others are related to ownership rights over seed resources. These are rights which seek to recognize the parentage of certain varieties and based on that, bestow certain exclusive marketing rights to the 'developers' of the seed (breeders' rights).
- The Plant Varieties Protection and Farmers' Rights Act expressly talks about farmers' rights in connection with seed even as it talks about breeders' rights. A legislation like the Consumer Protection Act 1986 is supposed to uphold the rights of farmers as consumers of inputs like seed, fertilizers, pesticides.
- The seed industry itself has grown rapidly and changed its profile substantially after the articulation of the National Seeds Policy of 2002 and prior to that, the New Policy on Seed Development in 1988. Legislations which have been enacted in recent times only work within an IPR framework to the advantage of seed companies, including the PPV & FR Act. Farmers' rights are more and more defined only in terms of residual rights, after rights to seed corporations are ensured.
- Private capital, including that of foreign seed companies, began to flow in even as mushrooming of several small Indian seed companies happened since the late 1980s. As the seed production and supply chain lengthened in terms of distance as well as number of players in the chain, the need for regulating the seed trade became more urgent and important. In this context, the existing Seed Act 1966 as well as the Seeds Control Order 1983 were found to be inadequate in regulating seed trade and ensuring provision of high quality seed. There are many reasons for this.
- The Seeds Act of 1966 is a legislation meant 'to provide for regulating the quality of certain kind of seeds for sale' and for matters connected therewith. The Act seeks to regulate quality of seed by first laying down minimum standards and then requiring all seed marketers to conform to such standards. The mark or label of the seed should indicate that the seed conforms to such minimum limits. No person can sell, offer for sale, keep for sale, barter or otherwise sell any seed of any notified variety unless the seed is identifiable to its kind or variety, that the seed conforms to the minimum standards and that the container of the seed bears in the prescribed manner the mark or label indicating the standards of the contents inside.
- The implement this law, there is an elaborate institutional set up (apart from the Central Seeds Committee and the Seed Certification Agencies) in the form of Central and State Seed Testing Laboratories, Seed Analysts and Seed Inspectors through which regulation towards good quality seed is sought to be achieved. A person upon conviction for contravention of the provisions of the Act could be punished for the first offence with fine which may extend to five hundred rupees and for subsequent offences with imprisonment for a term which may be up to six months or with fine which may extend to one thousand rupees or with both.
- While the Seeds Act 1966 might have met the regulation requirements in the situation that existed during that period, in the current situation, this legislation and its provisions are grossly inadequate. Today, the Indian seed industry has an annual turnover of about forty billion rupees. As the seed sector grew, the scope for more and more unscrupulous elements to enter the picture increased.

Incompatibility with other legislations and impact on Farmers' Rights

- The "registration" of plant varieties under the Seeds Bill is likely to create a parallel system to the PPV & FR registrations and create much confusion,

because the PPV & FR Act also allows for rights through "registration".

- The Seeds Bill has to resolve both contradictions in concepts and objectives as well as operationalisation conflicts with other laws.
- The Seeds Bill allows for "Registration" of seed varieties without first resolving issues related to parentage/origin of seed while granting rights of commercialization. The Bill could lead to a situation where plant varieties could be registered by anyone without the obligation of disclosure of origin or without prior informed consent. Ownership/parentage in the context of IPRs could then be claimed by the legitimization provided by the Seeds Bill. This would lead to biopiracy and would constitute a clear infringement of farmers' rights as breeders since all varieties that exist now have their origin in farmers' varieties. Once *de facto* breeder rights are appropriated, private interests could obtain exclusive marketing rights. In fact, exclusive marketing rights could be extended endlessly, given the provisions in the Bill.
- Unlike in the PPV & FR Act, this Bill also has no provision for regulating seed supply or seed pricing. These are two important requirements if the formal seed sector has to be regulated in a manner that farmers' interests are upheld.
- Furthermore, the Seeds Bill is also incompatible with the Environment Protection Act (EPA), the Biological Diversity Act (BDA) and so on. For example, it is the EPA which lays down the procedure for approvals and permissions related to genetically modified organisms. But the current bill seeks to circumvent those rules by talking about provisional registration for GM varieties.
- How the Seeds Bill could impact farmers' rights as breeders? The Seeds Bill asks farmers to compulsorily register themselves as "Seed Dealers" if they are engaged in saving and exchanging seeds. Secondly, the Bill says that farmers have to conform to the minimum standards laid down through this Bill. Both are clear infringements on the traditional rights of farmers who have always engaged in seed production and exchange with accountability systems that work out at the local level within the social structures of the community.
- In the first instance, the traditional seed saving and exchange system is not based on commercial interests and is usually a non-magnetized system. Farmers who seek seed select their choice of seed from other farmers after first seeing it perform in their fields. Certain farmers and even landless women are known for their seed selection and seed keeping skills and the others in the community trust their resource and knowledge. It is rare that such seeds fail due to deficient quality. Farmers do not knowingly supply deficient seed to other farmers. However, farmers engaged in seed exchange show that when such an instance of failure does happen, farmers who have borrowed the seeds pretty often assume that it is their management failure rather than the seed failure, especially if they see the same seed performing in other fields. Forcing the seed giver to pay compensation is somewhat rare given that it is perceived that the seed giver is actually doing a favour by lending her/his seed in the first instance. Still, in this traditional system, if a crop fails, the borrower could return any other variety to the seed giver.
- Coming to farmers as consumers of seed supplied by the formal seed sector, the Bill has no satisfactory clauses with regard to the institutional set up that will regulate and ensure the quality of seed produced and supplied nor satisfactory punitive clauses that will act as deterrents on unscrupulous seed traders. It also does not uphold the rights of farmers when it comes to compensation in case of seed failure. The Bill proclaims that farmers can claim compensation through Consumer Forums under the Consumer Protection Act 1986. If that was the case, there is no need to draft this legislation again.
- As is well known, it is not easy for the farmers of this country who are mostly illiterate to access and successfully obtain redressal through these Consumer Forums. A simplified and farmer-friendly redressal mechanism is needed to be provided in this Bill.
- As mentioned earlier, the Seeds Bill is also silent when it comes to seed pricing and seed supply regulations. With the Patents Act coming into force and monopolies being legitimized in the form of IPRs, seed prices are bound to spiral upwards increasing the overall cost of cultivation for farmers. In the case of transgenic varieties, the Seeds Bill has a confusing and unclear proposal called 'Special

Provision for Regulation of Transgenic Varieties' - it proposes a provisional registration for two years, subject to clearance under the Environment Protection Act. It is unclear why this provisional registration is being proposed and what the operationalisation implications are. While some have interpreted it as a violation of the EPA, others feel that it is probably a cautious approach to GMOs where only provisional registrations are provided. Genetic engineering is an irreversible and uncontrollable technology. Once released into the environment even for one season in a small scale, the potential for environmental damage and human health impacts could be tremendous. Transgenic contamination of seed stocks would become inevitable and irreversible in this country. The threat to original seed stock from where other varieties could be evolved is immense from GE and should be recognized for what it is.

- The development of Biotechnology has opened many vistas in the field of agriculture. The Department of Agriculture & Cooperation has appointed a Task Force on Application of Biotechnology in Agriculture under Dr. MS Swaminathan, the inter-ministerial consultations on the recommendations of the Task Force has been completed and the report has been examined for final decision. The Department of Agriculture and Cooperation is also placing its emphasis on the following subjects.

- The focus of strengthening capability till now has been on bio-safety and environmental safety infrastructure before commercial release of GM crops. With genetically modified cotton already released for commercial cultivation in the country and more crops being in pipeline and the fact that trade in genetically modified food grains will be increasing in future it is required to deal with GM seeds/crops on a much larger scale. This, *inter-alia*, calls for upgradation of the post-release monitoring infrastructure which is the responsibility of Department of Agriculture & Cooperation. In particular, there is a need for capacity building for training of manpower in advance techniques of risk assessment and management of GM crops particularly detection and analysis of LMOs, inspection, monitoring handling of GMO material, quarantine, issues relating to segregation, identity preservation and strengthening of institutions addressing issues of certification.

- The present Seed Act does not deal with the quality control of GM seeds as they are generally not notified. It is hoped that the new Seeds Bill will take care of this issue however, action against spurious GM seeds can always be taken under the Seeds Control Order and the EPA rules. As the GM seeds are very costly and sometimes farmers have been cheated, there is a strong urgency to develop protocol for determining the presence or absence of genes incorporated in the cultivars. Similarly, the procedure for testing of GM Seeds in the laboratories as well as in the fields is to be developed, strengthened and established with the State Government infrastructure. Strengthening of Seed Testing Laboratories will be undertaken in this context.

- The penalty clauses provided for offences are very mild and not deterrent enough. The bill proposes that the offender who sells sub-standard seed, upon conviction, be punishable with fine which shall not be less than five thousand rupees which may extend to twenty five thousand rupees. Offenders who sell spurious, misbranded or non-registered seeds are punishable with imprisonment for a term which may extend to six months or with fine which may extend to fifty thousand rupees or with both, according to the bill. Given that the spurious seed trade is worth crores of rupees, the small penalties being proposed are not likely to deter offenders.

- There should be a formula specified in the law itself for calculating the penalty applicable. For instance, the penalty should be based on the quantity of seed supplied or stocked with malicious/negligent intent and therefore, X-times the real loss or potential loss incurred by farmers and not a fixed amount irrespective of the magnitude of the offence. Each time a seed trader/company commits an offence under this law, there should be pro-active publicized data in front of farmers about the erring companies, warning them not to deal with such companies.

- The bill is completely inadequate when it comes to compensation to farmers in the case of seed failure. This Bill should take the opportunity to provide a mechanism for providing compensation to farmers in case of seed failure. Such compensation should be linked to a Seed Insurance system the premium for which is paid by the seed trader. Compensation should also be calculated based on a formula that

should be specified in the Legislation itself which should include the magnetized value of the expected performance as well as coverage of costs of cultivation incurred and not just the seed cost. Panchayats should have a role in certifying failures or losses since agricultural officials are not always available on time to verify the field level situation. Further, maximum time period for payment of compensation failing which more punitive clauses would apply should be specified in the legislation itself.

- Punitive and compensatory clauses should apply to misbranding, selling at prices higher than specified prices/MRP, failure of germination, lack of genetic purity etc. Misbranding should be defined to include failure to keep up promises made during marketing/ propaganda by the company and should include failure to reveal or keep up promises on expectable performance under different conditions as per the multi-locational agronomic trials as part of the packaging of seed.

Discrepancies

- The registration of all the seed varieties is not compulsory. Commercial and plantation crops and non-notified varieties are not covered. But why it is so important to "cover" all varieties is not explained. "This new Seed Bill emphasizes the use of only registered seeds. Why? Who registers their varieties? Who gets certification as producers? The seed companies, of course. Not the farmer." PPV & FR Act, 2001 described as one of its kind in the world as few countries have laws of this kind that protect farmers, has not yet been notified though the Act has been passed by both Houses of Parliament.
- Some critics allege that the notification of the PPV & FR Act is prevented primarily because of intense lobbying by the seed companies.
- The PPV & FR Act, for instance, mentions that based on the parentage of seeds, there will be benefit-sharing. It also mentions that farmers can claim compensation from breeders. It makes it mandatory upon the PPV & FR Authority to undertake "documentation, indexing and cataloguing of farmers' varieties".
- Most important, Section 39 of the Act states that the farmer 'shall be deemed to be entitled to save, use, sow, re-sow, exchange, share or sell his farm produce including seed of a variety protected under this Act in the same manner as he was entitled before the coming into force of this Act. Provided that the farmer shall not be entitled to sell 'branded' seed of a variety protected under this Act'. Also, in the PPV & FR Act, Section 43 specifies that the farmer cannot be prosecuted for infringement of the law if he can prove in court that he was unaware of the existence of such a right. The new Bill does not make such allowances to protect the farmers.
- Some portions of the Bill seem completely non-contextual. For instance, in Section 16, one of the grounds on which a sub-committee may cancel registration is the need to protect 'public order or public morality'. But which registrations will affect the 'public order or public morality' and how are not explained.
- It was also criticized that there is a fundamental flaw in the process and philosophy of this new Bill. Legislation relating to agriculture should ensure that farmers get access to seeds at reasonable cost; the needs of the seed industry should be subservient. But the new Seeds Bill questions the whole issue of ownership of seeds. The parentage of seed varieties is not required during registration which means that the seed companies could be using farmers' varieties and not giving credit, nor sharing profits.
- According to the existing provisions, it is necessary to make the registration of all seed varieties compulsory, especially given the need to enforce patent laws as specified by the World Trade Organization (WTO). Some critics have pointed out that India has already amended the Patent Act of 1970 to comply with the TRIPS agreement and PPV & FR Authority is in place. Thus, there is no further obligation to the WTO.
- India has a Genetic Engineering Approval Committee to regulate genetically modified (GM) crops. According to the Bill, provisional permission could be granted to transgenic varieties. This may violate biosafety principles.
- One of the demands of critics of the new Bill is that it be harmonized with the PPV & FR Act, 2001, and the Biodiversity Act, 2002, so that none of the rights already granted to farmers can be diluted. Also, stringent penalties should be imposed on seed manufacturers when spurious or under-

performing seeds are sold. Ironically, one of the stated objectives of the Bill is to impose harsher penalties - up to six months in prison or a fine of Rs. 50,000, or both. It has taken great care to protect itself, through a clause which says that 'no suit, prosecution or other legal proceeding shall lie against the government or any person for anything which is in good faith done or intended to be done'.

Seeds Bill should incorporate the following:

- Regulation should include seed pricing, seed supply and decentralized seed planning/production in addition to regulation of quality.
- Multi-locational agronomic trials undertaken in a scientific manner in all those locations where the seed is sought to be commercialized. The definition of "Agronomic Performance" should be included in the Act itself to cover many parameters like yield, growth, pest/disease/drought/other resistance. etc
- Each such licensing should be reviewed after 3-5 years and renewal should be allowed based on actual performance. The ICAR establishment should be used to conduct/ supervise the initial trials as well as the review of performance.
- Public access to information related to the grant of licenses for varieties as well as provisions for opposition to licenses granted to certain varieties if there is reason to believe that the variety is not what is claimed; information on revoking of licenses to be public too.
- Strong punitive clauses which act as deterrents, based on standard formulae to calculate penalties.
- Appropriate compensation clauses for speedy redressal to farmers who have incurred losses due to seed failure – this should be linked to an insurance system and should be based on calculations that consider loss in yields as well as cost of cultivation.
- Most importantly, the Seeds Bill should exclude traditional practices of farmers of seed production, sale and exchange from its purview.
- A role for panchayats in determining seed failure under various conditions – misbranding, spurious seed, sub-standard seed, seed sold above MRP etc.

Any legislation related to seeds must uphold and support the following:

- Farmers' rights of breeding, selecting, saving, using, exchanging/bartering, distributing and selling seeds. These should be seen as *inalienable primary rights* and not be given as residual rights. Equally importantly, such rights should not be denied or violated by any method. In other words, ownership and control should be in the hands of farmers over their seed resources.
- Farmer-level self sufficiency in the form of community seed banks and seed networks.
- Most importantly, the Seeds Bill should exclude traditional practices of farmers of seed production, sale and exchange from its purview.
- The right of access to good quality, affordable, desired seeds primarily from the public sector if not the informal sector.
- A role for panchayats in determining seed failure under various conditions – misbranding, spurious seed, sub-standard seed, seed sold above MRP etc.
- Increase in agro-biodiversity in particular and biodiversity in general; it should not seek to promote or end up promoting mono-cropping nor contribute to erosion of diversity.

Points to be Considered for Changes in the Seed Bill

- The Seed Bill should be harmonized with the Protection of Plant Variety and Farmers Rights Act (PPV & FR), 2001 and the Biodiversity Act, 2002.
- Nothing in the Seed Bill shall dilute the rights and protections granted to farmers under the PPV & FR.
- Registration of varieties under the Seed Bill shall require a sworn declaration of the parentage of the variety and make provisions for benefit sharing in harmony with the PPV & FR and the Biodiversity Act, when farmer varieties and public sector varieties are used.
- Registration for sale should be required only for new varieties as in the Seed Act 1966 which limits the requirement to notified varieties. No registration should be required for extant varieties and landraces.
- Wherever registration provides for marketing rights, there should be explicit provisions for ensuring adequate seed supply at a reasonable price.
- The compensation for non-performance of seed supplied by agencies must be regulated through the National Plant Variety Authority, not the District Consumer Courts.

- The duration of protection granted to registered varieties in the Seed Bill should be commensurate with what is granted under the PPV & FR. An extension of five years may be considered for those varieties that are very popular with farmers, provided the decision is taken transparently.
- The provisional permission granted to transgenic varieties is dangerous and violates principles of biosafety, it must be rescinded.
- Multilocation testing of varieties bred by the private sector may be done by the ICAR. It is proposed that industry contributes to a fund to pay for multi location testing but the testing itself should be done by the ICAR.
- The small token penalties for violations contained in the Seed Bill must be revised.
- When the declared source of registered material has been accessed illegally, registration would be cancelled and criminal and civil liability will be determined.
- To ensure transparency, a process for pre-grant opposition to registration of a seed variety must be included in the Seed Bill, like it is in the PPV & FR.
- A consultative process of governance should be established where the communities that will be affected are part of the decision making process.
- The Seed Bill contains several provisions biased in favor of a specific stakeholder; it is against the interest of farmers and in that sense, against the larger national interest.

Seed Laws in Selected Asian Countries

Afghanistan: The National Law on "Seed and Plant Quality" is in the process of being finalized by the Afghan Ministry of Agriculture, Animal Husbandry and Food. The government has been asked by FAO & ICARDA to set up a system for Seed Certification, Seed Testing, and Plant Quarantine in addition to setting standards of seed quality. According to the ICARDA draft law, for the formal sector registration and certification are mandatory for all crops. However, seeds from the informal sector are exempted as long as they are not sold.

Bangladesh: Bangladesh's first seed law was passed in 1977. Like India's existing law, Nepal, Pakistan, Sri Lanka and Thailand, only varieties notified by government are subject to regulation. Five notified crops (rice, wheat, sugarcane, potato and jute) were mainly handled by public institutions. Since an "Agriculture Sector Review" by FAO, UNDP, DANIDA & World Bank, greater participation of the private sector is planned. Under the Structural Adjustment Programmes agricultural input markets were substantially liberalised. By the 1997 amendment act and the 1998 Seed Rules the private sector can import and market any non-notified seeds, while seeds of notified crops may be brought in for trials, tested for suitability and then multiplied and sold.

Bhutan: Under the Seeds Act of Bhutan, 2000 the Royal Government of Bhutan regulates the seeds of notified kinds and varieties and certification is optional. The system is voluntary and there is no DUS criterion.

China: Under the Seed Law of 2000: all commercial seed production has to be registered and certified for sale. Though there is a blanket exception for peasants to exchange and sell their seeds and they do not require a seed operation license to do so. Also asserts State sovereignty over seed resources. The seed law was modified on 28 August 2004, it provides better market access to foreign seed companies in China.

India: The Seed Act of 1966, which only regulated notified varieties, is proposed to be replaced by the Seed Bill, 2004; according to the Bill all seed for sale must be registered on VCU criteria. Certification is optional. GM varieties may be registered subject to environmental clearance but there is a ban on Terminator GMOs. Express mention is made for the farmer's option to invoke consumer protection laws for liability on non-performance of seeds.

Nepal: The Seeds Act of 1988 & Seed Rules, 1996 deals with the registration and release of 153 varieties of plants. The government can require minimum procedures for the barter, sale and exchange of seeds of specific varieties and species, just like Pakistan. Otherwise, people are free to do what they want. Amendments to the seed law are under discussion.

Sri Lanka: The Seed Act of 2003 requires anyone "causing a seed to be placed in the market in Sri Lanka" to be registered with the Director of Seed Certification in the Department of Agriculture. Any locally produced seed has to conform to the rules of production of certified seed before its description and sale as "certified seed". Even though there is a blanket exception for farmer-to-farmer seed exchange and sale, if the farmer wishes

to sell seed in the open market they have to produce and sell certified seed. The FAO's post-tsunami rehabilitation project focuses on certified seed production and upgrade of seed testing and certification procedures.

Thailand : The Plant Act, 1992 regulates notified varieties through a licensing system for "controlled seeds". All other varieties are free from government control.

Pakistan: Under the Seeds Act of 1976, notified varieties of crops have to be registered and their sale, exchange & barter is subject to regulation. For all other varieties certification is optional. Over 350 crop varieties have been registered. The seed law is currently under revision.

Philippines: Republic Act No. 7308 *Seed Industry Development Act, 1992* was enacted to provide for the development of the domestic seed industry. Farmers can exchange and sell their varieties without certification.

The Republic Act No.7607 *Magna Carta of Small Farmers*, defines "good seeds" as "seeds that are the progeny of certified seeds so handled as to maintain a minimum acceptable level of genetic purity and identity and which is selected at the farm level". The High-Value Crops Development Act of 1995 encourages farmers to use non-traditional crops for which it gives several incentives including low-cost credit, tax exemptions & market linkages. The recommended (similar to 'notified' in South Asian countries) varieties must be registered and certified.

Conclusion

The New Seed Bill should not be looked at in isolation, but should be looked at in conjunction with other legislations and policies that India has, related to Seeds and Agriculture, like the Plant Varieties Protection and Farmers' Rights Act, 2001; Biological Diversity Act 2002; Environment Protection Act 1986 with its 1989 Rules pertaining to Genetically Modified Organisms and Patents Amendment Act, 2005. It should also be seen in the context of policies like National Biotechnology Development Strategy to understand the full implications of what lies ahead for Indian farmers in terms of their seed resources. Any new policy and legislation should first and foremost try and uphold the rights of farmers over Seed in terms of its ownership as well as its use and management. Such policies and legislation should also uphold the central and special role that women have always had when it comes to seeds.

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Ramification of Yield in Hallmark Wheat Germplasm of the Indo-Gangetic Plains of India

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The two mega-zones located in the Indo-Gangetic plains receive a great attention by the All India Coordinated Wheat and Barley Improvement Project in developing high yielding wheat varieties for timely sown irrigated conditions. Breeders from either zone can compete in releasing wheat varieties for both the zones. Even though varieties have been notified for the NEPZ in the recent past, release of new varieties has remained elusive in wheat bowl of the country. It has been difficult to break the yield plateau in the NWPZ whereas varieties in the adjoining NEPZ could be released and that too by breeders from the NWPZ. It is therefore necessary to understand the critical components that contribute to yield in either/one. By examining the hallmark germplasm of either zone, it was noted that the main yield determinants are different in these zones. Direct and indirect effect of those key characteristics and the inter-relationship with other components have been investigated to understand differences in yield route among the two group of varieties that have been widely accepted in the Indo-Gangetic plains.

Key words: Bread wheat, Yield components, Hallmark germplasm, Path analysis, Yield route

The Indo-Gangetic plains of India have a long history of wheat cultivation where a cool winter favours prospects of high productivity in this winter cereal. Wheat farming in the Gangetic plains, therefore, has proved vital in assuring food security in the country. Wheat occupies about 10 million hectares area under timely sown irrigated condition in this region. The All India Coordinated Wheat and Barley Improvement Project (AICW&BIP), therefore, imparts lot of importance to this region as instead of one, two national trials (NIVT 1A and NIVT IB) are conducted for initial yield evaluation of the new breeding materials. The whole region has been classified into two mega-zones i.e. North Western Plains Zone (NWPZ) and North Eastern Plains Zone (NEPZ) by the AICW&BIP. The NWPZ comprises the states of Punjab, Haryana, western Uttar Pradesh, Delhi, parts of Rajasthan as than (Alwar, Bharatpur and Sriganganagar), Ponta valley and Una district of Himachal Pradesh, while the states of Bihar, Jharkhand and eastern parts of Uttar Pradesh, West Bengal, Orissa and Assam constitute the NEPZ. Active wheat improvement centres located in both the zones enrol new bread wheat entries for wide scale initial evaluation in the Indo-Gangetic plains.

In the NWPZ, some very popular wheat varieties have been released for timely sown conditions. Among new varieties of the region, PBW 343 has created all time record as its acreage has gone over five million hectares. UP 2338 and WH 542 also had great seed demand in late nineties. In the past, HD 2329 was another highly popular variety in the eighties. However, the new varieties notified for timely sown condition have never become so popular in the adjoining NEPZ. Now when breeders from either zone are entitled to compete for variety release in whole of the Indo-Gangetic plain, it is important to realise the key traits that have contributed yield in the present day popular varieties of both the zones. Therefore, important yield attributes in the hallmark germplasm from this region have been investigated by utilising trial data generated by the AICRP on Wheat and Barley. This search to understand differences in the yield route under different environments will prove handy to the wheat breeders in developing suitable new varieties for two major zones of the country.

Material and Method

The All India Coordinated Wheat and Barley Improvement Project conducts Advance Varietal Trials (AVT) separately for the NWPZ and NEPZ. For comparison, the most popular varieties in the zone are included as checks. Varieties like PBW 343, HD 2687, WH 542, UP 2338 and HD 2329 are taken as checks for the normal sown AVT of the NWPZ. Five years zonal mean (AVT: 1996-97 to 2000-01) of these popular varieties of NWPZ was compared with corresponding check varieties of NEPZ i.e. MUW 468, K 9107, NW 1012, PBW 443, HP 1731 and HD 2733 (Progress Reports, AICRP on Wheat and Barley). According to guidelines mentioned by Rasmusson (1996), these superior varieties that have occupied cultivation in such a large area can be termed as hallmark germplasm. The trials are conducted under high fertility (120kg N, 60kg

P_2O_5 and 40kg K_2O per hectare) and irrigated condition in Randomised Complete Block Design where each has a plot size of 16.56 m^2.

For the purpose of present investigation, pooled data of each year was sorted out for each variety and 25 data files were created for a period of five years. Concerned data for both the zones were computed for statistical analysis i.e. multiple regression analysis by LSQ technique and path coefficient analysis with the purpose to identify the most significant yield contributing traits and analyse their direct and indirect effect on grain yield. Data pertaining to some important characteristics like per hectare grain yield, phenology, plant height, grain weight and grains per square meter were taken for detailed analysis. Since the high yielding varieties arc equally competitive in per hectare yield, differences in their physiological efficiency were therefore examined by partitioning the yield into two major components i.e. kernel number and kernel grain weight. As these traits arc highly dependent on growth period, per clay growth as suggested by Sayre *et al.*, (1998) and Przulj and Mladenov (1999), was also computed by deriving following parameters that can explain different attributes concerning physiological efficiency:

Height Gain Rate	(HGR)	Plant height/day during vegetative period (c)
Grain Formation	(GSR)	Grains formed/m/day during vegetative period (#)
Grain Growth Rate	(GDR)	Grain weight/day during grain filling period (mg)
Yield Filling Rate	(YFR)	Per hectare yield/day during grain filling period (kg)

Results

Varietal superiority and variability: Summary of five years overall performance of the Hallmark germplasm suggests that the NWPZ varieties have higher yield potential than the NEPZ varieties. Yield superiority in the NWPZ arises mainly due to longer vegetative period (a consequence of cooler winter) that results into higher bio-mass and more number of grains/in^2 (Table 1). Higher per day yield filling under NWPZ conditions suggests that these varieties are capable of fast translocation rate during grain ripening period. On the contrary, though the varieties cultivated under NEPZ suffer in yield due to less number of grains/m by virtue of short vegetative period as heading goes early due to relatively high temperature, they are fast in attaining height and filling of the grain. Even though the NEPZ varieties mature 20-25 days earlier when compared to NWPZ varieties, the grain ripening period remained almost similar i.e. around 45 days. It again emphasised that in relation to the total growth period, the NEPZ varieties could get proportionately more time for grain filling (36.2% of the total crop duration) in comparison to NWPZ where varieties got only 31.7% total maturity period for this purpose. The reverse stood true for the grain formation during vegetative period upto heading. Further examination of the results indicated that even though per hectare yield is less in NEPZ, the Hallmark germplasm enjoys more diversity as it throws more variability when compared to NWPZ varieties. The eastern material is distinctly diverse in height, yielding ability and per day growth rate i.e. physiological efficiency. This edge in varietal diversity under NEPZ environment not only gives more options in selecting right genotype for cultivation but also helps in minimising pressure from certain abiotic stresses.

Yield Associated Traits: Association of yield contributing traits with grain yield was examined for eleven traits in each zone (Table 1). In NWPZ, the crop phenology (days

Table 1. Performance, variability and association of component traits with yield

Variables	Overall performance		Coefficient of variability		Correlation with yield		Direct effect on yield	
	NWPZ	NEPZ	NWPZ	NEPZ	NWPZ	NEPZ	NWPZ	NEPZ
Yield (q/ha)	48.2	40.7	5.18	9.35	1.00	1.00	–	–
Days to heading	97.8	77.2	4.94	4.12	0.58**	0.14	–1.57	–0.77
Ripening period (days)	45.4	43.8	5.46	6.71	–0.56**	–0.43*	0.95	–0.91
Total duration (days)	143	121	2.85	1.90	0.35	–0.36	0.79	0.70
Vegetative phase (%)	68.3	63.8	2.96	3.67	0.65**	0.33	0.50	–0.37
Plant height (c)	93.4	89.7	5.07	10.6	0.41*	–0.17	0.00	0.08
Grain weight (mg)	37.5	38.3	8.17	9.7	0.28	0.32	–0.14	0.66
Grains/m^2 ('000)	12.9	10.7	8.60	10.6	0.27	0.56**	0.84	0.03
Height Gain Rate (c)	0.96	1.16	4.17	8.6	–0.25	–0.30	0.01	–0.11
Grain Formation Rale (#)	132	139	7.53	13.0	–0.07	0.42*	–0.55	0.32
Grain Growth Rate (mg)	0.83	0.88	8.43	13.6	0.60**	0.42*	0.42	–0.58
Yield Filling Rate (kg/ha)	106	93.7	8.55	13.7	0.86**	0.88**	1.55	1.08

Number of observations = 25, * Significant at 5% level, ** Significant at 1% level

to heading, grain filling period and % crop duration spent for days to heading i.e. % vegetative phase) and the rate of grain development and yield filling during ripening period showed highly significant correlation with yield. Plant height also had significant effect on the grain yield in this zone. Similar relationship in the NEPZ varieties could be noted only for three traits i.e. grain filling period, grain development rate and yield filling rate. In both the zones, grain filling period was negatively associated with grain yield. Unlike NWPZ, number of grains per unit area and the rate at which they were set during vegetative period were also very important in determining yield in the NEPZ. The rate at which height is attained, total crop duration and the grain size or weight was not correlated with grain yield in any of the zones. Surprisingly, even number of grains/m^2 remained unrelated to yield in NWPZ varieties. Since high grain number per unit area is always a common trait in varieties of this region, there may not be enough variability to register any significant effect on yield in the NWPZ varieties. Grain number per unit area, however, has great significance in the varieties of this region but the predominance of negative indirect effect on yield via certain other traits might have diluted a positive correlation with yield. As evident from the historical evidence, it is the grain number that has been consistently associated with increase in wheat yields. (Slafer *et al.*, 1994 and 1996; Villariel *et al.*, 1994 and 1995). The elite gene pool derived in this region comes largely from winter x spring gene pool recombination. Besides the 1B/1R translocation, a higher number of grains through either higher number of heads/m^2 or through bigger heads contribute to high yield in winter x spring wheat derived gene pool (Rajaram and Van Ginkel, 1996).

Determining the yield route through eleven traits is quite a complex exercise and it is not easy for the breeders to exercise selection with so many yield components. Also, judging importance of any yield component trait with yield through correlation studies may not necessarily reflect real importance of a given trait as its overall impact on yield can also be influenced by certain other associated traits. Investigation was further carried to identify the key components in each set of varieties and multiple regression analysis by LSQ technique was applied (Table 2). This technique provides combined effect of key yield components by studying real importance of concerned traits after separating the indirect influence that any involved trait could have had on the yield.

Yield Governing Traits

NWPZ varieties: It was interesting to note that out of the six traits that had registered significant or highly significant correlation with yield in the NWPZ varieties, only two of them i.e. ripening period and yield fill rate played the most crucial role in determining grain yield. With a very high multiple regression coefficient (R^2=0.958), these two components could be seen as the deciding factor in high yield potential of the NWPZ varieties. Ripening period even though showed negative contribution and association with yield (r=-0.57) but at its own it regressed positively with yield direct its direct effect on yield was positive and quite high (0.95). These two attributes not only aid to high physiological efficiency of NWPZ varieties but also to attain quick ripening-thereby enhancing the genotype ability in negotiating abiotic stress especially terminal heat. Contribution of yield filling rate was found the most predominant yield parameter in the NWPZ varieties. It proved that physiological efficiency during grain ripening plays a most crucial role in realising genetic yjeld potential of the wheat varieties cultivated in the NWPZ.

NEPZ varieties: Multiple regression analysis presented a different yield route in the NEPZ varieties where four traits i.e. yield fill rate, grain weight, grain development rate and proportionate vegetative phase were noted as crucial yield governing factors (R^2 = 0.997). Among

Table 2. Multiple regression analysis by LSQ technique

Character (Predictor)	% contribution of the predictor to the R^2 value	Correlation of the predictor with regression function	Regression coefficient value	SE (b)	t value (b)
NWPZ (R^2 = 0.958)					
Ripening period	-62.64	-0.57	1.08	0.10	10.88
Yield Filling Rate	162.64	0.86	0.50	0.03	1.84
NEPZ (R^2 = 0.997)					
% vegetative phase	-5.25	0.33	-0.26	0.08	3.96
Grain weight	24.20	0.32	0.78	0.05	15.25
Grain Growth Rate	-45.38	0.42	-33.17	2.45	13.57
Yield Filling Rate	126.43	0.88	0.42	0.01	72.34

these, two characters registered a negatively contribution to the overall yield i.e. proportionate vegetative phase and the rate of grain filling i.e. grain development rate. Unlike NWPZ, grain filling period failed to emerge as a crucial yield component even when it was significantly (-ve) correlated with grain yield. Among phenological traits, the vegetative phase registered a negative impact on grain yield. It means that longer vegetative period for a given maturity duration adds negative impact in NEPZ. Percent duration for grain filling was higher in these varieties (63.8%) when compared to corresponding varieties of NWPZ. This trait, however, failed to establish a significant correlation with yield perhaps due to the over riding positive effect that this trait might have had on the associated characters. The grain weight made a positive contribution to yield in these varieties even when significant positive correlation with yield was not registered. Third important yield attribute of the NEPZ varieties was grain development rate. Its contribution to yield was negative and it also regressed negatively with yield. It showed that rapid filling in the individual grain proves detrimental to yield of the varieties under cultivation in NEPZ. It needs slow filling in each grain whereas the existing eastern varieties have grain filling (0.88mg/day) faster than the NWPZ (0.83mg/day). The only common factor between the two sets of varieties was the yield fill rate and at its own, this single factor had maximum contribution to grain yield in both the zones. It reflects that movement of sink to source during grain filling period is high in both kinds of varieties. High yield filling rate even when fast grain development hinders grain yield, makes the NEPZ varieties complex and so special.

Effect of key components on yield route in different environments: The traits identified as crucial factors in governing grain yield were further studied in detail for their indirect effect on yield via other traits (Table 3). It was interesting to note that except plant height (total as well as per day gain), all other traits had a high direct effect on yield even when correlation with yield could not be established. It showed that indirect effect on an individual trait via associated characters was also paramount. Though a number of traits had shown significant correlation with yield, their importance can still differ as a few of them actually played a crucial role in determining yield. Since selection for some of the traits like grain development rate, yield filling rate and percent vegetative phase can not be exercised in the field, the correlation matrix and their direct and indirect effect on yield via other traits were closely examined. Very low residual effect under both the environments (NWPZ=0.0383 and NEPZ=0.0018) assured that the characteristics under investigation, covered majority of the traits that are useful for grain yield. Besides better understanding of the yield route in this elite germplasm, such an exercise also simplifies the selection criteria to be adopted in the breeding material.

Grain filling period: A major key component that emerged as a limiting factor in governing yield of the NWPZ varieties is the grain ripening period. However it appeared to be a ticklish characteristic as regression coefficient with yield stood positive even when correlation with yield was negative. Further investigation through path coefficient analysis revealed that the grain ripening period did have a high direct positive impact on yield that is why at its own it regressed positively with yield (Table 3). However, high indirect negative effect through certain other traits like grain size and yield filling rate negated its favourable impact. No indirect high effect on yield was observed via either grain weight or grain development rate. The correlation matrix made it further clear as the ripening period had a significantly negative correlation with days to heading, number of grains/m^2, grain setting rate and yield filling rate (Table 4). It means that by curtailing grain filling period through fast grain ripening, grain number per unit area is enhanced in the NWPZ varieties. The duration of grain ripening failed to appear as the key yield contributor in the hallmark germplasm of NEPZ where its direct effect on yield was quite in contrast to the effect that the NWPZ varieties had in the adjoining zone. Ripening period was the only trait that carried indirect high and positive effect on yield via days to heading in each zone. It shows that any attempt to curtail heading carry adverse impact on yield via ripening period as well.

Yield filling rate: This characteristic had a very high positive direct effect on yield and correlation with yield was also highly significant in both types of varieties. However, divergence for this particular parameter was quite conspicuous between the two sets of varieties when its indirect effect on yield was examined. In the NWPZ varieties, it had a high positive indirect effect on yield via grains/m' and vegetative phase whereas it was the grain filling period that registered a positive indirect effect on yield in the NEPZ varieties. Similarly, characters adding indirect negative effect on yield were also different

in both the production conditions. Heading had a very high indirect negative effect on yield in the NWPZ varieties (-1.01) whereas in the other group, this type of negative effect was milder (-0.35). Besides, grain filling period also had a high negative indirect effect on yield in the NWPZ varieties whereas in the other group, the focus was shifted to grain development rate. So the indirect effect of grain filling period was high and positive in the NWPZ varieties whereas it turned opposite (high, -ve) in the NBPZ varieties. Diversity among the zones was visible for the common trait yield fill rate when its correlation was examined for certain other important traits. In the NWPZ, yield filling rate registered negative correlation with height gain rate. It implies that the varieties with slow vertical growth were benefited in yield filling rate under NWPZ conditions. Slow vertical growth aids lateral/horizontal growth that is manifested in more tillering and biomass production and better physiological efficiency in the zone. In NEPZ, the yield-filling rate was also correlated positively with grain weight and negatively with crop duration. Varieties with longer maturity period and small grain size, therefore, fail to draw any yield advantage in NEPZ.

Grain weight: Size of the grain was important for good yield in wheat varieties of the NEPZ. This key yield determinant in the NEPZ varieties regressed positively with yield as it had high direct positive effect. However, it failed to exhibit any correlation with yield. An examination of indirect effects revealed that a high negative indirect effect via some important traits like heading and rate of grain development nullified the direct positive effect and converged to an insignificant correlation with grain yield. A close look on the correlation matrix shows that bolder grains in the NEPZ hallmark germplasm were recorded in the varieties that had long grain filling period/ higher proportion of vegetative phase/ total duration/ plant height where as such correlation failed to exist in the NWPZ varieties.

Grain growth rate: The fourth important factor that governed yield in the NEPZ varieties was the rate at which filling in the individual grain take place. Grain weight in wheat is the product of rate and duration of grain filling (Nass and Reiser, 1975). Przulj and Mladenov (1997) found no strong connection between grain fill duration and grain fill rate, which enables the combining of these two traits in the process of cultivar development. They have suggested that in regions with shorter growing season, the yield can be more easily raised by increasing grain fill rate while in the temperate regions different values of these parameters can be combined. By this study, grain fill rate appeared to be a complex trait as its contribution to grain yield was negative. It regressed with yield in negative direction and its direct effect was also high and negative. However, it did register a significant positive correlation with yield. A positive correlation with yield was observed in NWPZ varieties also (r=0.60) but the direct effect on yield was also positive in that environment (0.42). Its high indirect positive effect on yield in the NEPZ varieties via gram filling period, grain size/weight and yield filling rate were the basis of shaping positive correlation. The correlation matrix in NEPZ showed that grain development rate in the prevalent varieties is highly influenced by phenological traits as it improves with delayed heading (r=0.79) and falls when grain filling period gets longer (-0.76). Such a correlation between phenological traits and grain development rate was not established in NWPZ.

Vegetative phase: The NEPZ hallmark germplasm was special in many other respects. Even though there was no correlation between yield and the percent crop duration utilised for vegetative growth, this phenological attribute registered a high and negative direct effect on yield (-0.37). And this crucial yield determinant regressed negatively with grain yield in the NEPZ varieties. It also drew negative indirect effect on yield via heading and rate of grain development, however, an indirect positive effect via grain filling period, grain weight and yield filling rate nullified the positives effect in the final analysis. This was in total contrast to the NWPZ varieties where a high direct positive effect (0.50) and positive correlation with yield (0.65) were established for this trait, indirect effect on yield via other traits was also different for most of the traits in the NWPZ varieties. The conspicuous differences between two groups of varieties were also observed in the correlation matrix. It appeared that vegetative phase has an important role to play in different environments. In the NWPZ varieties, it was positively correlated with total duration, plant height and grain number per unit area (Table 4). It means that an increase in the percent time spent in vegetative phase, adds to the grains per unit area and bio-mass of the NWPZ varieties. No such effect was visible in the NEPZ varieties. Negative selection for this trait in NEPZ can be exercised by enhancing the grain ripening period.

Table 3. Direct and indirect effect of yield contributing traits in the timely sown varieties of NWPZ and NEPZ

Characteristic	Zone	Effects via											Correlation
		1	2	3	4	5	6	7	8	9	10	11	with yield
1. Days to heading	NWPZ	**-1.57**	-0.51	0.67	0.42	0.00	0.02	0.39	0.00	0.06	0.09	1.00	0.58**
	NEPZ	**-0.77**	0.66	0.32	-0.33	0.03	0.41	-0.01	-0.00	-0.21	-0.46	0.50	0.14
2. Ripening period	NWPZ	0.84	**0.95**	-0.02	-0.44	-0.00	-0.03	-0.44	-0.00	0.14	-0.16	-1.39	-0.56**
	NEPZ	0.55	**-0.91**	0.20	0.35	-0.02	-0.22	-0.00	-0.00	0.05	0.44	-0.86	-0.43*
3. Total duration	NWPZ	-1.35	-0.03	**0.79**	0.24	0.00	-0.00	0.19	0.00	0.16	0.01	0.33	0.35
	NEPZ	-0.35	-0.26	**0.70**	0.00	0.02	0.28	-0.02	-0.01	-0.23	-0.07	-0.42	-0.36
4. Vegetative phase (%)	NWPZ	-1.36	-0.85	0.38	**0.50**	0.00	0.03	0.48	0.00	-0.05	0.14	1.37	0.65**
	NEPZ	-0.68	0.88	0.00	**-0.37**	0.03	0.31	-0.00	-0.00	-0.12	-0.48	0.77	0.33
5. Plant height	NWPZ	-1.11	-0.18	0.57	0.25	**0.00**	-0.04	-0.05	-0.00	0.29	0.17	0.52	0.41*
	NEPZ	-0.32	0.23	0.17	-0.12	**0.08**	0.42	-0.02	-0.10	-0.21	-0.34	0.03	-0.17
6. Grain weight	NWPZ	0.18	0.22	0.00	-0.10	0.00	**-0.14**	-0.70	-0.00	0.47	0.34	-0.00	0.28
	NEPZ	-0.48	0.31	0.30	-0.17	0.05	**0.66**	-0.02	-0.04	-0.22	-0.50	0.43	0.32
7. Grains per unit area	NWPZ	-0.73	-0.50	0.18	0.28	-0.00	0.11	**0.84**	0.00	-0.45	-0.20	0.74	0.27
	NEPZ	0.32	0.07	-0.47	0.05	-0.05	-0.40	**0.03**	0.06	0.30	0.23	0.43	0.56**
8. Height sain rate	NWPZ	0.61	0.44	-0.14	-0.24	0.00	-0.07	-0.57	**0.01**	0.28	0.09	-0.64	-0.25
	NEPZ	-0.03	-0.01	0.05	-0.00	0.07	0.24	-0.01	**-0.11**	-0.13	-0.16	-0.20	-0.30
9. Grain setting rate	NWPZ	0.18	-0.24	-0.23	0.05	-0.00	0.12	0.69	0.00	**-0.55**	-0.28	0.20	-0.07
	NEPZ	0.52	-0.15	-0.51	0.14	-0.05	-0.45	0.02	0.05	**0.32**	0.33	0.20	0.42*
10. Grain develop, rate	NWPZ	-0.34	-0.37	0.01	0.17	0.00	-0.11	-0.40	-0.00	0.37	**0.42**	0.84	0.60**
	NEPZ	-0.61	0.69	0.09	-0.30	0.05	0.57	-0.01	-0.03	-0.18	**-0.58**	0.73	0.42*
11. Yield filling rate	NWPZ	-1.01	-0.85	0.17	0.44	0.00	0.00	0.40	0.00	-0.07	0.23	**1.55**	0.86**
	NEPZ	-0.35	0.73	-0.27	-0.26	0.00	0.26	0.01	0.02	0.06	-0.40	**1.08**	0.88**

Residual effect: NWPZ = 0.0383, NEPZ = 0.0018, Bold figures signify direct effect, * Significant at 5% level of probability, ** Significant at 1% level of probability

Table 4. Correlation matrix of different traits in the timely sown varieties of the NWPZ and NEPZ

Characteristic	Zone	1	2	3	4	5	6	7	8	9	10	11	12
1. Grain yield	NWPZ	1.00	**0.58**	**-0.56**	0.35	**0.65**	**0.41**	0.28	0.27	-0.25	-0.07	**0.60**	**0.86**
	NEPZ	1.00	0.14	**-0.43**	-0.36	0.33	-0.17	0.32	**0.56**	-0.30	**0.42**	**0.42**	**0.88**
2. Days to heading	NWPZ	**0.58**	1.00	**-0.54**	**0.86**	**0.86**	**0.71**	-0.12	**0.47**	**-0.39**	-0.12	0.21	**0.64**
	NEPZ	0.14	1.00	-0.72	**0.46**	**0.89**	**0.41**	**0.62**	-0.42	0.05	**-0.68**	**0.79**	0.46
3. Ripening period	NWPZ	-0.56	-0.54	1.00	-0.03	**-0.89**	-0.19	0.23	-0.53	**0.46**	-0.25	**-0.39**	-0.90
	NEPZ	-0.43	-0.72	1.00	0.29	-0.96	-0.25	-0.34	-0.08	0.01	0.16	-0.76	-0.80
4. Total duration	NWPZ	0.35	**0.86**	-0.03	1.00	**0.48**	**0.73**	0.01	0.23	-0.18	-0.29	0.02	0.22
	NEPZ	-0.36	**0.46**	0.29	1.00	0.00	0.24	**0.42**	-0.68	0.07	-0.72	0.13	-0.39
5. Vegetative phase (%)	NWPZ	**0.65**	0.86	-0.89	**0.48**	1.00	**0.50**	-0.21	0.57	-0.48	0.09	0.34	**0.88**
	NEPZ	0.33	**0.89**	-0.96	0.00	1.00	0.34	**0.48**	-0.13	0.01	-0.39	**0.82**	0.71
6. Plant height	NWPZ	**0.41**	0.71	-0.19	0.73	**0.50**	1.00	0.31	-0.07	0.38	-0.52	**0.40**	0.34
	NEPZ	-0.17	**0.41**	0.25	0.24	0.34	1.00	**0.65**	-0.67	**0.89**	-0.67	**0.59**	0.03
7. Grain weight	NWPZ	0.28	-0.12	0.23	0.01	-0.21	0.31	1.00	-0.83	**0.53**	-0.86	**0.80**	-0.00
	NEPZ	0.32	**0.62**	-0.34	**0.42**	**0.48**	**0.65**	1.00	-0.60	0.37	-0.68	**0.87**	**0.40**
8. Grains per unit area	NWPZ	0.27	0.47	-0.53	0.23	**0.57**	-0.07	-0.83	1.00	-0.68	**0.82**	-0.47	**0.48**
	NEPZ	**0.56**	-0.42	-0.08	-0.68	-0.13	-0.67	-0.60	1.00	-0.53	**0.95**	-0.40	**0.40**
9. Height gain rate	NWPZ	-0.25	-0.39	**0.46**	-0.18	-0.48	0.38	**0.53**	-0.68	1.00	-0.52	0.22	-0.41
	NEPZ	-0.30	0.05	0.01	0.07	0.01	**0.89**	-0.37	-0.53	1.00	-0.42	0.27	-0.19
10. Grain setting rate	NWPZ	-0.07	-0.12	-0.25	-0.29	0.09	**-0.52**	-0.86	**0.82**	**-0.52**	1.00	-0.66	0.13
	NEPZ	**0.42**	-0.68	0.16	-0.72	-0.39	-0.67	-0.68	**0.95**	**-0.42**	1.00	-0.57	0.19
11. Grain develop, rate	NWPZ	**0.60**	0.21	-0.39	0.02	0.34	**0.40**	**0.80**	-0.47	0.22	-0.66	1.00	**0.54**
	NEPZ	**0.42**	**0.79**	-0.76	0.13	**0.82**	**0.59**	**0.87**	**-0.40**	0.27	-0.57	1.00	**0.68**
12. Yield filling rate	NWPZ	**0.86**	**0.64**	**-0.90**	0.22	**0.88**	0.34	-0.00	**0.48**	**-0.41**	0.13	**0.54**	1.00
	NEPZ	**0.88**	**0.46**	**-0.80**	**-0.39**	**0.71**	0.03	**0.40**	**0.40**	-0.19	**0.19**	**0.68**	1.00

Bold figures denote significant correlation at 5% level of probability

Discussion

The north-western plain zone known as wheat bowl of the country, has a kind of environment that help in exploiting genetic yield potential of a genotype to the maximum. Information generated by the AICW&BIP, and computer simulations on the attainable yield indicates that NWPZ has potential of 7.0t/ha grain yield (Nagarajan, 1998). PBW 343 has recorded productivity of such a magnitude at many places in the yield trials of the zone. This variety has been notified for the whole Indo-Gangetic region and it has covered over five million hectare cultivation in the in the NWPZ alone. However, this zone

could not get any other alternate variety of such a wider adaptation ever since the release of PBW 343 in 1995. For such an important zone, only one more variety i.e. HD 2687 was notified four years later but it could not catch on to PBW 343. The NWPZ needs varietal diversity under timely sown conditions, as only a few varieties occupy very large area. Avoiding threats of mono-culture in NWPZ has captured attention of the breeders but the suitable alternative are not coming. The percentage of new materials promoted to Una I stage testing and found to yield better than the best check is too low in NWPZ whereas the NEPZ is comfortably placed for wheat varieties of timely sown condition (Jag Shoran *et al.* 1998, Mohan *et al.* 2001). Some of the impediments that come in the way of finding new varieties for this region have been thrown to light by this investigation.

The present study has revealed that quick ripening and high yield fill rate are the two important yield determinants for wheat varieties of the NWPZ. In another study, the authors have indicated that wider adaptation and ability to exploit favourable conditions to yield advantage through high number of grains/m is an in-built advantage tagged to the elite wheat material developed in the north-western region (Mohan and Jag Shoran, 2002). To harness the benefit of large number of grains per unit area, high physiological efficiency is needed during grain ripening. This kind of physiological efficiency is ensured through high yield fill rate (Sayre *et al.*,1998). Quick ripening, so essential to escape terminal heat at the time of grain maturity, also guarantee development of good grain size through tolerance against abiotic stress. A manifestation of both these attributes is the wheat variety PBW 343 (Mohan *et al.*, 2004). The study revealed that the grain filling period is an important but highly complex attribute and its contribution to yield varies in accordance with the environment. Since the direct effect for this trait is very high and positive in the NWPZ, direct selection for this trait can be exercised even when correlation is negative. Yield fill rate has not only high and positive correlation with yield but the direct effect is also very high and positive. However, a direct selection for this parameter will be difficult in the field. Indirect selection to cash on the positive effects on yield under NWPZ conditions can be exercised for yield fill rate through grains per unit area and well-partitioned phenology with more packing for vegetative growth. However, the indirect high to very high negative effect that yield fill rate gets through phonological attributes like heading (-1.01) and ripening period (-0.85) can not be overlooked though it can be minimised to certain extent through more grains per unit area and vegetative phase.

It looks relatively easy to breed varieties for the NEPZ where the yield is ultimately controlled by four traits i.e. grain size, grain development rate, vegetative phase and the yield fill rate. Besides direct selection, yield gain through grain size can also be maximised by indirect selection via heading and grain ripening period. By selecting genotypes of early flowering and extended ripening period, even the correlation of grain size with yield in the NEPZ can be established. Selection for such traits will also minimise the negative contribution that the % vegetative phase has on grain yield. With no compromise on grain size, varieties with similar phenology (early flowering, longer grain filling duration and less packing of vegetative phase) shall be suitable for slow rate of grain filling. Similar phenology in combination with good grain size but low rate of grain filling will indirectly strengthen the already very high effects of yield fill rate. Phenological development therefore, carries importance for varieties of the NEPZ. Role of phenological development and its manipulation for increasing wheat yield potential has been emphasised by many wheat workers (Renolds *et al.*, 1996; Slafer *et al.*, 1996; Richard 1996). The study supports the view point that it is relatively more convenient to capitalise on the characteristics that build yield under NEPZ conditions even if the breeding efforts are made under prevailing conditions of NWPZ. Wheat in the NEPZ region comes to heading 20 days earlier when compared to wheat grown in the NWPZ. When flowering goes early, there remains sufficient time to translocate the food reserves to the grains formed during short vegetative period. So the grain filling duration does not remain a limiting factor as in the adjoining zone. The authors have also noted earlier that the material bred in the NWPZ has an edge over NEPZ bread materials in terms of grains/m^2 and the elite gene pooled developed in these two regions express these attributes in general (Mohan and Jag Shoran, 2002). So when the material rich in grains/m^2 (as in case of NWPZ bred material) is tested in the NEPZ, the prospects of finding a better manifestation of genetic yield potential become brighter. The breeders from the NWPZ could release three varieties (I ID 2733, PBW 443 and PBW 343) in the adjoining zone since 1999 whereas it has been difficult for them to overtake the yield potential of PBW 343, a variety that reins NWPZ.

Conclusion

The hallmark germplasm suitable for timely sowing under irrigated condition have shown high yield potential in their respective zones falling within the Indo-Gangetic plains. Making use of the cool winter, the NWPZ varieties exert good yield potential through longer vegetative period that aids good tillering, biomass and eventually more number of grains per unit area. However, there is not much diversity for the yield component traits in varieties of this region and the varieties of adjoining NEPZ offer more choice to the farmers as they are not only more diverse in yield, plant height and grains per unit area but also register better growth rate that is crucial in varietal adjustment against abiotic pressures.

The yield route examined through direct or indirect effects on the yield and the inter-trait relationship in the hallmark germplasm of each zone is quite diverse. Among different yield components, grain filling period (fast ripening) and yield filling rate are the most crucial characters that govern yield in the NWIV, varieties. Even though combining these two attributes is not distinctly impossible as PBW 343 has stood all tests in this aspect, but high physiological efficiency through high yield fill rate can certainly be seen as a good reason for not finding a matching gene combination. Besides, yield filling rate that contributes maximum to grain yield in the whole Indo-Gangetic plains, yield in varieties of the adjoining zone i.e. NEPZ is also determined by grain weight, grain development rate and percent vegetative phase. Unlike NWPZ, varieties in this zone have longer grain filling period and slow filling in the individual grain will be desirable. Even for yield filling rate, a common trait in both the zones, the contributing traits are not common in two zones. While longer vegetative phase, slow vertical growth and higher grain number per unit area are the important traits related to yield fill rate in the NWPZ varieties, the route is quite different in the other zone. In NEPZ varieties, even though emphasis is on the longer grain filling period but this duration is to be enhanced without increasing the total duration. There is a ceiling on the total maturity period in the NEPZ also it correlates negatively with yield filling rate. Besides, breeder should never loose sight of grain weight in developing varieties for the eastern region.

The present analysis has made it clear that even though common trials are being conducted by the AICW&BIP for the Indo-Gangetic plains of India; the route to yield seems to be quite different in the constituent zones. This study to understand direct and indirect effect of the key characters and the inter-trait relationship in the existing popular varieties will help the wheat breeders in shaping their research programme for different needs of the mega-zones covered in the Indo-Gangetic plains.

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Occurrence of Two Races of Black Pepper in Southern Region of India

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Out of a 192 accessions of black pepper, 103 including 48 named clones, 12 wild clones and 43 unnamed clones from Western Ghats region were observed for 12 quantitative and 7 qualitative passport and spike and berry characters. The collection based on two very important qualitative characters such as berry shape and pace of ripening colour change, which are closely associated with each other along with distribution pattern could be divided into two races (race 1 with 7 accessions and race 2 with 96 accessions). These races are named as race 'Kariyilanchi' and 'Karimunda' respectively after the local varietal names of two prominent accessions each representing a race. Numerical taxonomic study based on the above characters could substantiate the racial classification with 6 accessions of the first race falling under a single group in the dendrogram. One chemical parameter, oleoresin content is lesser (30.03%) in race 1 as compared to 41.36% in race 2.

Key words: Black pepper, Races, Karivilanchi, Karimunda

Formal taxonomy has failed most conspicuously at the infra-specific level in cultivated plants (Harlan, 1975). Infra-specific classification of cultivated plants involves fitting a set of man-made categories to the man-influenced products of earlier domestication and the resultants of later evolutionary processes, which apparently produces a hierarchic series of discontinuities. Thus, according to Barbara Pickersgill there is a need for full and systematic classification of cultivated plants, which will have either a general or commercial value as a system of identification. Cultivated plants fall under two major groups such as sexually (through seeds) and asexually (through vegetative means) propagated ones. A race might have originated in some geographic region at some point of time in the history of the crop evolution. As a biological unit, it is not clearly separable as a species but has distinct cohesion of morphology, geographical distribution, ecological adaptation and frequently breeding behaviour. The race is a group of useful cultivars in a crop. In the present study, an attempt has been made to identify two races of black pepper of commerce having vegetative mode of propagation coupled with sexual in the wild and run wild forms in its centre of origin on the basis of spike and berry characters.

Black pepper (*Piper nigrum* L.) having a monocentric origin in a limited geographic area in tropical region with high rainfall on the western slopes and plateau region of Western Ghats has a short history as a crop but has longer commercial history as a forest produce. It has spread to very far off areas in South East Asia and South America without any appreciable secondary centres of diversity. Its spread to the other tropical areas in Brazil, Malaysia, Thailand and Vietnam is comparatively a recent development. This crop has originated from the wild ones through domestication and selection (Ravindran et al., 2000). Cultivar diversity is richest in Kerala followed by Karnatatka. The cultivars are mostly bisexual as against the dioecious wild ones. Intermediate populations of various species and their segregating progenies probably arising through natural hybridization and segregation have been noticed to occur in pockets of Western Ghats. Escape of cultivated ones through birds and establishment of bisexual types in forest areas has also been observed. Nearly hundred cultivars have been reported from Southern region of India. There is an overlapping of local names in relation to regions, places, situations, dialects and spike and berry characters. Though *Piper* species of Western Ghats has been subjected to numerical taxonomic analysis and isoenzyme analysis with a view to group them. However, no report on the existence of different races in the crop has been made so far. Morphometric analysis of 44 black pepper cultivars and 7 wild accessions using 22 characters to classify them into 11 groups has been furnished by Ravindran (1991) and Ravindran et al. (1997a, b). Ravindran et al. (2000) has also attempted to furnish spike and berry characters of 14 species of the genus from Western Ghats. A comprehensive report on all the cultivars with distinguishing key characters is still needed in this crop. Thus as a part of characterization and documentation of collections made from southern region, observation of the first author on various pepper cultivars and wild population during his survey and collection trips in southern region indicated that the most prominent character of the cultivated pepper

is the shape and size of its berries and changing colour on ripening. These appear to be two important characters probably have an evolutionary significance in the crop.

Materials and Methods

Out of a total of 192 accessions of black pepper maintained in the National Bureau of Plant Genetic Resources (NBPGR), Regional station's farm at Vellanikkara, 103 accessions belonging to 48 named clones (Tables 1 and 2) were observed for 12 quantitative and 7 qualitative spike and berry characters at the time of harvesting during January to March, in 2002 and 2003. The collections were divided subjectively into two races (race 1 and race 2) based on two associated characters such as berry shape

Table 1. Race wise list of collections of black pepper

S.No.	Tcno	Collno	Icno	Local Names	Locality	District	State
Oval berried types							
1	300	V90/P-90	266416	Kariyilanchi	Payyakode	Kollam	Kerala
2	301	V90/P-92	266417	Kariyilanchi	Ithikkara	Kollam	Kerala
3	331	V91/P-207	266404	Kariyilanchi	Kunnakkad	Palakkad	Kerala
4	421	VB/2001-69	373830	Karivilanchi	Mavila	Kollam	Kerala
5	425	VB/2001-75	373836	Elamaravan	Ummannur	Kollam	Kerala
6	427	VB/2001-68	373829	Nadan	Mavila	Kollam	Kerala
7	438	VU/2001-8	373754	Ayimpiriyan	Vengola	Thiruvananthapuram	Kerala
Round berried types							
1	1	V3613	85313	–	Edamalayar	Idukki	Kerala
2	6	V3643	85318	Nadan	Kuttampuzha	Idukki	Kerala
3	8	V3646	85320	Karimunda	Puyamkutti	Idukki	Kerala
4	12	V3654	85324	Karimunda	Adimali	Idukki	Kerala
5	19	V3671	85331	–	Kallar	Idukki	Kerala
6	21	V3675	85333	–	–	Idukki	Kerala
7	23	V3677	85335	–	Ayiram Acre	Idukki	Kerala
8	26	V3686	85338	Nedumundi	Ayiram Acre	Idukki	Kerala
9	27	V3688	85339	Narayakkodi	Ayiram Acre	Idukki	Kerala
10	29	V3690	85341	Kuthiravali	Ayiram Acre	Idukki	Kerala
11	41	V3712	85353	Karimundi	Nedunkandam	Idukki	Kerala
12	42	V3713	85354	Vattamundi	Nedunkandam	Idukki	Kerala
13	45	V3717	85357	Neelamundi	Nedunkandam	Idukki	Kerala
14	49	V3722	85361	Vellamundi	Nedunkandam	Idukki	Kerala
15	50	V3724	85362	Wild	Nedunkandam	Idukki	Kerala
16	51	V3725	85363	Vellamundi	Perumpazham	Idukki	Kerala
17	54	V3728	85366	Vellamunda	Thekkady	Idukki	Kerala
18	58	V3735	85370	Ottamundi	Kumili	Idukki	Kerala
19	59	V3726	85371	Thevanmundi	Kumili	Idukki	Kerala
20	63	V3740	85375	Narayakkodi	Peermed	Idukki	Kerala
21	64	V-3741	85376	Vellamundi	Peermed	Idukki	Kerala
22	65	V3742	85377	Thevanmundi	Peermed	Idukki	Kerala
23	69	V3749	85381	Vattamundi	Chinnar	Idukki	Kerala
24	74	V3756	85386	Malamundi	Thadiyanpad	Idukki	Kerala
25	75	V3757	85387	Karimunda	Thadiyanpad	Idukki	Kerala
26	80	V3774	85392	Narayakkodi	Ranni	Pathanamthitta	Kerala
27	84	V3805	85396	Chomala	Mekkazhoor	Pathanamthitta	Kerala
28	85	V3807	85397	Karimunda	Perinadu	Pathanamthitta	Kerala
29	86	V3808	85398	Valiyaramunda	Perinadu	Pathanamthitta	Kerala
30	89	V3811	85401	Valiyamunda	Kochandi	Pathanamthitta	Kerala
31	90	V3812	85402	Palikkodi	Kochandi	Pathanamthitta	Kerala
32	91	V3819	85403	Wild	Muahiar	Pathanamthitta	Kerala
33	94	V3841	85406	Valiyaramunda	Vadasserikkara	Pathanamthitta	Kerala
34	99	V3852	85411	–	Chittar	Pathanamthitta	Kerala
35	100	V3854	85412	Neelamunda	Chittar	Pathanamthitta	Kerala
36	103	V3858	85415	–	Konni	Pathanamthitta	Kerala
37	105	V3861	85410	Narayakkodi	Konni	Pathanamthitta	Kerala
38	106	V3865	85418	Karivally	Konni	Pathanamthitta	Kerala

S.No.	Tcrno	Collno	Icno	Local Names	Locality	District	State
39	108	V3867	85420	Karinthakara	Konni	Pathanamthitta	Kerala
40	110	V3873	85422	Arimani	Adoor	Pathanamthitta	Kerala
41	112	V3879	85424	Konnamankara	Pandalam	Pathanamthitta	Kerala
42	114	V3885	85426	Kotta	Moduveli	Pathanamthitta	Kerala
43	115	V3888	85427	–	Aranmula	Kottayam	Kerala
44	116	V3891	85428	–	Kuttoor	Pathanamthitta	Kerala
45	117	V3892	85429	–	Kuttoor	Pathanamthitta	Kerala
46	121	V3899	85433	Cholakkodi	Chambakkara	Kottayam	Kerala
47	122	V4031	85434	Ottanadan	Kallara	Kottayam	Kerala
48	127	V4060	85437-a	Wild	Kudajadiri	Udupi	Karnataka
49	175	V4168	85487	–	Mukkali rd.	Palakkad	Kerala
50	176	V4174	85488	–	Mukkali Rd	Palakkad	Kerala
51	216	V4288	85528	Arivally	Panniyur	Kannur	Kerala
52	217	V4289	285529	Karimundi	Panniyur	Kannur	Kerala
53	218	V4290	85530	Arakalamundi	Panniyur	Kannur	Kerala
54	219	V4291	85531	Vattamundi	Panniyur	Kannur	Kerala
55	221	V4293	85533	Kanjiramundi	Panniyur	Kannur	Kerala
56	224	V4296	85536	Kuttianikkodi	Panniyur	Kannur	Kerala
57	225	V4297	85537	Kottanadan	Panniyur	Kannur	Kerala
58	226	V4298	85538	Kutching	Panniyur	Kannur	Kerala
59	228	V4300	85540	Kalluvalli	Panniyur	Kannur	Kerala
60	232	V4304	85544	Vokkale	Panniyur	Kannur	Kerala
61	233	V4305	85545	Cul.331	Panniyur	Kannur	Kerala
62	275	V4108	266411	Wild	Charmadighat	S.Kanara	Karnataka
63	276	V90/P-1	266410	Karimunda	Mandiram	Pathanamthitta	Kerala
64	288	V90/P-76	266414	Wild	Kallar estate	Kollam	Kerala
65	290	V90/P-79	266415	–	–	Kollam	Kerala
66	303	V90/P-94	266418	Kariyilanchi	Ithikkara	Kollam	Kerala
67	305	V/90—96	266419	–	Ochira	Kollam	Kerala
68	306	V91/P-99	266379	Wild	Makkootta	Kudagu	Karnataka
69	309	V91/P-137	266382	–	Sullya	S.Kanara	Karnataka
70	310	V91/P-138	266383	–	Sullya	S.Kanara	Karnataka
71	321	V91/P-188	266394	–	Malampuzha	Palakkad	Kerala
72	322	V91/P-189	266395	Wild	Malampuzha	Palakkad	Kerala
73	324	V91/P-191	266397	Wild	Malampuzha	Palakkad	Kerala
74	327	V91/201P-202	266400	–	Kappunakam	Malapppuram	Kerala
75	329	V91/P-205	266402	–	Thachanatukara	Palakkad	Kerala
76	330	V91/P-206	266403	–	Kunnakkad	Palakkad	Kerala
77	332	V91/P-180	266405	–	Moozhiar	Pathanathitta	Kerala
78	334	V91/P-179	266407	Wild	Palaruvi	Kollam	Kerala
79	343	V92/P-256	266438	–	Appangala	Kudagu	Karnataka
80	356	Kuthiravlly II	266441	–	PRS, Panniyur	Kannur	Kerala
81	363	Cul-406	266445	Cul-406	IISR, Calicut	Kozhikkode	Kerala
82	364	Vally	266446	Vally	PRS, Panniyur	Kannur	Kerala
83	367	Kottanadan II	266447	Kottanadan-II	PRS, Panniyur	Kannur	Kerala
84	371	Kaniakadan	266451	–	PRS, Panniyur	Kannur	Kerala
85	380	Arakalamunda	266455	Arakalamunda	PRS, Panniyur	Kannur	Kerala
86	383	Karimunda IV	266456	Karimunda-I	PRS, Panniyur	Kannur	Kerala
87	385	Perumkkodi	266457	Perumkodi	PRS, Panniyur	Kannur	Kerala
88	390	TMB-XII	266459	TMB-XII	PRS, Panniyur	Kannur	Kerala
89	426	VB/2001-67	373828	Ottamaniyan	Ariyankavu	Kollam	Kerala
90	431	VU/2001-19	373770	–	Onthupacha	Kollam	Kerala
91	432	VU/2001-9	373575	Vadakkan	Kulathupuzha	Kollam	Kerala
92	435	Panniyur-1	–	Panniyur-1	PRS, Panniyur	Kannur	Kerala
93	441	Panniyur2	–	Panniyur-2	PRS, Panniyur	Kannur	Kerala
94	442	Panniyur4	–	Panniyur-4	PRS, Panniyur	Kannur	Kerala
95	444	Panniyur5	–	Panniyur-5	PRS, Panniyur	Kannur	Kerala
96	445	V3656	85331A	–	Kallar	Idukki	Kerala

and colour change in ripening. The subjective classification resulted in inclusion of seven collections in race 1 and 96 collections in race 2. The quantitative data was computed for range, mean, SD and phenotypic CV% separately for each race and furnished separately for races 1 and 2 in Table 3. Frequency class distribution of 7 qualitative data was made. Finally data on 12 quantitative and 8 qualitative characters (including the codes for races) were used for sequential, agglomerative, hierarchical and tested clustering (SAHN) based on computed similarity or dissimilarity indices (SIMINT) using linearly transformed rectangular data matrix in NTSYS 2.2 package. A tree dendrogram showing the clustering pattern in the collection is furnished in Figure 3. Three samples representing round berried type and four of oval berried type (replicated thrice) were subjected to estimation of essential oil content and oleoresin content and mean values were given in Table 4 for race 1 and 2 respectively. Diagrammatic representation of the two berry shapes is furnished in Figure 2 and a photograph of the two types in Plate 1. Geographic distribution of the two races has also been furnished in Figure 3. The present information has been interpreted in view of the available information of berry shape in related species of the genus distributed naturally in forests of the Western Ghats and based on the evidences available in literature.

List of descriptors and their states

S.No.	Character	Codes for descriptor states		
1	Race	1-Race 1	2- Race 2	
2	Status	1-Cultivated	2-Wild	
3	Berry shape	1-Round	2-Oval	
4	Berry size	1-Small	2-Medium	3-Large
5	Fruit pungency	1-Low	2-Medium	3-High
6	Seed shape	1-Round	2-Oval/conical	
7	Seed size	1-Small	2-Medium	3-Large
8	Berry colour change	1-Fast	2-Slow	
9	Berry length (mm)			
10	Berry width (mm)			
11	Single spike wt. (g)			
12	Fresh berry wt./ spike (g)			
13	100 berry volume (ml)			
14	100 berry fresh wt.(g)			
15	100 berry dry wt. (g)			
16	100 seed fresh wt. (g)			
17	100 seed dry wt. (g)			
18	Seed length (mm)			
19	Seed width (mm)			
20	Berry dry wt.%			

Results and Discussion

On the basis of berry shape and the time taken for berry colour change in ripening berries, two distinct cultivar groups such as oval and spherical berry bearing types were identified. The passport information is listed in Table 1. The oval berried cultivars were mostly confined to southern most districts of Kerala (Fig. 2). The one such sample was collected from an estate in Palkkad district. This might be as a result of spread of this type from Southern Kerala through the newly settled farming communities. Only three cultivars such as Karivilanchi, Nadan and Elamaravan belong to the first group. Oval berry shape is closely associated with the slow pace of colour change in ripening berries. However, few collections falling under the race 2 with round berry shape such as IC 85402 ('Palikkodi') from Pathanthitta, IC 266418 (wild) from Kallar estate in Kollam, IC 266400 from Malappuram, IC 466407 (wild) Palaruvi in Kollam, IC 266456 ('Karimunda-II', a variant of typical 'Karimunda') kept by a Research Station also exhibited the slow pace of colour change. Thus, the evolutionary significance of both berry shape and the colour change in ripening berry appear to have close association that can be possibly traced back to the species/ crop origin and domestication. Such types are rarely noticed in the forest and in farmers' fields.

The first group hailing from southern Kerala contained seven accessions with oval berries, more pronounced and uniform yellow colour of mature berries and uniformly larger berries. The large berry size is commercially a

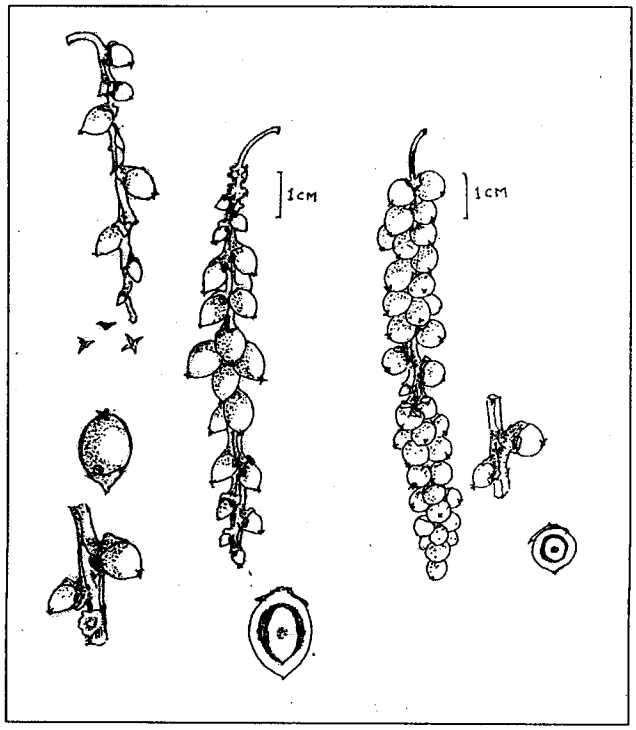


Fig. 1: Diagrammatic representation of oval and round fruits

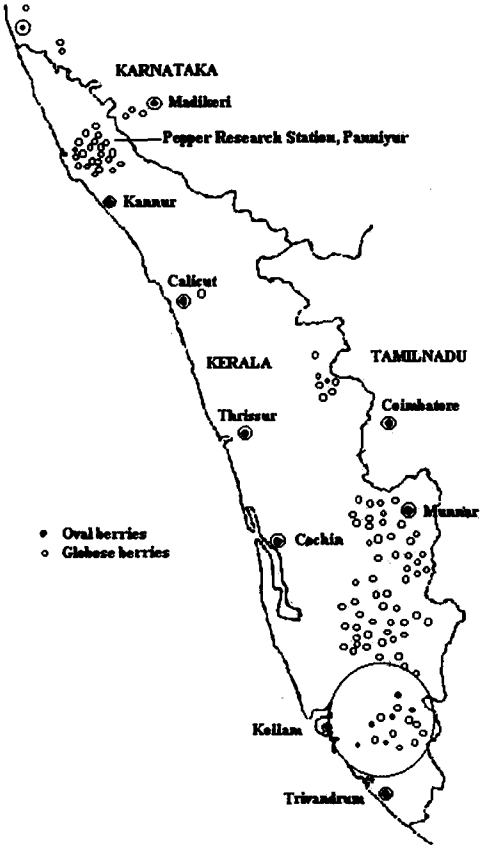


Fig. 2: Distribution of black pepper races in southern region

useful character. The second group included ninety six accessions with round berry, less uniform yellow colour in mature berries and with highly varying berry size from small to large. This group is uniformly distributed all over in the pepper growing areas in Kerala and Karnataka and as wild in forest areas. Diagrammatic representation of the berry of each group is given in Figure 1 and photographs in Plate 1. The variation noticed in race 2 is very high as compared to race 1 as evident from range, mean, SD and CV% for 12 quantitative characters in Table 2. In race 1, higher amount of phenotypic CV% values *viz.* 68.21%, 120.81% and 66.64% were noticed in the case of single spike weight, fresh berry weight/ single spike and 100-berry volume respectively. The range of CV% varied from 23.08% in berry dry weight% to 120.81% in the case of fresh berry weight per spike. With respect to race 2 greater CV% values *viz.* 62.06, 50.61% 59.97% and 50.61% were obtained in berry length, berry width, seed length and seed width respectively.

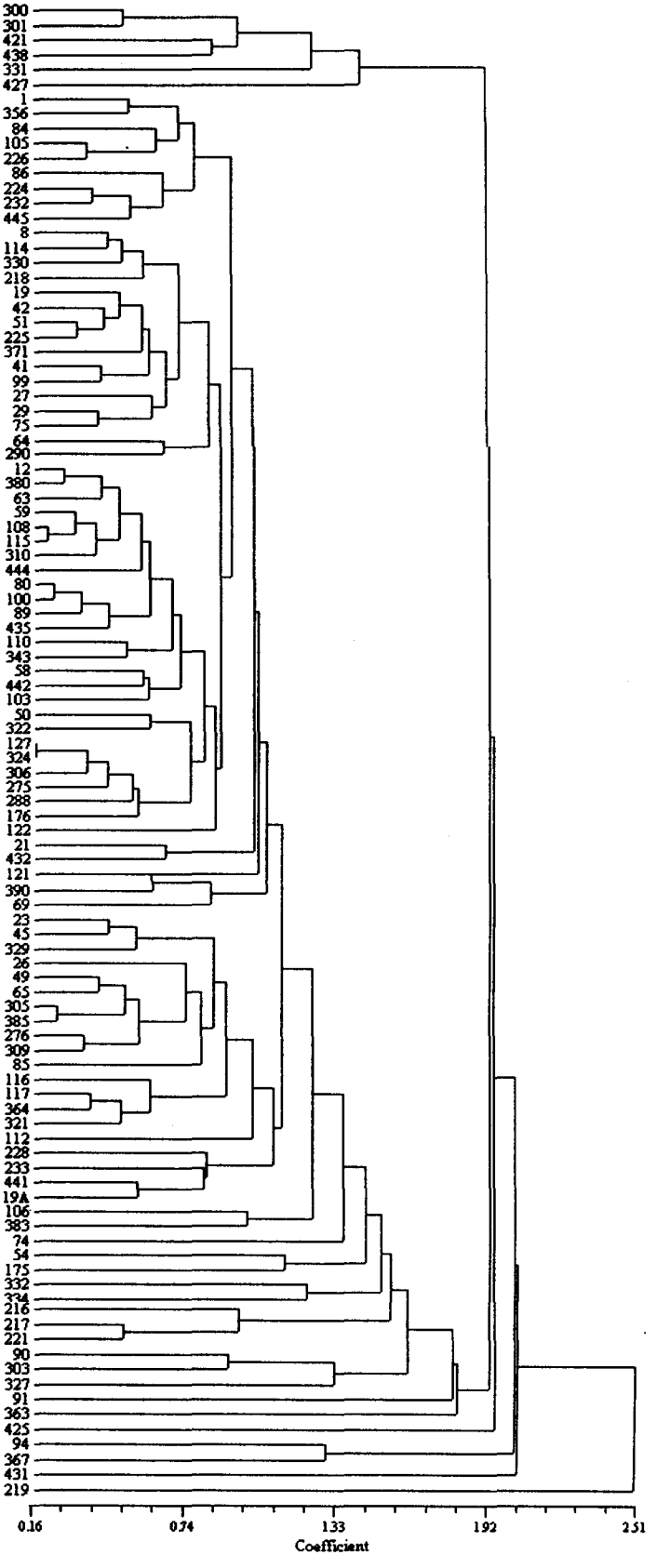
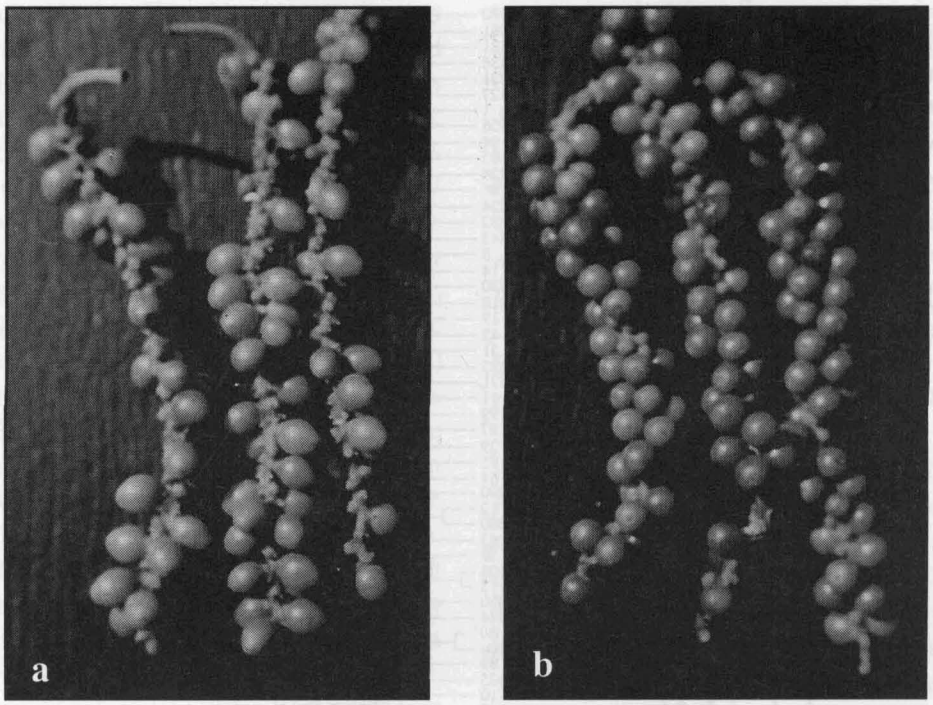


Fig. 3: Dendrogram of black pepper cultivars



IC 266217 (Race 1- 'Kariyilanchi') *IC 85320 (Race 2- 'Karimunda')*

Plate 1. Black pepper with oval/oblong fruit and that with round fruit

Table 2. Showing range, mean, SD and CV% in round berry bearing type

Race-1 (Oval berried types)						
	Berry length (cm)	Berry width (cm)	Single spike wt. (g)	Berry wt./ spike (g)	Hundred berry wt. (g)	Hundred dry berry wt. (g)
Min	0.53	0.47	1.70	1.44	2.62	2.44
Max	7.40	7.30	36.90	72.00	27.04	12.00
Mean	5.23	5.00	5.93	5.76	12.70	5.14
S.D	1.940	1.851	4.05	6.95	3.84	1.55
CV%	37.10	37.03	68.21	120.81	30.26	30.29
	Hundred berry volume (ml)	Hundred fresh seed wt. (g)	Hundred dry seed wt. (g)	Deed length (cm)	Seed width (cm)	Berry dry wt. %
Min	3	3.60	2.08	0.43	0.40	21.62
Max	143	20.40	5.80	6.67	5.45	56.08
Mean	14.57	6.51	4.00	4.08	3.84	39.70
S.D	15.45	2.80	0.83	1.49	1.37	9.16
CV%	106.04	42.95	20.77	36.37	35.93	23.08
Race-2 (Round berried types)						
	Berry length (cm)	Berry width (cm)	Single spike wt. (g)	Berry wt./ spike (g)	Hundred berry wt. (g)	Hundred dry berry wt. (g)
Min	0.62	0.54	3.23	2.88	6.4	4.72
Max	7.80	6.11	7.50	6.72	15.92	7.76
Mean	4.43	3.88	5.29	4.77	11.51	6.22
S.D	2.75	2.34	1.49	1.33	3.01	1.10
CV%	62.06	60.28	28.19	27.92	26.12	17.63
	Hundred fresh volume (ml)	Hundred dry seed wt. (g)	Deed length seed wt. (g)	Seed width (cm)	Berry dry (cm)	Hundred berry wt. %
Min	6	4	2	0.46	0.41	28.35
Max	16.40	16.40	8.10	5.20	4.51	48.70
Mean	12.44	9.64	4.95	3.41	3.07	39.83
S.D	3.67	4.88	1.71	2.04	1.82	6.21
CV%	29.53	50.61	34.61	59.97	59.20	15.59

Table 3. Frequency distribution of various qualitative characters

Parameter	Classes	Class description	Number	Total
Status	1	Cultivars	87	103
	2	Wild	12	
	3	Improved	4	
Fruit shape	1	Globose	93	103
	2	Oval	10	
Fruit size	1	Small	10	103
	2	Medium	60	
	3	Large	33	
Pungency	1	Low	20	103
	2	Medium	61	
	3	High	22	
Seed shape	1	Globose	91	102
	2	Oval/conical	11	
Seed size	1	Small	29	100
	2	Medium	48	
	3	Large	23	
Fruit colour	1	Green to yellow to red fast	92	103
	2	Green to yellow to red slow	11	

Table 4. Chemical characters of black pepper races

Berry shape		Essential oil content	Oleoresin content
Round berry (race 2)	Mean	3.83	41.36
	SD	0.47	1.80
Oval berry (race 1)	Mean	4.33	30.06
	SD	0.35	3.03

Table 5. Berry shape in related species as per the taxonomic reports

Species	Berry shape	Colour change	
Piper schmidtii	Oblong/oval	Ripening black	Small
Piper wightii	Conical/shperical	Ripening orange yellow to red	Large
Piper tricho stachyon	Oblong/spherical	Ripening orange yellow to red	Large
Piper galeatum	Oblong/spherical	Ripening orange yellow to red	Large
Piper bababudanii	Oblong/oval	Ripening orange yellow to red	Large
Piper sugandhi	Oblong/oval	Ripening orange yellow to red	Large
Piper pseudonigrum	Spherical	Ripening orange yellow to red	Large

The range of CV% varied from 15.59% in berry dry weight to 62.06 in berry length. The berry dry weight% showed a CV% range of 28.35 to 48.7. Thus in both the groups berry dry weight % had good range of variation.

All the above given 20 characters (8 qualitative including the race code based on subjective observation and 12 quantitative were used for clustering and the dendrogram (Fig. 3) indicated that all the 6 collections of race 1 clustered together at 1.5 CEC. However, a cultivar from Kollam was far away separated along with collections falling under race 2. Thus 6 collections were categorised in race 1.

The two chemical parameters such as essential oil content and oleoresin content in representative samples of both the races also exhibited some difference. The oleoresin content which is more (41.36) in the second type than that in the first (30.06%). The actual difference will have to be studied in detail.

Black pepper as a wild species and as crop has a monocentric origin in and around forests of Western Ghats. Its gene pool based on breeding behaviour is yet to be worked out. Diversity of closely related species and varieties to black pepper are maximum noticed in Western Ghats. Ravindran (1991) proposed two probable bases for the origin of black pepper through natural hybridization and suggested that *P. wightii* x *P. galeatum* gave rise to *P. nigrum* with 2n =52 and *P. wightii* x *P. nigrum* var. *hirtullosum* with 2n=52 chromosomes. The picture of natural hybridization of these species as drawn by him may not be very true as the existing ecological niches of the above species are much-differentiated altitudinally in the mountain. Further, the grouping and clustering of species on the basis of morphology has given different pictures in the past as reported by Rahiman (1981) and Ravindran *et al.* (1991). Rahiman's study indicated that *P. nigrum* and *P. bababudanii* were closer where as that of Ravindran et al. (1991) indicated that *P. nigrum* and *P. sugandhi* were closer. *P. psuedonigrum* and *P. sugandhi* are morphologically very close and greater distribution all over Western Ghats in Kerala, Karnataka and Tamilnadu along with intermediate types. *P. galeatum, P. trichostachyon, Piper nigrum, P. nigrum* var. *hirtullosum, P. sugandhi / P. pseudonigrum* and *P. bababudanii* could be noticed in forests of Coorg district. Glabrous forms of *P. pseudonigrum* and *P. sugandhi* are almost similar. Hairy forms of *P. pseudonigrum* are almost similar to *P. nigrum* var. *hirtullosum*. Thus there is very dynamic and turbulent situation of closely occurring species in evergreen forests at middle elevations of Western Ghats especially at 1000 m. elevation. Such situations occur in Coorg, Nilgiris, Coimbatore, Idukki, Pathanamthitta, Kollam, Thiruvananthapuram and Tirunelveli districts. Some of the intermediate types were doubted for *P. nigrum* earlier. *P. wightii* usually occur in rare pockets

in above 2000 m elevation in Nilgiris, Anamalays and Munnar. It is gradually becoming eroded too due to habitat distruction. Further, *P. nigrum* var. *hirtullosum* is also very much related to *P. pseudonigrum* which have greater distribution in areas where natural population of *P. nigrum* is less. True natural population of *P. nigrum* is usually noticed up to 900 m elevation; above, which either cultivated *P. nigrum* or its run wild populations occur along with *P. sugandhi, P. pseudonigrum, P. galeatum, P. trichostachyon* etc. Pepper as a crop probably was domesticated from the wild clones and this process is still going on in Uttar Kannada forests in Karnataka. There is a possibility of domestication of intermediate natural hybrid progenies by vegetative means in the past and these clones might remain without much change in farming areas around the vicinity of the original home. Thus the occurrence of oval berried types in eastern parts of Kollam district of Kerala can be attributed to original domestication of similar types involving natural hybrid population arising from chance interspecific hybridization in forest areas between round berried wild *P. nigrum* and those species with oval berries. *P. schmidtii, P. wightii, P. trichostachyon, P. galeatum, p. bababudanii* and *p. sugandhi* have been reported to have the oval, hemi-spherical, oblong berries. Variation within the species with respect to berry shape may be also present.

Since *P. nigrum* is a polymorphic species having good amount of morphological variation and chromosome numbers reportedly varying from 2n = 52 to 128, existence of interspecific hybrids in wild and cultivated populations having different genomes cannot be ruled out. This obviously is a point for detailed study including interspecif hybridization, morphological and molecular characterization of the wild species, interspecific hybrids and their back crosses involving wild and cultivated *P. nigrum* and others in order to clearly define the gene pool of black pepper and its relatives in Western Ghats. It is probable that the oval berry shape noticed in both in cultivated and wild *P. nigrum* has an evolutionary significance while studying the origin of the crop through natural hybridization. According to Harlan (1975), in dynamics of crop domestication the effects of selection pressure in vegetatively propagated crops are absolute and immediate as against those in seed crops. As black pepper is a good example of pure form of 'vegeculture' Harlan's point is quite acceptable in order to assume instant domestication of such cultivated types from the wild clones in rare pockets. The two races identified in the present study have been named as 'Kariyilanchi' for race 1 and 'Karimunda' for the race 2 as these were representative common cultivars of black pepper in the region.

Race 1. 'Kariyilanchi'

Standard representative specimen: Live specimen Collectors No. V90/P-92; IC 266417

Distribution : Ithikkara, Kollam, Kerala, India

Race 2. 'Karimunda'

Standard representative specimen: Live specimen: Collector's No. V-3646; IC 85320

Distribution: Puyamkutti, Idukki, Kerala, India

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Selecting Accessions in Soybean Collection with High Diversity

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The paper suggests a diversity efficient and computationally convenient procedure for selecting distinct accessions for breeding as well as core-set formation purpose. Soybean germplasm data comprising of 270 accessions, evaluated for seven important quantitative traits were used for the study. Thirty entries scoring the highest inertia values in individual clusters, when selected, resulted in highest pooled Shannon Diversity Index as well as coefficient of variability for individual characters.

Key words: Soybean, Diversity, Principal component

Plant breeders look for distinct and unique variability out of the large number of accessions available with them with an aim of increasing the level of expression of economic traits in the crossed combinations. Their primary concern is how to select the desired variability to carry out the breeding programme preferably with low number of accessions keeping in view the time and resource constraints. Thus, choice of parents for hybridization is one of the most critical factors in deciding the outcome. This is important because it determines the kind of variability expected in segregating generations, thereby setting the limits for improvement. The choice of parents largely depends upon the objectives. Various methods of selecting parents in *Triticum aestivum* have been discussed by Bhatt (1973). These methods are based on either ecogeographic diversity (Cox and Worall, 1987), character compensation (Grafius, 1965), early generation testing (Thurling and Ratinam, 1987) or measures of combining ability. These methods generally consider few parents. Many breeding programmes in the major crop species have reached a stage where yield improvement is slow or has almost reached a plateau. In this situation, a different strategy has to be adopted to increase the pace of improvement. A narrow genetic base among released cultivars and the practice of using elite line x elite line crosses has been implicated in slowing the rate of genetic advance for yield (Lal and Rana, 2000). There are two potential ways of overcoming the yield barrier. One is to look for traits/genes, which can enhance the adaptability of the cultivar in a specific production system/agro-climatic region. The other way is to use genetically diverse parents. Clustering germplasm into various groups using hierarchical or non-hierarchical algorithms based on multivariate statistical techniques, and sampling from within discrete groups is a common method for maximizing diversity. What and how many entries to be selected from each group, particularly when the population is large, is again cumbersome procedure. Various strategies have been proposed to select a number of entries from each group, particularly in relation to developing core sets (Brown, 1989; Schoen and Brown, 1995). In an empirical analysis, these authors ranked the various strategies according to the highest to the lowest expected allele retention and found the M Maximization) strategy to be superior. Principal Component Score Strategy (PCSS) suggested by Hamon and Noirot (1996), Noirot *et al.* (1996), Mahajan *et al.*, 1996), Srivastava *et al.*, (1999), Sapra and Lal (2003) and others, based on quantitative traits for selecting the accessions. Sapra and Lal (2003) discussed the issue of minimum sample size and estimated, under certain assumptions, the required target population size for including variability ranging from low to high. Inertia score has been used to select accessions to maximize the variability in the sample. The suggested approach slightly differs from above as it makes use of both i.e. the inertia score as well as is the grouping done based on *K-Means Clustering* for ensuring high and representative variability in the sample.

Materials and Methods

Data on 270 lines representing Indian as well as exotic variability. The crop was grown in 5 m rows during *kharif* (crop season beginning with the arrival of *monsoon* in July) 2004 in an augmented design (Federer, 1956) with five checks. Data was recorded on seven quantitative and four qualitative traits. However, the quantitative data was subjected to Principal Component Analysis (PCA) to calculate inertia scores (defined below). First three Principal Components with an Eigen value of one or more

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were extracted. The Relative Contribution (RC) for each accession was determined as follows:

Let Y_{ij} be the score through PCA for i^{th} (i = 1, 2 . . . N) accession and j^{th} (j = 1, 2 . . . k) principal component. The inertia of the i^{th} accession is defined as

$P_i = \Sigma_j Y_{ij}^2$ The relative contribution for the i^{th} accession is given by $RC_i = P_i /Nk$. Accessions were arranged in descending order of inertia.

The data was also subjected to classification using *K-Means Clustering* after applying the z- transformation. The number of clusters (k) was taken equal to the number that is approximately equal to the 10% of the collection size, a number normally required for developing germplasm core set for retaining at least 70% or more allelic diversity in the sample. In our case 30 clusters were formed. The quantitative data for all the characters was converted into qualitative one by dividing the individual character range into five equal intervals. The pooled Shannon Diversity Index (pooled over the characters) was chosen as the measure of diversity and for comparison purpose.

Proposed Selection Procedure

(i) Select a single entry from each cluster whose inertia score is the highest in the cluster.

(ii) Count the frequencies of each character state and calculate the individual SDI for all the characters. Pooled SDI is the sum of individual SDIs.

Results and Discussions

The first three principal components could explain 71% of the total variation, whereas the first two components around 56%. Graph 1 and 2 give the spread in a two dimensional space of all the 270 data points as well as the points related to 30 accessions selected from 30 clusters and top 30 points in terms of inertia score respectively. If we examine the top 30 points in Graph 2, it is clear that these points are distantly located from the centre and hence play significant role in the divergence and that is why the top entries have higher values of diversity index as compared to that of the whole collection (Table 2). The points, which are located near the centre of the graph, have low inertia score and contribute less to the diversity. The pooled diversity decreases from top to bottom i.e., from 9.070 to 5.732 (Table 2). However, the diversity of individual characters does not show a declining trend for all the characters when we move from top to bottom (Table 2). For example the middle 30 accessions show lower values of SDI for plant height and pods/plant as compared to those of bottom accessions. The basic objective here is to look for those points, which can give higher diversity than that of the top 30 entries.

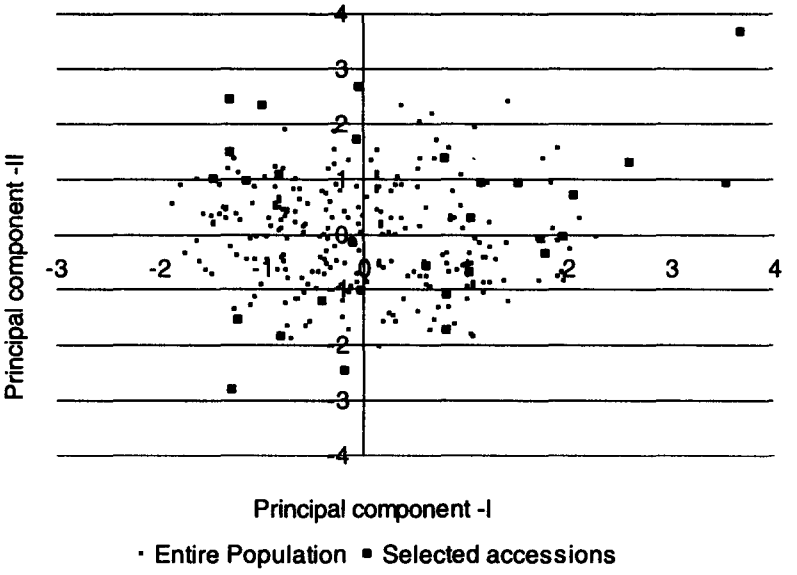
Graph 1 indicates the 30 points having the highest inertia and located in the 30 disjoint-clusters. On comparing the two graphs we find that nearly 60% of the points are common. Some of the points have come closer to the centre. *K-Means Clustering* divides the 270 objects into 30 clusters such that some metric relative to the centroids of the clusters is minimized. Thus, the selected points represent the homogenous clusters, are bound to give better representation of the variability in the sample. If we compare the values of SDIs between top 30 entries and clusters points, the values are higher for all the characters except for plant height. The sample of cluster points resulted in the highest pooled SDI (9.463). Table 3 gives a comparative view of the variation in terms of range and coefficient of variation (%) for the entire collection and cluster points. The range for individual characters is either equal to that of entire collection or almost approaching it. The CV (%) values are higher for all the traits for cluster-selected-points. Thus, selection based on inertia score and clustering could be an appropriate choice if the objective is to maximize the diversity for a given sample size. This procedure is diversity efficient, computationally convenient and

Table 1. Eigen value and variation

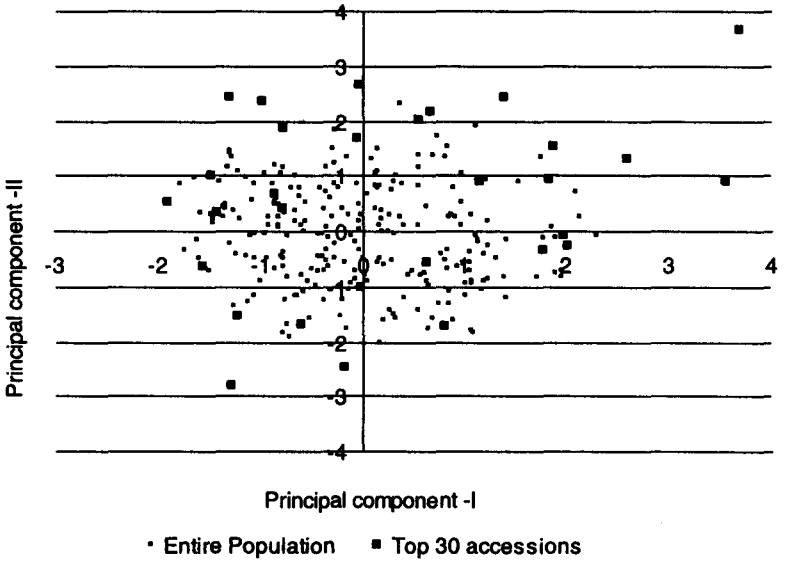
Principal Component	Eigen value	Variance (%)	Cumulative %
I	2.55	31.872	31.87
II	1.917	23.96	55.83
III	1.214	15.171	71

Table 2. Shannon Diversity Index for various samples, and entire collection for individual traits

	Days to 50% flowering	Days to maturity	Plant height	Number of branches	Number of pods/plant	Number of seeds	Yield per plant	Pooled SDI
Population	1.377	1.316	1.480	1.224	0.897	1.156	0.994	8.444
Top 30	1.448	1.320	1.431	1.328	1.111	1.200	1.232	9.070
Middle 30	0.976	1.239	1.067	1.012	0.543	1.198	0.730	6.766
Bottom 30	0.887	0.822	1.198	0.722	0.703	0.778	0.623	5.732
Clusters points	1.407	1.458	1.367	1.477	1.152	1.206	1.395	9.463



Graph 1: *Spread of entire population and accessions from 30 clusters in a two dimensional space*



Graph 2: *Sperad of entire population and top 30 accessions in a two dimensional space*

straight forward. The procedure can be easily adopted for large collections, particularly, where the information on geographical diversity is lacking or unavailable. Selection of entries from the non-hierarchical groups is not optional but logical as the entry with the highest inertia is included in the sample.

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Table 3. Showing variation in quantitative traits for the entire collection and cluster selected points (bold)

	Minimum	Maximum	Mean	CV(%)
Days to 50%	33	55	44.10	9.41
Flowering	35	55	43.67	12.36
Days to maturity	87	115	100.23	5.54
	87	115	99.63	8.30
Plant Height (cm)	18.67	97	61.01	27.60
	20.00	90	56.95	37.57
Number of Branches	0.67	9	4.13	33.13
	0.67	9	4.81	43.13
Number of Pods/plant	6.5	171.5	41.69	45.49
	6.5	171.5	51.17	63.43
Seeds/pod	1.2	2.73	1.99	12.47
	1.4	2.53	2.01	14.84
Yield/plant	0.42	22.43	4.92	72.95
	0.42	22.43	6.66	87.05

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Morphological Characterization of *Sesbania* Accessions using Multivariate Analysis

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Forty accessions of *Sesbania* belonging to 13 species tracing their origin to India, Brazil, Australia and Philippines, were evaluated for 15 agro-morphological characters in Randomized Block Design with three replications. Accessions showed significant genetic variability for all the 15 characters. Euclidean distance (D^2) between all possible pairs (780 pair comparisons) of accessions were calculated and used in unweighted pair group method with arithmetic average cluster analysis. The accessions were delineated into 7 clusters. The highest inter-cluster distance (33.44) was present between cluster 1 and 7 followed by distance of cluster 7 with cluster 2 and 3. Cluster 7 contained only one accession of *bispinosa* species and was isolated from other clusters. Majority of *S. rostata* species were grouped together in one cluster. Other clusters were heterogeneous. The composition of clusters indicated that geographic diversity is not the sole factor for determining the genetic diversity. The botanical origin of the species needs to be established. The study suggested that grouping of *Sesbania* accessions would facilitate in maintaining and utilizing the germplasm resources. Some potential pairs of accessions are suggested for their utilization in hybridization programme.

Key words: *Sesbania*, Characterization, Cluster analysis, Euclidean distance, Multivariate analysis

The genus *Sesbania*, one of the important genera of legumes, is ecofriendly and has a great potential for sustaining of agriculture. It is an organic biofertilizer due to its heavy root nodulation and helps to improve soil physical structure, texture and prevents leaching and loss of nutrients. *Sesbania* species have many other uses like ruminant fodder, fire wood and medicines (Veasey *et al.*, 1999). Considering the immense importance of the *Sesbania* species, there is renewed interest in utilization and genetic improvement of this genus. Germplasm characterization of *Sesbania* will be of great help in maintaining and utilizing germplasm resources and initiating a sound breeding programme of this important genus. However, very limited information is available on this aspect of *Sesbania* germplasm. Therefore, this study is aimed to present characterization of a set of 40 diverse accessions of *Sesbania* using 15 agro-morphological traits in field testing.

Materials and Methods

Forty land races of *Sesbania* comprising 16 indigenous and 24 exotic belonging to 13 species represented a wide spectrum of variability. These accessions had their origin from Australia, Brazil, India and Philippines. The material was planted in Randomized Block Design in three replications at the experimental area of Department of Pant Breeding, CCS HAU, Hisar. Each plot was of 3 m length with row to row spacing of 45 cm and plant to plant spacing of 15 cm. Five plants were randomly selected from each accession in each replication for recording the observation on 15 agro-morphological traits viz., plant height at 20 days after sowing (20 DAS), plant height at 60 DAS, green biomass at 60 DAS, number of root nodules at 60 DAS, fresh weight of root nodules at 60 DAS, number of leaves per plant at 50% flowering, number of leaflets at 50% flowering, leaf length at 50% flowering, plant height at maturity, number of pods per plant, pod length, number of seeds per pod, dry biomass of plant, 100-seed weight and seed yield per plant. Euclidean distances (D_i^2) between all possible pairs of accessions were calculated based on 15 characters (Mahalanobis, 1948) and used in unweighted pair group method with arithmetic average (UPGMA) cluster analysis (Romesburg, 1984).

Results and Discussion

Significant differences were observed for the characters among accessions (Table 1). This indicated a substantial genotypic variability to further pursue the cluster analysis. Cluster analysis of the 40 accessions of *Sesbania* was performed using D^2 statistics based on Euclidean distances. The analysis delineated the accessions into 7 clusters (Fig. 1 and Table 2). The composition and geographic origin of the accessions in different clusters are depicted in Table 1. The clusters appeared to be homogeneous within themselves but differed from each other. Cluster 1 contained 9 accessions. All these accessions were exotics except one indigenous accession

Table 1. ANOVA for 15 quantitative traits in 40 *Sesbania* accessions

Mean square for	Source of variation		
	Replication (2)	Treatment (39)	Error (78)
Plant height at 20 DAS (cm)	78.59	52.64*	28.61
Plant height at 60 DAS (cm)	2696.56	2245.48*	254.63
Green mass at 60 DAS (g)	38.50	6852.38*	161.85
No. of root nodules	45.30	2393.97**	17.28
Weight of root nodules (g)	0.83	0.88**	0.08
No. of leaves at 50% flowering	82.95	6408.92**	61.24
No. of leaflets per leaf	7.37	162.43**	26.33
Leaf length at 50% flowering (cm)	42.96	165.31**	6.06
Plant height at maturity (cm)	1010.06	9807.62**	2041.76
No. of pods	426.53	11909.89**	1551.74
Pod length (cm)	6.48	24.00**	3.68
No. of seeds per pod	22.01	47.39**	11.25
Dry weight at 60 DAS (g)	87.26	55.90**	12.96
100-seed weight (g)	0.05	0.71**	0.16
Seed yield per plant(g)	51.74	1430.33**	58.71

*Significant at 5 per cent level.
**Significant at 1 per cent level.

Table 2. Cluster composition based on clustering on morphological characters and geographic origin of *Sesbania* accessions (T)

Cluster	Acc. (No.)	Coded Acc.	Species	Accession	Origin/source
1	9	T4	*S. rostrata*	EC 223312	IRRI, Philippines
		T6	*S. rostrata*	EC 218472	IRRI, Philippines
		T5	*S. rostrata*	EC 178342	IRRI, Philippines
		T8	*S. sesban*	EC 213473	IRRI, Philippines
		T2	*S. rostrata*	EC 331973	IRRI, Philippines
		T3	*S. rostrata*	IC 277784	PAU, Ludhiana
		T14	*S. sesban*	EC 509439	Brazil
		T15	*S. exasperata*	EC 599434	Brazil
		T16	*S. virgata*	EC 509442	Brazil
2	7	T10	*S. aculeata*	IC 277777	PAU, Ludhiana
		T12	*S. aculeata*	IC 277782	PAU, Ludhiana
		T7	*S. rostrata*	EC 213472-A	IRRI, Philippines
		T36	*S. aculeata*	IC Pant-3	Uttaranchal
		T37	*S. aculeata*	NBPGR-3	Najafgarh, New Delhi
		T32	*S. macrantha*	EC 493701	Australia
		T35	*S. aculeata*	IC Pant-1	Uttaranchal
3	9	T29	*S. simpliciuscula*	EC 493667	Australia
		T31	*S. cannabina*	EC 493700	Australia
		T33	*S. macrantha*	EC 493702	Australia
		T34	*S. speciosa*	EC 493706	Australia
		T38	*S. aculeata*	PDCSR-2	Modipuram (UP)
		T39	*S. aculeata*	NIC 4149	India
		T40	*S. aculeata*	NIC 4223	India
		T18	*S. aculeata*	SES H-1	Haryana
		T1	*S. rostrata*	EC 331970	IRRI, Philippines
4	3	T23	*S. exaltata*	EC 493664	Australia
		T26	*S. leptocarpa*	EC 493676	Australia
		T28	*S. exasperata*	EC 493688	Australia
5	4	T9	*S. aculeata*	IC 277791	Modipuram (UP)
		T22	*S. simplicuscula*	EC 493666	Australia
		T11	*S. aculeata*	IC 277786	PAU, Ludhiana
		T25	*S. exasperata*	EC 493687	Australia
6	7	T13	*S. aculeata*	IC 277776	PAU, Ludhiana
		T20	*S. aculeata*	IC 277789	PAU, Ludhiana
		T17	*S. aculeata*	Ses H-9	Haryana
		T19	*S. aculeata*	Ses H-6	Haryana
		T21	*S. simpliciuscula*	EC 493668	Australia
		T27	*S. campylocarpa*	EC 493695	Australia
		T30	*S. exaltata*	EC 493662	Australia
7	1	T24	*S. bispinosa*	EC 493681	Australia

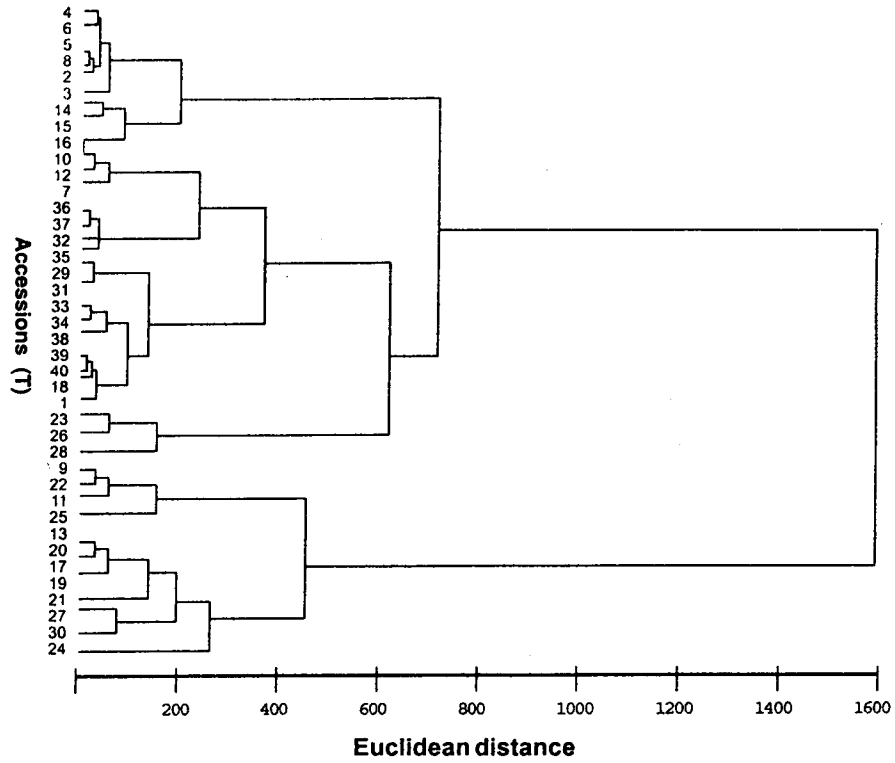

Fig. 1: Dendrogram from cluster analysis with 15 quantitative characters

from Punjab. This cluster contained majority of accessions from Philippines (5 accessions) and three accessions from Brazil. Five accessions of this cluster belonged to *rostrata* species, two belonged to *sesban* and remaining two belonged to *exasperata* and *virgata* species each. Cluster 2 consists of 7 accessions. Majority of them were indigenous. This cluster had two exotic accessions, one each from Philippines and Australia. Cluster 3 had nine accessions: 4 from Australia, one from Philippines and 4 from India. Three accessions, all belonging to Australia were grouped together in cluster 4. Each of these accessions belonged to three different species (*exalata*, *leptocarpa* and *exasperata*). Cluster 5 had 4 accessions, two each from India and Australia. Seven accessions comprising 4 from India and 3 from Australia, were grouped together in cluster 6. These accessions belonged to 4 different species. Cluster 7 was very unique containing only one accession belonging to bispinosa species from Australia.

Intra- and inter-cluster distances are shown in the Table 3. Cluster 4 appears to be more heterogeneous as it had maximum intracluster distance (14.75). The minimum intracluster distance was found among accessions belonging to cluster 3. The highest intercluster distance (33.44) was present between cluster 1 and 7. This was followed by the distances of cluster 7 from cluster 2 and cluster 3. In general, cluster 5 also exhibited substantial intercluster distances from other clusters.

The mean values of clusters for different agro-morphological characters are given in Table 4. The salient features of the clusters for different characters are summarized hereafter.

Cluster 1

Cluster 1 comprised accessions with low mean values for green mass at 60 DAS, number of root nodules, weight of root nodules, number of leaves at 50 per cent flowering, number of leaflets per leaf, pod length and seed yield. It had medium mean values for plant height at maturity, number of pods per plant, number of seeds and 100-seed weight.

Cluster 2

It is characterized by accessions with higher plant height at 60 DAS, higher green mass, high number and weight of root nodules, high number of leaflets, high mean value of plant height at maturity, high number of pods, more number of seeds per pod, low plant dry weight, bold seeded accessions and medium mean value of seed yield.

Table 3. Euclidean intra and inter cluster distances

	Cluster-1	Cluster-2	Cluster-3	Cluster-4	Cluster-5	Cluster-6	Cluster-7
Cluster-1	10.03	16.50	14.28	20.33	25.48	20.24	33.44
Cluster-2		11.19	12.90	22.71	17.13	15.84	27.91
Cluster-3			09.19	16.64	19.80	14.89	26.16
Cluster-4				14.75	25.58	19.07	24.58
Cluster-5					12.32	17.37	21.68
Cluster-6						11.69	18.81
Cluster-7							00.00

Table 4. Mean values of clusters for 15 quantitative traits in 40 *Sesbania* accessions

Cluster	Plant height at 20 DAS (cm)	Plant height at 60 DAS (cm)	Green mass at 60 DAS (g)	No. of root nodules	Weight of root nodules (g)	No. of leaves at 50% flowering	No. of leaflets/ leaf at 50% flowering	Leaf length at flowering (cm)	Plant height at flowering (cm)	No. of pods/ plant	Pod length maturity (cm)	No. of seeds/ plant	Dry weight at 60 DAS (g)	100-seed weight (g)	Seed yield/ plant (g)
1	02.59	139.47	69.90	17.94	0.88	55.67	24.03	22.05	475.24	84.49	18.81	29.57	18.42	2.03	24.68
2	23.26	176.82	135.91	53.07	1.50	42.51	37.98	28.82	528.16	104.25	22.73	34.32	17.90	2.41	45.80
3	22.77	177.79	155.07	29.82	1.14	83.87	35.80	28.83	496.21	86.91	20.08	30.64	23.07	2.15	27.10
4	23.53	163.48	136.19	25.26	0.72	171.87	32.29	19.53	414.53	78.81	19.82	27.53	20.59	1.37	25.42
5	22.57	156.62	124.62	98.67	1.55	78.18	38.36	30.16	475.46	104.56	21.81	30.82	20.63	1.96	31.42
6	21.01	161.95	139.35	56.55	1.50	117.53	36.74	35.56	528.52	176.46	23.44	34.49	22.99	2.47	71.11
7	21.33	155.60	195.13	90.17	2.97	207.17	42.03	40.60	513.67	115.67	22.41	32.10	22.53	1.90	59.17

Cluster 3

Majority of accessions of this cluster were tall at 60 DAS with higher green mass, more number of leaves and leaflets, more plant height at maturity, moderately high number of seeds, more dry weight of plant and accession with low seed yield.

Cluster 4

Cluster 4 consisted of mainly accessions with tall plants at 60 DAS, high green mass, low values for number and weight of root nodules, high number of leaves, medium plant height maturity, low number of pods per plant, small pod length, less number of seeds per pod, small seeded plants and low seed yield.

Cluster 5

The accessions belonging to this cluster were characterized with medium plant height at 60 DAS, medium mean value of green mass, high values for number and weight of root nodules, moderately high number of leaflets, medium plant height at maturity, moderately high number of pods, medium pod length, medium number of seeds and medium mean value for 100-seed weight and seed yield.

Cluster 6

Accessions of this cluster had high average value of plant height and green mass at 60 DAS, medium mean value for number and weight of root nodules, tall plants at maturity, high number of pods per plant, more pod length, more number of seeds, bold seeded plants with high seed yield.

Cluster 7

This cluster consisted of only one accession belonging to the species *bispinosa* from Australia. This accession is characterized with highest mean values for green mass, number and weight of root nodules, number of leaves and leaflets, tall plants at maturity, moderately high number of pods, larger pod size and moderately high seed weight.

In the present study, majority of the *S. rostrata* species were grouped together in cluster 1. All these accessions were from Philippines. Two remaining accessions of *S. rostrata* were grouped in two different clusters i.e. cluster 2 and cluster 3 each. The separation of accessions of the same species into different clusters has also been reported in *Sesbania* by Veasey *et al.* (2001, 2002). On the other hand accessions from Brazil belonging to three different species were grouped together in cluster 1. The other clusters were also heterogeneous having different species together. This warranted further detailed investigation on species relationship in *Sesbania*. Species nomenclature in *Sesbania* has been questioned by Backer and Van den Brink (1963), Markila (1980) and Evans and Rotar (1987). The accessions from Australia tended to be together but split into three different groups. Thus, the complex composition of clusters indicates that the geographic diversity is important but not the sole factor

determining the genetic diversity. Factors other than geographic diversity might also be responsible for different grouping of accessions. This is in agreement with the findings of Gupta and Singh (1970) and Malhotra *et al.* (1974). A plausible explanation is given by Clausen and Hiesey (1958) who demonstrated that even a single component of environment such as the temperature could cause difference between and within the race. Similarly, Murthy and Arunachalam (1966) were of the opinion that the genetic drift and selection in different environments may also cause greater diversity than geographic origin influenced the clustering pattern.

In addition, the reproductive biology of the species may also affect grouping of accession. In *Sesbania* species *sesban* and *virgata* have been reported to be partial allogamous (Heering, 1994; Veasey *et al.*, 2002; Girma *et al.*, 2002). Besides, grouping of subjects (accessions) into clusters may be rather sensitive to the particular choice of variables (characters) used in clustering. A different choice of variables, apparently equally reasonable, may give different clusters (Manly, 1998). The characters related to floral morphology and other taxonomic characters are more relevant to the botanical origin of the species.

The inter-cluster distances and the mean performance of accessions suggested that improvement in yield may be achieved by use of T3 accession from cluster 1 and T24 from cluster 7 as parents in the crossing programme. Similarly, accession T37 (NBPGR-3) belonging to cluster 2 with high green mass should be crossed with accession T24 for genetic improvement of green mass for manuring. The other potential pairs of parents are: T3 from cluster 1 with T11 from cluster 5, and T23 from cluster 4 with T11 from cluster 5. These pairs of parents have high mean values for green biomass with high genetic divergence between them.

It is evident from the study that measurement of divergence between accessions and grouping them according to similarity will facilitate the selection of potential parents for hybridization. This information supplemented with passport data would be useful to *Sesbania* breeders for proper maintenance and exploitation of the germplasm in crop improvement programme.

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Characterization of *Capsicum* spp. Germplasm

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A total of 53 accessions of *Capsicum* spp. collected from Kanyakumari district of Tamil Nadu was characterized for 38 characters. The frequency was very high for four characters *viz.* absence of anthocyanin spots over fruits, neck at base of fruit and fruit blossom end appendage, and lanceolate-shaped cotyledonous leaf. Predominance of single descriptor state was found in more than 50 per cent accession for 25 characters. Wide variability was exhibited in all the quantitative characters studied except for the trait fruit bearing period. Importance of studied characters in utilization is narrated.

Key words: Chilli, Characterization, Utilization, Western Ghats

Hot pepper (*Capsicum annuum* L.) is one of the most commercially grown vegetables in the tropics. It was probably introduced by Portuguese into southern parts of India as evidenced by the fact that there were only three races of chilli being cultivated in India by the year 1642 AD (Heiser, 1976). Cultivation spread throughout the country by the end of 19th century. Due to continuous selection, long history of cultivation and popularity of the crop, sufficient genetic variability has been generated. Now India is believed to be one of the secondary centres of diversity for *Capsicum annuum* L. (Gupta *et al.*, 1996). Other species occurring in India include *C. frutescens* L. (Hooker, 1885) and *C. baccatum* L. var. *pendulum* (IBPGR, 1983). Rich variability in morphological traits in hot pepper occurs throughout India particularly in the south Peninsular region, north eastern foothills of Himalayas and Gangetic plains. Gupta *et al.* (1996) reported that the germplasm collection of chilli is prioritised owing to its cultivated status, widespread distribution, high variability and moderate genetic erosion status. Kanyakumari district of Tamil Nadu (8°03' to 8°35'N latitude & 77°15' to 77°36'E longitude) lies relatively nearer to equator and covers a part of Western Ghats, experiencing typical tropical humid climate with an average rainfall of 1450mm. Under National Agricultural Technology Project on Plant Biodiversity (1999-2004), a huge variation in plant, leaf, flower and seed characters available in the entire district was collected. In this study, the germplasm accessions assembled in the Department of Vegetable Crops, Horticultural College and Research Institute (HC&RI), Coimbatore were characterized for 38 traits.

Investigation was carried out at the orchard of Horticultural College and Research Institute, TNAU, Coimbatore during December 2001 and May 2002. All the 53 accessions collected from Kanyakumari district of Tamil Nadu were included in the study. The experiment was laid out in a completely randomized design (pot culture) involving three replications with a minimum of ten plants per treatment (accession). Forty five day old seedlings were transplanted into pot (one seedling/pot) which consists of four kg substrate containing a mixture of loam soil and farmyard manure in the ratio of 3:1. Recommended cultural practices were taken up during the study period. A total of 38 characters (Tables 1 & 2) including few quantitative ones useful for management, maintenance and utilization of germplasm were characterized by adopting the descriptor jointly developed by IPGRI, AVRDC and CATIE (1995). In case of quantitative characters, mean value of five observations in each treatment was taken into account. Frequency distribution of various qualitative characters and variability parameters for quantitative characters were worked out.

Characterization of germplasm indicated that out of 32 qualitative characters studied, the frequency was very high (96.23%) for four characters *viz.* absence of anthocyanin spots over fruits, neck at base of fruit and fruit blossom end appendage followed by lanceolate cotyledonous leaf shape (94.34). Frequency was high (>80%) in traits like purple hypocotyl, number of locules per fruit and lengthy placenta i.e. placenta more than half the length of fruit. More than 50 per cent of germplasm accessions exhibited solitary erect flowers, white-coloured corolla spot, campanulate-shaped corolla,

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Table 1. Frequency distribution of 53 accessions of *Capsicum* spp. for different descriptors

S. No.	Descriptor state	Descriptor code	Absolute frequency	Relative percentage
1	2	3	4	5
1	**Hypocotyl colour**			
	White	1	–	–
	Green	2	8	15.09
	Purple	3	45	84.91
2	**Hypocotyl pubescence**			
	Sparse	3	25	47.17
	Intermediate	5	26	49.06
	Dense	7	2	3.77
3	**Cotyledonous leaf colour**			
	Light green	1	–	–
	Green	2	20	37.74
	Dark green	3	–	–
	Light purple	4	14	26.42
	Purple	5	6	11.32
	Dark purple	6	13	24.53
	Variegated	7	–	–
	Yellow	8	–	–
	Other	9	–	–
4	**Cotyledonous leaf shape**			
	Deltoid	1	–	–
	Ovate	2	–	–
	Lanceolate	3	50	94.34
	Elong–deltoid	4	3	5.66
5	**Stem colour**			
	Green	1	13	24.53
	Green with purple stripes	2	26	49.06
	Purple	3	14	26.42
	Other	4	–	–
6	**Number of flowers per axil**			
	One	1	32	60.38
	Two	2	12	22.64
	Three or more	3	8	15.09
	Many flowers in bunch	4	–	–
	Others	5	1	1.89
7	**Flower position**			
	Pendant	3	7	13.21
	intermediate	5	10	18.87
	Erect	7	36	67.92
8	**Corolla colour**			
	White	1	18	33.96
	Light yellow	2	15	28.3
	Yellow	3	–	–
	Yellow-green	4	–	–
	Purple with white base	5	9	16.98
	White with purple base	6	–	–
	White with purple margin	7	–	–
	Purple	8	20	37.74
	Other	9	–	–
9	**Corolla spot colour**			
	White	1	27	50.94
	Yellow	2	3	5.66
	Green–yellow	3	16	30.19
	Green	4	–	–
	Purple	5	7	13.21
	Other	6	–	–
10	**Corolla shape**			
	Rotate	1	21	39.62
	Campanulate	2	32	60.38
	Other	3	–	–
11	**Anther colour**			
	White	1	–	–
	Yellow	2	–	–
	Pale blue	3	36	67.92
	Blue	4	7	13.21
	Purple	5	10	18.87
	Other	6	–	–
12	**Filament colour**			
	White	1	19	35.85
	Yellow	2	5	9.43
	Green	3	–	–
	Blue	4	–	–
	Light purple	5	–	–
	Purple	6	29	54.72
	Other	7	–	–
13	**Calyx pigmentation**			
	Absent	0	34	64.15
	Present	1	19	35.85
14	**Calyx margin**			
	Entire	1	2	3.77
	Intermediate	2	22	41.51
	Dentate	3	29	54.72
	Other	4	–	–
15	**Anthocyanin spots or stripes over fruits**			
	Absent	0	51	96.23
	Present	1	2	3.77
16	**Fruit colour at intermediate stage**			
	White	1	–	–
	Yellow	2	10	18.87
	Green	3	11	20.75
	Orange	4	–	–
	Purple	5	32	60.38
	Deep purple	6	–	–
	Other	7	–	–
17	**Fruit set**			
	Low	3	10	18.87
	Intermediate	5	30	56.60
	High	7	13	24.53
18	**Fruit colour at mature stage**			
	White	1	–	–
	Lemon-yellow	2	–	–
	Pale orange-yellow	3	–	–
	Orange-yellow	4	1	1.89
	Pale Orange	5	–	–
	Orange	6	3	5.66
	Light red	7	5	9.43
	Red	8	28	52.83
	Dark red	9	16	30.19
	Purple	10	–	–
	Brown	11	–	–
	Black	12	–	–
	Other	13	–	–
19	**Fruit shape**			
	Elongate	1	18	33.96
	Almost round	2	10	18.87
	Triangular	3	12	22.64
	Campanulate	4	1	1.89
	Blocky	5	12	22.64
	Other	6	–	–
20	**Fruit shape at pedicel attachment**			
	Acute	1	–	–
	Obtuse	2	20	37.74
	Truncate	3	30	56.60
	Cordate	4	3	5.66
	Lobate	5	–	–

1	2	3	4	5
21	**Neck at base of fruit**			
	Absent	0	51	96.23
	Present	1	2	3.77
22	**Fruit shape at blossom end**			
	Pointed	1	33	62.26
	Blunt	2	19	35.85
	Sunken	3	1	1.89
	Sunken and pointed	4	–	–
	Other	5	–	–
23	**Fruit blossom end appendage**			
	Absent	0	51	96.23
	Present	1	2	3.77
24	**Fruit cross-sectional corrugation**			
	Slightly corrugated	3	42	79.25
	Intermediate	5	9	16.98
	Corrugated	7	2	3.77
25	**Number of locules per fruit**			
	2	1	43	81.13
	3	2	8	15.09
	4	3	1	1.89
	5	4	1	1.89
	>5	5	–	–
26	**Fruit surface**			
	Smooth	1	39	73.58
	Semi-wrinkled	2	8	15.09
	Wrinkled	3	6	11.32
27	**Pedicel persistence with ripe fruit**			
	Slight	3	–	–
	Intermediate	5	36	67.92
	Persistent	7	17	32.08
28	**Placenta length**			
	<1/4 fruit length	1	–	–
	1/4 -1/2 fruit length	2	7	13.21
	>1/2 fruit length	3	46	86.79
29	**Seed colour**			
	Deep yellow	1	36	67.92
	Brown	2	17	32.08
	Black	3	–	–
	Other	4	–	–
30	**Seed surface**			
	Smooth	1	39	73.58
	Rough	2	2	3.77
	Wrinkled	3	12	22.64
31	**Seed size**			
	Small	3	7	13.21
	Intermediate	5	40	75.47
	Large	7	6	11.32
32	**Number of seeds per fruit**			
	<20	1	6	11.32
	20-50	2	22	41.51
	>50	3	25	47.17

pale blue anther, purple filament colour, no pigmentation in calyx, dentate calyx margin, purple fruit color at intermediate stage, medium fruit set, red fruit color at maturity stage, truncate-shape at pedicel attachment with fruit, pointed fruits at blossom end, slightly corrugated fruits with smooth surface, medium pedicel persistence with ripe fruit, and deep yellow, medium sized and smooth seeds. All the descriptor states mentioned in IPGRI, AVRDC and CATIE (1995) were exhibited by characters *viz.* hypocotyl pubescence, flower position, calyx pigmentation, presence or absence of anthocyanin spots over fruits, neck at base of fruits and fruit blossom end appendages, fruit set, fruit cross-sectional corrugation, fruit surface texture, seed size and number of seeds per fruit indicating wide diversity existed in the studied germplasm for those characters.

The study also showed that in the germplasm, wide variability (>15% CV) was exhibited in all the quantitative characteristics studied (Table 2) except for one character i.e. the fruit bearing period. Fruit length varied from 1.23 to 8.10cm whereas width from 0.83 to 3.10cm. The main objective of this characterization study is two fold *viz.* to have an easy and quick discrimination of phenotypes; the other is to simply correlate with practical utilization. In this regard, those traits expressed in seedling stage such as hypocotyl and cotyledonous leaf color, hypocotyl pubescence, stem color before transplanting can be utilized to know and discard any varietal admixture at a very early stage, or as a marker for early selection of hybrid provided genetics of these traits known. Thin walled fruits dry quickly hence may be of good use for dry chilli purpose. Smooth fruit surface is well preferred for canning purpose. Capsaicin content is more in placenta followed by seeds, and hence, accessions with lengthy placenta and more number of seeds per fruit may be useful in breeding for high pungency. Rajagopal and Muthukrishnan (1977) also reported the importance of high seed weight in breeding high pungent chilli.

Table 2. Variability parameters for different quantitative traits in 53 *Capsicum* spp. accessions

Feature	Fruit bearing period	Fruit length (cm)	Fruit width (cm)	Fruit pedicel length (cm)	Fruit wall thickness (mm)	Seed diameter (mm)
Mean ± SE	65.33 ± 0.76	3.26 ± 0.22	1.75 ± 0.07	2.46 ± 0.07	1.50 ± 0.07	3.15 ± 0.09
Range	80.00 - 54.33	8.10 - 1.23	3.10 - 0.83	3.60 - 1.37	2.50 - 0.50	4.53 - 2.03
CV (%)	8.62	50.47	29.46	22.25	33.62	20.25

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Agro-morphologic Traits as Selection Parameters for Improvement of Upland Rice

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Fifty-seven upland rice genotypes were studied to estimate the degree of character association by correlation and path analysis on basis of 14 agro-morphological characters. Genotypic correlation coefficients were higher as compared to the phenotypic correlation coefficients. The grain yield was significantly and positively correlated with flag leaf length and area, grain number/panicle, spikelet fertility, 1000-grain weight, biological yield and harvest index. In addition to high correlation to grain yield, the characters having positive direct effect on grain yield were grain number/panicle, harvest index, 1000-grain weight biological yield and flag leaf length, thus utilization of these traits as selection parameters and strengthening the predictive value of phenotypic selection for yield improvement in upland rice.

Key words: Rice, GCV, PCV, Biological yield, Harvest index

The knowledge about the extent and nature of association of plant characters among themselves and with yield would provide a better understanding in improving yield through selection. Grain yield in rice is a complex character being highly influenced by environmental changes. Therefore, direct selection for yield would not give expected results. The estimation of correlation coefficient among yield and its components has been useful to the breeders in selecting suitable plant types. However, this simple association does not provide the exact basis of simultaneous improvement of the different traits. Under such conditions, path coefficient analysis is a technique which facilitates the partitioning of the correlation coefficients into different components of direct and indirect effects. Further, the quantitative characters being more vulnerable to environmental changes are lively to exhibit differential relationship among themselves. It is for this reason the present study was undertaken in two *kharif* seasons i.e. *kharif* 2002 and 2003 to estimate the genotypic correlation among the 14 characters and to determine the direct and indirect effects of component traits on yield in *57* upland rice genotypes.

Materials and Methods

The experimental material consisted of 57 upland rice genotypes including 32 local rice germplasm collections from 8 hilly districts of Orissa (Table 1). The experiment was laid out in randomized block design with three replications at the Central Research Station, Orissa University of Agriculture & Technology (OUAT) Bhubaneswar, Orissa during *kharif* season in 2002 and 2003. The genotypes direct seeded in 5 rows of 3-m length with row-to-row 20 cm and plant-to-plant 10 cm spacing. Observations were recorded on 14 quantitative characters *viz.*, days to heading, plant height (cm), flag leaf Length (cm), flag leaf area (cm^2), panicle length (cm), panicles per meter square, no. of filled grain/panicle, spikelet fertility, 1000-grain weight (g), grain length (mm), Grain L/B ratio, grain yield (g) and harvest index (%). The data were subjected to statistical analysis. Correlation coefficient at genotypic and phenotypic level and path coefficient were worked out following the method suggested by Goulden (1952) and Dewey and Lu (1959), respectively.

Results and Discussion

The correlation coefficients at the phenotypic and genotypic levels for the characters are presented in Table 2. In respect of most of the character pairs, there was close correspondence between phenotypic and genotypic correlation coefficients, indicating less masking effect of environment on the character expression.

At the genotypic level, the correlation of grain yield with other characters reflected similar pattern of association as the phenotypic correlation. But the genotypic correlation coefficients were higher in magnitude (direction remaining same) as compared to phenotypic values in all the thirteen character pairs. Thus, higher correlation coefficient values at genotypic level having positive association and lower in case of negative association would reinforce selection based on phenotype. At phenotypic level, grain yield exhibited significant positive correlation with flag leaf length, flag leaf area, grain number, spikelet fertility, 1000-grain weight, biological yield and harvest index. Similar results have

Genotype	IC No	Parentage	Plant height (cm)	Place of origin/adaptation
KCM73	298382	Local collection	Tall	Dugudi, G.Udyagin. Kandhamal, Orissa
KCM 74	298383	Local collection	Tall	Dugudi, G.Udyagiri, Kandhamal, Orissa
KCM75	298384	Local collection	Tall	Dugudi, G.Udyagiri, Kandhamal, Orissa
KCM76	298385	Local collection	Tall	Gamuli, G.Udayagri, Kandhamal, Orissa
KCM93	298402	Local collection	Tall	Garnuli, G.Udayagri, Kandhamal, Orissa
KCM 104	298413	Local collection	Tall	Badabandha.Tumudibandha,Kandhamal, Orissa
KCM 105	298414	Local collection	Tall	Badabandha.Tumudibandha Kandhamal, Orissa
KCM 106	298415	Local collection	Tall	Badabandha.Tumudibandha, Kandhamal, Orissa
KCM 107	298416	Local collection	Tall	Badabandha, Tumudibandha.Kandhamal, Orissa
KCM 129	298438	Local collection	Tall	Sikharpadu, Rayagada. Rayagada, Orissa
KCM 130	298439	Local collection	Tall	Sikharpadu, Rayagada, Rayagada, Orissa
KCM 143	298452	Local collection	Tall	Madanpur, Kolhnara, Rayagada, Orissa
KCM 158	298467	Local collection	Tall	Rupakana. Rayagada. Rayagada, Orissa
KCM 170	298479	Local collection	Tall	Mahantaput, Baipariguda, Koraput, Orissa
KCM 176	298485	Local collection	Tall	Utakapadu, Rayagada, Rayagada, Orissa
KCM 186	298495	Local collection	Tall	Sunabahal, Malkanagiri, Malkanagiri, Orissa
KCM 187	298496	Local collection	Tall	Pandripani, Malkanagiri, Malkanagiri, Orissa
KCM 188	298497	Local collection	Tall	Pandnpani, Malkanagiri, Malkanagiri, Orissa
KCM 327	321742	Local collection	Tall	Biswanathpur, Lanjiguda, Kalahandi, Orissa
KCM 336	321753	Local collection	Tall	Phulajhari, Umarkot, Nawarangpur, Orissa
KCM 378	–	Local collection	Tall	Keshanbida, Umarkot, Nawarangpur, Orissa
KM 2	–	Mutant from Kalakeri	Tall	OUAT, Bhubaneswar, Orissa
KM 6	256528	Mutant from Kalakeri	Short	OUAT, Bhubaneswar, Orissa
PB16	256533	Local collection	Tall	Deogarh, Orissa
PB21	256537	Local collection	Tall	Deogarh, Orissa
PB25	256578	Local collection	Tall	Deogarh, Orissa
PB66	256585	Local collection	Tall	Sundargarh, Orissa
PB73	256614	Local collection	Tall	Sundargarh, Orissa
PB102	256650	Local collection	Tall	Sundargarh, Orissa
PB138	256652	Local collection	Tall	Sundargarh, Orissa
PB140	256653	Local collection	Tall	Sundargarh, Orissa
PB141	256660	Local collection	Tall	Sundargarh, Orissa
PB148	256672	Local collection	Tall	Sundargarh, Orissa
PB 160	–	Local collection	Tall	Sundargarh, Orissa
JD6	–	Mutant from (Dular x N 22)	Short	IARI, New Delhi
JD 13	–	Mutant from (Dular x N 22)	Short	IARI, New Delhi
N22	–	Pure line selection	Tall	Uttar pradesh
Blackgora	–	Pure line selection	Tall	Bihar
Kalakeri	–	Pure line selection	Tall	Orissa
Dular	–	Pure line selection	Tail	West Bengal
Annapurna	–	PTB 10/T(N) 1	Short	Kerala
Rudra	–	Parijat/IET3225	Short	OUAT. Bhubaneswar, Orissa
Shankar	–	Parijat/IET3225	Short	OUAT, Bhubaneswar, Orissa
Parijat	–	TKM6/T(N, 1	Short	OUAT. Bhubaneswar. Orissa
Subhadra	–	T(N)1/SR26B	Short	OUAT Bhubaneswar, Orissa
Pathara	–	COIfi/Hema	Short	OUAT, Bhubaneswar, Orissa
Ghanteswari	–	IR2G61-628/N 22	Short	OUAT, Bhubaneswar, Orissa
Lalitgiri	–	Badami/IR 1996-364	Short	OUAT, Bhubaneswar, Orissa
Udayagir	–	IRAT 138ATR 13543-66	Short	OUAT, Bhubaneswar, Orissa
Bhatta Sel. 2	–	Pureline selection	Tall	Orissa
Kalinga 3	–	AC 540/Ratna	Tall	CRRI, Cuttack Orissa
Annada	–	MTU 15/Yai Kyaku Kantoku	Short	CRRI, Cuttack, Orissa
Heera	–	CR 404-48/CR 289-1208	Short	CRRI, Cuttack, Orissa
Neela	–	CR 94-1512-6/Pusa 2-21	Short	CRRI, Cuttack, Orissa
Sneha	–	Annada/CR 143-2-2	Short	CRRI, Cuttack, Orissa
Vandana	–	C 22/Kalaken	Tall	CRRI, Cuttack, Orissa
Vanaprava	–	ARC 12422/ARC 12751	Tall	CRRI.Cuttack, Orissa

been reported in rice by Chauhan *et al.* (1986), Marimuthu *et al.* (1990), Shivani and Reddy (2000), Kavitha and Reddi (2001) and Shrirame and Muley (2003). Association of plant height and panicle length with grain yield was positive but not significant.

Inter-relationship among the yield components at phenotypic level was significant in 42 out of 78 characters pairs. Days to heading showed significant positive correlation with plant height, panicle length and biological yield while significant negative correlation with spikelet

Table 2. Phenotypic (r_p) and genotypic (r_g) correlation among 14 characters pooled over years

Character		PH	FLL	FLA	PL	PN	GN	SF	GW	GL	GL/B	BY	HI	GY
DH	r_p	0.313*	0.067	0.267	0.530**	-0.098	0.212	-0.534**	-0.364**	0.072	0.159	0.282**	-0.481**	-0.119
	r_g	0.327	0.073	0.283	0.604	-0.198	0.240	-0.565	-0.377	0.073	0.164	0.304	-0.548	-0.122
PH	r_p		0.683**	0.720**	0.723**	-0.566**	0.660**	0.271*	0.170	-0.106	-0.080	0.699**	-0.037	0.342**
	r_g		0.75	0.762	0.821	-1.000	0.786	0.286	0.181	-0.116	-0.084	0.761	-0.040	0.363
FLL	r_p			0.821**	0.494**	-0.328**	0.579**	0.435**	0.307*	-0.030	-0.007	0.679**	-0.229	0.475**
	r_g			0.838	0.617	-0.776	0.711	0.495	0.337	-0.032	-0.008	0.771	-0.286	0.525
FLA	r_p				0.609**	-0.495**	0.791**	0.373**	0.153*	-0.185	-0.037	0.827**	-0.284*	0.589**
	r_g				0.728	-1.000	0.935	0.418	0.164	-0.213	-0.040	0.906	-0.330	0.628
PL	r_p					-0.559**	0.678**	0.001	-0.108	0.118	0.204	0.674**	-0.142	0.253
	r_g					-1.000	0.878	0.418	-0.121	0.136	0.233	0.798	0.174	0.294
PN	r_p						0.745**	0.212	0.157	0.021	-0.142	0.314*	-0.154	0.267*
	r_g						1.000	0.392	0.320	0.004	-0.307	-0.667	0.413	0.541
GN	r_p							0.484**	-0.204	0.137	0.307*	0.561**	0.228	0.402*
	r_g							0.559	-0.238	0.148	0.346	0.652	0.275	0.452
SF	r_p								0.411**	-0.228	-0.170	0.373**	0.520**	0.487**
	r_g								0.434	0.238	-0.175	0.410	0.599	0.515
GW	r_p									-0.154	-0.381**	0.577**	0.425**	0.532**
	r_g									-0.171	-0.394	0.613	0.476	0.547
GL	r_p										1.000**	-0.171	-0.022	-0.099
	r_g										1.000	-0.183	-0.029	-0.102
GL/B	r_p											-0.054	0.016	-0.038
	r_g											-0.057	0.011	-0.039
BY	r_p												0.859**	0.953**
	r_g												1.000	0.989
HI	r_p													0.914**
	r_g													1.000

* and ** significant at the levels of 5% and 1% respectively.

DH=Days to heading, PH=Plant height. FLL=Flag leaf length (cm). FLA=Flag leaf area, PL=Panicle length, PN=Panicle numbers/m². GN=Grain numbers/panicle, SF=Spikdet fertility. GW=1000-grain weight, GL=Grain length. GL/B=Grain length/breadth ratio, BY=Biological yield/meter, HI=Harvest index. GY=Grain yield/meter

Table 3. Genotypic path indicating direct (diagonal) and indirect effects of component traits on grain yield pooled over years

Character	DH	PH	FLL	FLA	PL	PN	GN	SF	GW	GL	GL/B	BY	HI	Correlation with yield
DH	-0.004	0.029	-0.004	0.026	-0.079	-0.003	0.006	0.015	-0.010	-0.004	0.014	0.149	-0.258	-0.122
PH	-0.001	0.090	-0.037	0.071	-0.107	-0.021	0.810	-0.008	0.005	0.006	-0.007	0.374	-0.019	0.363
FLL	0.000	0.067	-0.049	0.078	-0.081	-0.013	0.017	-0.013	0.009	-0.002	-0.00!	0.380	0.135	0.525
FLA	-0.001	0.068	-0.041	0.093	-0.095	-0.020	0.022	-0.011	0.004	0.011	-0.003	0.445	0.156	0.628
PL	-0.002	0.074	-0.030	0.067	-0.131	-0.024	0.002	0.000	-0.003	-0.007	0.020	0.393	-0.082	0.294
PN	0.001	-0.107	0.038	-0.104	0.184	0.017	-0.040	0.010	0.008	0.000	-0.027	-0.328	-0.195	-0.054
GN	-0.001	0.071	-0.035	0.087	-0.115	-0.030	0.023	-0.015	-0.006	-0.008	0.030	0.321	0.130	0.452
SF	0.002	0.026	-0.024	0.039	0.00 1	-0.007	0.013	-0.027	0.011	0.012	-0.015	0.202	0.282	0.515
GW	0.001	0.016	-0.017	0.015	0.016	0.006	-0.006	-0.012	0.025	0.009	-0.034	0.302	0.225	0.547
GL	0.000	-0.010	-0.002	-0.018	-0.018	0.000	0.003	0.006	-0.004	-0.051	0.098	-0.090	-0.014	-0.102
GL/B	-0.001	-0.008	0.000	-0.004	-0.030	-0.005	0.008	0.005	-0.010	-00.58	0.086	-0.028	0.005	-0.039
BY	-0.001	0.008	-0.038	0.084	-0.104	-0.012	0.015	-0.011	0.160	0.01	-0.005	0.492	0.475	0.989
III	0.002	-0.004	-0.014	0.031	0.023	-0.007	0.006	-0.016	0.012	00.02	0.001	0.496	0.471	1.003

Residual=00854

DH=Days to heading, PH=Plant height. FLL=Flag leaf length (cm). FLA=Flag leaf area, PL=Panicle length, PN=Panicle numbers/m². GN=Grain numbers/panicle, SF=Spikdet fertility. GW=1000-grain weight, GL=Grain length. GL/B=Grain length/breadth ratio, BY=Biological yield/meter, HI=Harvest index. GY=Grain yield/meter

fertility, 1000-grain weight and harvest index. Plant height had significant positive association with flag leaf length and area, panicle length, grain number, spikelet fertility and biological yield but it showed significant negative association with panicle number. Flag leaf length and area had significant positive association between them as well as with panicle length, grain number, spikelet fertility and biological yield while both had significant negative association with panicle number. Flag leaf length exhibited significant positive association with 1000-grain weight whereas flag leaf area showed positive association with 1000-grain weight although not significant statistically. Association of panicle length was significantly positive with grain number and biological

yield, indicating selection of this trait would be reliable accompanied by high number of grains/panicle and high biological yield. Panicle number showed significant negative association with grain number and biological yield. Grain number/panicle had significant positive correlation with spikelet fertility, grain L/B ratio and biological yield whereas negative association with 1000-grain weight. Besides, above-mentioned characters, spikelet fertility had significant positive association with 1000-grain weight, biological yield land harvest index. 1000-grain weight showed significant negative association with grain L/B ratio while with biological yield and harvest index was positive and significant, indicating its important role in selection for yield improvement. High significant positive association between biological yield and harvest index suggesting their contribution in yield improvement. Characters having strong correlation values on grain yield are useful as selection parameters. Besides high positive and significant association of these traits with other yield attributing traits may be useful for simultaneous selection of many characters while selecting these traits. The contribution of grain number/panicle, panicle length, flag leaf length, 1000-grain weight, biological yield and harvest index towards grain yield in the present study is well corroborated by the results obtained in rice by Paul and Nanda (1994), Yolanda and Das (1995), Biao *et al.* (2002) and Shanthala *et al.* (2004).

The estimates of direct and indirect effects at the genotypic level are presented in Table 3. From the table it is observed that a positive direct effect was highest for biological yield (0.492) followed by harvest index (0.471). The direct positive effect of flag leaf area, plant height, grain L/B ratio, 1000-grain weight, grain number and panicle number were of lower magnitude at genotypic level. All characters except panicle number, grain length and grain L/B ratio had substantial positive indirect effect via biological yield at genotypic level. Flag leaf length and area, grain number, spikelet fertility, 1000-grain weight and biological yield had positive indirect contribution through harvest index. Direct and indirect effects of yield component traits on grain yield have also been reported earlier by Shivani and Reddy (2000), Kavitha and Reddi (2001), Biao *et al.* (2002), Shanthala *et al.* (2004) and Shashidhar *et al.* (2005).

In the present study high genotypic correlation coefficients as compared with the phenotypic correlation coefficients were observed. Significant positive correlation of flag leaf length and area, grain number spikelet fertility, 1000-grain weight, biological yield and harvest index with grain yield in the present study suggest that the selection based on these characters would be effective and reliable. From path coefficient analysis, it could be inferred that biological yield, harvest index, grain number, panicle number and 1000-grain weight contributed substantially towards grain yield both at phenotypic as well as genotypic level, thus suggesting that selection based on these characters would be more effective for yield improvement of early rice varieties for rainfed upland ecosystem.

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Choice of Clones in Early Clonal Generations in Sugarcane (*Saccharum* complex Hybrids) Breeding

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Eighty four clones including three checks in first and second consecutive clonal generations were undertaken with the objective to identify reliable yield attributing traits for formulation of selection indices and selection of suitable clones in early clonal generation. A consistent trend for the significance of mean sum of square due to checks, entries, check vs entries, range of variation and coefficient of variation was observed in both clonal generations. Correlation coefficient study revealed that only three quantitative traits i.e., number of shoots at 120 days, number of millable cane at harvest and single cane weight showed consistent trend of significant association with cane yield in both the clonal generations. Path coefficient analysis revealed that number of millable cane at harvest and single cane weight were major direct contributor in both clonal generations. Multiple regression analysis revealed that single cane weight act as most reliable traits in predicting performance in early clonal generations. Preliminary selection in early clonal generation should be based on quantitative traits i.e. single cane weight, number of shoots at 120 days and number of millable canes and quality traits should be delayed to latter generation till the character stabilize.

Key words: Sugarcane, Selection criteria, Early clonal generation, Correlation, Path analysis, Multiple regression

Sugarcane is one of the most important cash crops in India. The importance of sugarcane increased tremendously in recent years, as Government of India decided to mix ethanol in suitable proportion to petroleum fuel. Plant breeders responsibility has enhanced tremendously for genetic improvement of this crop to cope with changing ecological and economical necessity of country. Breeding cycle which usually takes ten years, i.e., from making crosses to final evaluation trial, can be shortened to much lower extent if breeders will be able to predict the promising genotypes in early stage of screening.

Thus the present investigation was conducted to predict the performance of genotypes for yield and quality attributes in early clonal generations, with objectives: (a) To study variability and association of quantitative traits with yield; (b) to generate information on direct and indirect effects of yield and quality components in different clonal generations; (c) to identify reliable yield attributes for formulation of selection indices in early clonal generation; and d) to identify reliable clones in early clonal generation.

Materials and Method

In the present investigation, eighty one clones with three checks, i.e. B0110, B0128 and BO130 of sugarcane (*Saccharum complex* hybrids) were grown in augmented design in two consecutive clonal generation, i.e., first clonal and second clonal generation during spring season of 2003-2004 and 2004-2005 respectively. The experimental materials were grown in research farm of Rajendra Agricultural University, Pusa, Samastipur, (Bihar). In first clonal generation, experimental materials were planted in two rows of 3 m x 90 cm apart. In second clonal generation, all experimental materials were planted in four rows of 6 m x 90 cm apart. All the recommended package of practices for north Bihar condition were followed throughout the crop season.

Data were recorded for germination per cent at 45 days, number of shoots per hectare at 120 days, number of millable canes per hectare, cane height at harvest, single cane weight, cane diameter at harvest, refractometric brix (in mid November, December and January, sucrose per cent in juice in January), commercial cane sugar (CCS) per cent in January and the cane yield. The mean data collected were subjected to statistical analysis for variance and variability were found. Correlation and path coefficient analysis were worked out as per the method described by Wright (1921) and Dewey and Lu (1959).

Results and Discussion

There was consistent trend of significant variation for almost all the characters in first and second clonal generation among eighty one entries except cane diameter at harvest and refractometric brix in mid December in second clonal generation and for sucrose percent in juice

in first clonal generation (Table 1). Regarding variation among check varieties, similar trends of significant variations were observed in both the generations for the characters germination percent at 45 days, number of shoots per hectare at 120 days, single cane weight, refractometric brix in mid November, CCS per cent in January and cane yield (t/hec). However, the traits such as number of millable cane per hectare represented similar trend of non significant variation in both the generations. Remaining traits showed dissimilar trend of variation in either generations. The presence of substantial variability for agronomic and quality characters was reported by Nagarajan *et al.* (2000). Presence of variability in germination percent, variability in number of millable canes, cane height, single cane weight and number of shoots was also reported by Kamat and Singh (2001). The presence of variability in quality character, refractometric brix was also reported by Mishra (1988) were as Verma *et al.* (1999) reported variability in CCS per cent in January.

This trend of variability was expected, as the entries are the crosses among highly heterozygous parents for most of the loci, such characteristics are the complex interaction of hereditary and environmental elements, as genes cannot be responsible for an observed character in absence of suitable environmental conditions for its to appear, nor can any association of environmental conditions alone cause a character to develop in absence of necessary genes.

The range of variation showed almost similar trend in both the clonal generations, for example the highest range of variation was observed for number of millable cane per hectare followed by cane yield, germination percent, number of shoot per hectare at 120 days in both the clonal generations. Almost similar trends were observed for coefficient of variation for all the traits in both clonal generations. In second clonal generation, a decrease in average mean for quantitative traits were recorded whereas it was more for quality traits. This trend of change in the mean performance of clones of first and second clonal generation for both qualitative and quantitative characters can rather be distinguished as "Settle down behaviour" as suggested by early workers (Hill, 1935).

Correlation coefficient for both quantitative and qualitative traits with cane yield and among themselves were studied (Table 2). The quality traits which showed positive significant correlation among themselves in both the clonal generations were: Refractometric brix in mid

Table 1. Analysis of variance for twelve quantitative characters in sugarcane (first and second clonal generation)

Sl. No.	Character / Degree of freedom	Generation	Mean sum of square due to Block	Check	Entries	Check Vs entries
			8	2	80	1
1.	Germination percent at 45 days	I	1.126	29.427**	143.407**	2965.710**
		II	0.805	49.090**	98.545**	33.511**
2.	No. of shoots per hectare at 120 days (in thousand)	I	73487055**	346863133**	12697752717**	1503078437**
		II	49142969	197366575*	4734697528**	11732728947**
3.	No. of millable canes per hec (in thousand)	I	14802855	12512098	575765508**	5782926520**
		II	23360863	8246447	385504354**	20351748791**
4.	Cane height at harvest (cm)	I	331.676	172.259	1006.228*	51302.25**
		II	156.917	892.111**	1756.936**	35031.361**
5.	Cane diameter at harvest (cm)	I	0.012	0.230**	0.064*	0.933**
		II	1.707	1.174	0.102	0.252
6.	Single cane weight (kg)	I	0.0003**	0.007**	0.018**	0.008**
		II	0.0002	0.012**	0.013**	0.022**
7.	Refractometric brix (mid November)	I	0.644	11.574**	3.084*	10.311**
		II	0.714	2.935*	2.624**	7.922**
8.	Refractometric brix (mid December)	I	0.953	12.218**	2.148**	8.059**
		II	1.173	2.973	1.955	6.362*
9.	Refractometric brix (mid January)	I	1.330	8.917**	2.145**	1.467
		II	0.328	0.606	1.582**	0.001
10.	Sucrose percentage in juice (in January)	I	1.156	0.145	2.207	18.395**
		II	0.042	1.139**	13.135**	0.025**
11.	CCS percent in January	I	0.010	0.374**	1.052**	15.230**
		II	0.008	0.414**	0.830**	0.028**
\2.	Cane Yield (t/hec)	I	2.782	52.742**	215.651**	1386.818**
		II	5.236	83.834**	165.917**	5138.314**

*, **: Denote significance at 5% and 1% probability level respectively
I&II: Denote first and second clonal generation respectively

Table 2. Phenotypic correlation coefficient between pair of twelve quantitative characters (first and second clonal generation)

Characters		Generation	No. of shoots at 120 days	No. of millable canes	Cane height (cm)	Cane diameter (cm)	Single cane weight (kg)	Brix (mid Nov)	Brix (mid Dec)	Brix (mid Jan)	Sucrose percent	CCS%	Cane yield
Germination percent at 45 days	(X_1)	I	0.482**	0.085	0.159	-0.238*	0.045	-0.095	0.033	0.125	0.325**	0.277*	0.331**
		II	0.027	0.00	-0.050	-0.201	-0.129	-0.039	-0.109	-0.098	0.077	0.064	-0.002
No. of shoots at 120 days	(X_2)	I		0.247*	0.169	-0.104	0.071	-0.217*	-0.141	-0.147	0.021	0.12	0.683**
		II		0.958**	0.184	0.054	-0.013	-0.080	-0.020	-0.054	-0.022	0.019	0.791**
No. of millable canes at harvest	(X_3)	I			0.299	-0.003	0.222*	-0.200	-0.292**	-0.292**	-0.179	-0.192	0.319**
		II			0.158	0.034	-0.061	-0.093	-0.028	-0.103	-0.108	-0.053	0.815**
Cane height at harvest (in cm)	(X_4)	I				-0.227*	0.079	-0.096	-0.167	-0.071	0.125	0.070	0.195
		II				0.112	0.045	-0.042	-0.004	0.178	0.152	0.117	0.137
Cane diameter at harvest (in cm)	(X_5)	I					0.074	-0.053	-0.005	-0.042	-0.084	-0.064	-0.057
		II					-0.081	0.098	0.049	0.213	-0.131	-0.092	0.023
Single cane weight (kg)	(X_6)	I						-0.140	-0.098	-0.008	0.178	0.195	0.558**
		II						0.202*	0.308**	0.236*	0.088	0.095	0.238*
Brix in mid November	(X_7)	I							0.764**	0.654**	0.418**	0.385**	-0.328**
		II							0.865**	0.526**	0.259*	0.229*	0.048
Brix in mid December	(X_8)	I								0.796**	0.457**	0.411**	-0.226*
		II								0.515**	0.202	0.202	0.079
Brix in mid January	(X_9)	I									0.571**	0.512**	-0.151
		II									0.302**	0.219*	-0.029
Sucrose percent in juice in January	(X_{10})	I										0.956**	0.035
		II										0.917**	0.047
CCS% in juice in January	(X_{11})	I											0.043
		II											0.087

*, **: Denote significance at 5% and 1% probability level respectively
I & II: Denote first and second clonal generation respectively.

November with refractometric brix in mid December and mid January, sucrose percent in juice and CCS percent in January. Refractometric brix in mid December with refractometric brix in mid January. Refractometric brix in mid January was found to be correlated with sucrose percent in juice and CCS percent in January. Sucrose percent in juice was correlated with CCS percent in January. The significant negative association of brix in mid November and December with cane yield changed in second clonal generation to non significant. While taking quantitative traits into consideration, three traits which showed positive significant correlation with yield in both the clonal generations were number of shoots at 120 days, number of millable canes at harvest and single cane weight. The component traits number of shoots at 120 days and number of millable canes were found positively and significantly correlated among themselves in both the clonal generations. The present finding of significant correlation of brix with commercial cane sugar (CCS) had also been reported by Battan *et al.* (1985), sucrose and CCS percentage were also reported to be positively correlated by Das ef til. (1997). Puncet *et al.* (2002) also reported that the interrelationship between the quality traits was high and positive which supports present findings. Kumar and Singh (1999) had reported positive and significant correlation among yield vs among shoots at 120 days, whereas correlation among yield and number of millable cane was also reported by Ramesh and Varghese (1995). The component traits, number of millable canes per hectare and number of shoots at 120 days were also reported to be positively and significantly correlated by Kumar and Singh (1999).

Perusal of Table 3 revealed that only the single cane weight and the number of millable canes at harvest had positive direct effects towards cane yield in both clonal generation and out of these two traits, only the single cane weight was positive direct contributor in both clonal generation. Indirect effect of number of shoots per hectare at 120 days via number of millable canes and cane height at harvest via number of millable canes was positive and more in second clonal generation. No consistent contribution of different qualitative and quantitative traits towards cane yield were observed in both the clonal generations. For instance, the trait, number of shoots per hectare at 120 days had positive direct and larger effect towards cane yield in first clonal generation whereas it was having negative little direct effect in second clonal generation. Similar case was observed with other traits namely germination percent at 45 days, cane height, cane diameter and quality traits.

Table 3. Direct (Diagnol) and indirect effect of different quantitative characters towards cane yield in first (I) and second (II) clonal generation

Characters		Gene-ration	Germin-ation percent	No. of shoots at 120 davs	No. of millable canes	Cane height (cm)	Cane diameter (cm)	Single cane weight (kg)	Brix (mid Nov.)	Brix (mid Dec.)	Brix (mid Jan.)	Sucrose percent in Jan.	CCS% in Jan.	Cane vield
			X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	Y
Germination percent		I	–0.0053	0.2916	0.0029	0.0059	0.0079	0.0222	0.0140	0.0004	0.0078	–0.0331	0.0175	0.3310**
at 45 days	(X_1)	II	0.0123	–0.0027	0.0000	0.0003	–0.0071	–0.0257	–0.0066	0.0104	0.0067	0.0102	–0.0002	–0.0020
No. of shoots at		I	–0.0025	0.6050	0.0083	0.0063	0.0035	0.0350	0.0320	–0.0017	–0.0082	–0.002 1	0.0076	0.6830**
120 days	(X_2)	II	0.0003	–0.0986	0.9021	–0.0013	0.0019	–0.0026	–0.0136	0.00i9	0.0037	–0.0029	–0.0001	0.7910**'
No. of millable		I	–0.0040	0.1494	0.0336	0.0111	0.0001	0.1095	0.0295	–0.0036	–0.0164	0.0183	–0.0121	0.3190**
canes at harvest	(X_3)	II	0.0000	–0.0945	0.9416	–0.0011	0.0012	–0.0121	–0.0158	0.0027	0.0071	–0.0143	0.0001	0.8150**
Cane height at harvest		I	–0.0008	0.1022	0.0101	0.0372	0.0075	0.0390	0.0141	–0.0021	–0.0040	–0.0127	0.0040	0.1950
(in cm)	(X_4)	II	–0.0006	–0.0181	0.1488	–0.0068	0.0040	0.0090	–0.0071	0.0004	–0.0122	0.0201	–0.0003	0.1370
Cane diameter at		I	0.0013	–0.0629	–0.0001	–0.0085	–0.0332	0.0365	0.0078	–0.0010	–0.0024	0.0086	–0.0040	–0.0570
harvest (in cm)	(X_5)	II	–0.0025	–0.0053	0.0320	–0.0008	0.0355	–0.0161	0.0166	–0.0047	–0.0146	–0.0173	0.0003	0.0230
Single cane weight		I	–0.0002	0.0430	0.0075	0.0029	–0.0025	0.4933	0.0206	–0.0012	0.0004	–0.0182	0.0123	0.5580**
(kg)	(X_6)	II	–0.0016	0.0513	–0.0574	–0.0003	–0.0029	0.2490	0.0342	–0.0295	–0.0162	0.0117	–0.0003	0.2380*
Brix in mid November	(X_7)	I	–0.0005	–0.1313	–0.0067	–0.0036	–0.0018	–0.0691	–0.1474	0.0094	0.0367	–0.0426	0.0243	–0.3280**
		II	–0.0005	0.0079	-0.0876	0.0003	0.0035	0.0402	0.1694	–0.0828	–0.0361	0.0343	–0.0006	0.0480
Brix in mid December	(X_8)	I	–0.0002	–0.0853	–0.0098	–0.0062	0.0002	–0.0483	–0.1126	0.0123	0.0446	–0.0466	0.0260	–0.2260*
		II	–0.0014	0.0020	–0.0264	0.0000	0.0017	0.0613	0.1465	–0.0957	–0.0354	0.0267	–0.0005	0.0790
Brix in mid January	(X_9)	I	–0.0007	–0.0889	–0.0077	–0.0026	0.0014	0.0039	–0.0964	0.0098	0.0561	–0.0582	0.0324	–0.1510
		II	–0.0012	0.0053	–0.0970	–0.0012	0.0076	0.0470	0.089!	–0.0493	–0.0687	0.0400	–0.0006	–0.0290
Sucrose percent in		I	–0.0017	0.0127	–0.0057	0.0047	0.0028	0.0878	–0.0616	0.0056	0.0320	–0.1020	0.0604	0.0350
juice in January	(X_{10})	II	0.0010	0.0022	–0.1017	–0.0010	–0.0047	0.0175	0.0439	–0.0193	–0.0207	0.1324	–0.0025	0.0470
CCS% in juice in		I	–0.0015	0.0073	–0.0065	0.0026	0.0021	0.0962	–0.0567	0.0050	0.0287	–0.0975	0.0632	0.0430
January	(X_{11})	II	0.0008	–0.0019	–0.0499	–0.0008	–0.0033	0.0189	0.0388	–0.0193	–0.0150	0.1214	–0.0027	0.0870

I & II : Denotes first mid second clonal generation respectively. (Residual effect- first generation=0..5071 & second generation=0.5241)

The present findings of positive direct effect of number of millable cane per hectare and single cane weight on cane yield was reported by various workers time to time viz. Balasundram and Bhagyalakshmi (1978), Hooda *et ai* (1988), Bakshi and Choudhary (2000) and Krishna and Singh (2004) etc.

The efficiency of multiple regression equation (Table 4 and 5) in present study for first and second clonal generation were observed to be same i.e r^2 (Cn)=74.7, r^2 ($C|_2$)=72.7, r^2 (C_2i)=72.5 and r^2 (C_{22})=70.8, where r^2 (C_{11}) and r^2 (C_{21}) were degree of determination for observed cane yield by taking all eleven characters in first and second clonal generation respectively and r^2 (C_{12}) and r^2 (C_{22}) were degree of determination of predicted cane yield by taking two characters (number of shoots per hectare at 120 days and single cane weight) *in first clonal generation and three characters (number of* millable cane per hectare, single cane weight and refractometric brix in mid November) in second clonal generation. These stated that efficiency of selection remained almost unaffected even after deleting nine characters in first clonal generation and eight character in second clonal generation.

Rank correlation between ranking of clones in both clonal generations based on selection indices also remained strong as more than fifty percent of identified clones in first clonal generation and more then eighty percent of identified clones in second clonal generation were found quite closer in ranking in both the criteria. Top ten ranking clones of first clonal generation (Table 6) viz, CoX02120, CoX02138, CoX02177, CoX02244, CoX02129, CoX02027, CoX02058, CoX02217, CoX02061 and CoX02007 were found on the basis of eleven cane yield component characters. Top ten ranking clones after considering two cane yield *component characters in first clonal generation were as* follow: CoX02117, CoX02120, CoX02121, CoX02314, CoX02027, CoX02138, CoX02289, CoX02244,

Table 4. Partial regression coefficient for first clonal generation

Sl. No.	Characters	When all eleven characters were included	After deleting nine characters
1.	Germination percent at 45 days	0.01652±0.08654	
2.	Number of shoots per hectare at 120 days	–0.00006+0.00014	0.00024±0.00002
3.	Number of millable canes per hectare	0.00059+0.00015	
4.	Cane height at harvest (in cm)	–0.00235±0.02072	
5.	Cane diameter at harvest (in cm)	1.4817±2.9361	
6.	Single cane weight (in kg)	19.818+6.9359	57.938±6.7094
7.	Refractometric brix in mid November	1.3243+1.0637	
8.	Refractometric brix in mid December	–0.75505+L0730	
9.	Refractometric brix in mid January	–0.66779+0.83316	
10.	Sucrose percent in juice in January	1.3856±1.8547	
11.	CCS percent in juice in January	–0.00257+2.3188	
	R^2	74.7	72.7

$Y = 3.910–0.136X, +0.00023X_2 + 0.000002\ X_3 + 0.0164\ X_4 - 1.578\ X_5 + 0.0000056\ X_6 - 1.196\ X_7 + 0.1102\ X_8 + 0.6452, X_9 – 0.9589\ X_{10} + 0.7276\ Xn$

$Y = -11.299 + 0.00024\ X_2 + 57.940\ X_6$

Table 5. Partial regression coefficient for second clonal generation

Sl. No.	Characters	When all eleven characters were included	After deleting nine characters
I.	Germination percent at 45 days	–0.01362±0.09934	
2.	Number of shoots per hectare at 120 days	0.00022±0.00027	
3.	Number of millable canes per hectare	0.00002±0.00004	0.00052±0.000038
4.	Cane height at harvest (in cm)	0.01614±0.02972	
5.	Cane diameter at harvest (in cm)	–1.5775±3.0907	
6.	Single cane weight (in kg)	55.881±7.5069	16.945±6.2741
7.	Refractometric brix in mid November	–1.1957±0.81962	0.07168±0.04978
8.	Refractometric brix in mid December	0.11022±1.2757	
9.	Refractometric brix in mid January	0.64527±1.2369	
10.	Sucrose percent in juice in January	–0.95885±2.5297	
11.	CCS percent in juice in January	0.72756±3.1605	
	R^2	72.5	70.8

$Y = 27.592 + 0.0166\ Xi - 0.000642\ X_2 + 0.000592\ X_3 - 0.00236\ X_4 + 1.48\ X_5 + 0.198\ X_6 + 1.32\ X_7 - 0.755\ X_g - 0.668\ X_9 + 1.39\ X_{10} - 0.00257\ Xn$

$Y = -18.232 + 0.000518\ X_3 + 0.7168\ X_7 + 16.95\ X_6$

Table 6. Top ten genotypes ranked on the basis of observed value in first clonal generation

Sl. No.	Genotypes	X-value	X-rank	Y value	Y rank
1.	CoX02120	85.90	1	80.35	2
2.	CoX0213S	79.11	2	70.07	6
3.	CoX02177	78.87	3	80.84	1
4.	CoX02244	76.32	4	68.36	8
5.	CoX02129	70.37	5	65.00	11
6.	CoX02027	68.54	6	72.74	5
7.	CoX02058	67.66	7	61.42	15
8.	CoX02217	66.82	8	56.43	18
9.	CoX02061	66.63	9	55.28	21
10.	CoX02007	65.18	10	61.83	13

X- value = Observed yield value
Y-value = Predicted yield value

CoX02243 and CoX02238. Among the top ten ranking clones in first clonal generation CoX02117, CoX02120, CoX02027, CoX02138 and CoX02244 were having almost similar ranking under both criteria.

Similarly, in case of second clonal generation top ten ranking clones (Table 7) on the basis of eleven component traits were CoX02217, CoX02177, CoX02182, CoX02150, CoX02058, CoX02148, CoX02001, CoX02307, CoX02176 and CoX02027 and top ten ranking clones on the basis of three yield components are CoX02150, CoX02182, CoX02155, CoX02058, CoX02027, CoX02001, CoX02148, CoX02217, CoX02130 and CoX02177. Among the top ten ranking clones in second clonal generation CoX02150, CoX02182, CoX02058, CoX02027, CoX02001, CoX02148, CoX02217 and CoX02177 were having almost similar ranking under both the criterias.

Obviously, in the selection programme stress on number of shoots per hectare at 120 days and single cane weight in first clonal generation will be easier to follow and equally-rewarding than taking all eleven characters. Similarly stress given to the characters single cane weight, number of millable cane per hectare and refractometric brix in mid November in second clonal generation will be easier to follow and equally rewarding than taking all eleven characters. The standard partial regression coefficient in both first and second clonal generation for single cane weight was high valued, while formulation of selection criterion by deducing non-significant cane yield contributing traits so trend in third and subsequent clonal generation might be studied to get reliable results.

Bakshi and Choudhary (2000) reported number of millable canes or number of shoots as most reliable character for selection. Single cane weight was also reported as best criterion for selection in the breeding program by Bakshi and Kumar (1999). Similar observations were also reported by Krishna and Singh (2004) while studying genotypic variability in sub-tropical sugarcane. Overall this study of two consecutive generations suggested that selection in early clonal generation should be done on the basis of single cane weight coupled with number of shoots at 120 days as well as number of millable canes. Single cane weight was most reliable trait for selecting genotypes

Table 7. Top ten genotypes rankedon the basis of observed value in second clonal generation

Sl. No.	Genotypes	X-value	X-rank	Y-value	Y-rank
1.	CoX02217	66.17	1	58.21	8
2.	CoX02177	65.64	2	57.82	10
3.	CoX02182	64.64	3	61.35	2
4.	CoX02150	64.53	4	62.12	1
5.	CoX02058	64.42	5	59.73	4
6.	CoX02148	64.15	6	58.67	7
7.	CoX02001	63.02	7	59.31	6
8.	CoX02307	60.70	8	48.05	20
9.	CoX02176	60.58	9	45.88	24
10.	CoX02027	58.46	10	59.35	5

X-value = Observed yield value; Y-value = Predicted yield value

in both the generations. The positive and significant correlation among number of shoots at 120 days and number of millable canes in both the generations advocated its inclusion in selection procedure as these were among the major contributor to cane yield. Consideration of settling behaviour of individual character is also advocated to make selection more effective in early generations.

The changing behaviour of correlation of brix in mid November and mid December with cane yield in both the generations and non-significant association of other quality traits with cane yield advocate preliminary selection on the basis of cane yielding ability than to score these for juice quality. It can also be suggested that the scoring of genotypes for quality traits should be delayed to later generation till the stabilize.

Finally, two clones, *viz* CoX02217 and CoX02177 were selected for subjecting directly for varietal evaluation trial and as parent in hybridization programme for improvement of sub-tropical sugarcane. Details about these two clones in comparison to best check BO 128 are listed in Table 8.

Table 8. Mean performance of a top two identified genotypes of second clonal generation for all the twelve quantitative traits in both the generations

Sl. No.	Character	Genotypes					
		CoX02217		CoX02177		BO 128	
		1st gen	2nd gen	1st gen	2nd gen	1st gen	2nd gen
1.	Germination percent at 45 days	43.33	42.52	66.53	45.75	31.56	32.88
2.	No. of shoot per hectare at 120 days (in thousand)	106.30	109.79	184.35	106.75	121.49	115.72
3.	No. of millable canes per hectare (in thousand)	96/78	96.49	101.51	97.63	101.86	110.49
4.	Cane height at harvest (in cm)	247	217	238	248	213	219
5.	Cane diameter at harvest (in cm)	2.27	2.86	2.67	2.39	2.16	1.89
6.	Single cane weight (in kg)	0.730	0.635	0.829	0.708	0.587	0.595
7.	Refractometric brix in mid November	17.90	21.88	15.30	21.01	20.78	19.80
8.	Refractometric brix in mid December	19-16	20.49	18.56	22.02	21.64	20.82
9.	Refractometric brix in mid January	22.04	21.92	19.70	22.46	22.07	21.82
10.	Sucrose percent in juice in January	15.02	16.21	16.86	16.21	17.28	17.29
11.	CCS percent in juice in January	10-32	11.10	11.52	11.33	11.95	11.93
12.	Cane yield (t/ha)	66.82	66.17	78.87	65.64	59.60	59.41

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Genetic Variability and Character Association Analysis in Tomato

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Genetic variability, heritability (h^2), genetic advance, character association and path analysis were carried out in 17 accessions of tomato (*Solanum lycopersicum* Mill.) during 2000-2001. Significant genotypic differences were observed for all characters under study as indicated by the high genotypic coefficient of variation for number of fruits per plant, average fruit weight, number of locules per fruit, acidity percentage, length of fruits and yield of fruits per plant. The characters with high genotypic coefficient of variation had also high heritabilities. This indicates the possibility of genetic improvements for such traits through selection based on phenotype. Association studies indicated that the yield of fruits per plant positively correlated with plant height, number of branches per plant, number of fruits per plant, average fruit weight, fruit length, number of locules, TSS and ascorbic acid content. Pericarp thickness and acidity percentage are negatively correlated with yield. Path coefficient analysis revealed that plant height, number of branches per plant, width of fruit, number of fruits per plant and average fruit weight exhibited the maximum positive direct effect on yield. Thus an increase in selection on these traits may lead to an over all increase in the yield. Quality traits except pericarp thickness and TSS did not play any significant direct and indirect role. Therefore, a genetic improvement of yield can be initiated by putting positive selection pressure on plant height, number of branches per plant, width of fruit, number of fruits per plant and average fruit weight.

Key words: Tomato, Variability, Correlation, Path analysis, Heritability, Yield

Tomato (*Lycopersicon esculentum* Mill.) is one of the important vegetables grown throughout the world. Though the area and production of tomato are increasing annually yet its average yield remains low. Therefore, for improving yield potential there is a need of systemic breeding approach. Hence knowledge of the magnitude and kind of variability existing in the germ pool for yield and its attribute is essentially important. Heritability examines the extent of heritable portion of variability, while study of genetic advance predicts the possible yield through selection. Keeping in view of this, an attempt was made to know the nature and magnitude of genetic variability existing for yield and its contributing characters in the available germplasm of tomato. The fruit yield in tomato as in other field crops is a very complex character and is dependent on a number of yield components. An attributing trait has been of immense practical interest in the field of plant breeding. This among different yield attributes and for predicting yield in correlation between the related variables. Path coefficient analysis allows partitioning the correlation coefficient into direct and indirect effects of the traits contributing towards the dependent attributes. Selection based on suitable selection indices is more efficient than the selection of different attributes individually. Thus, contribution of suitable indices adopting statistical tools is an essential aspect of plant improvement.

Materials and Methods

The present investigation was carried out at the research farm of the Horticulture Allahabad Agricultural Institute, during 2000-2001. Seventeen hybrids consisting of some released/ pre released varieties were taken for the study. Experiment was laid out in randomized block design with three replications. Seedlings were transplanted in the field during September. A spacing of 75 x 60 cm was given and all the recommended agronomic practices were followed. The observations were recorded on three randomly selected plants per replications for each hybrid on twelve important characters. The analysis of variance was carried out as suggested by Panse and Sukhatme (1997) were used for calculating other genetic parameters. Genotypic and Phenotypic coefficient of variation were calculated as per the formula suggested by Burton and Devane (1953).

Results and Discussion

The analysis of variance indicated highly significant differences among genotypes for all the characters (Table 1). The extent of variability present in seventeen hybrids of tomato was measured in term of range, grand mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, (broad sense) and genetic advance. All the varieties differed significantly with respect to different characters studied. There was close relationship between PCV and GCV

Table 1. Analysis of variance

Source of variation	Plant height (cm)	Branches/ plant	Fruits/ plant	Avg. fruit wt. (gm)	Fruit length (cm)	Fruit width (cm)	Locules/ fruit	TSS %	Acidity %	Yield/ plant (kg)
Replication	26.37	0.58	9.20	1.49	0.58	0.03	0.07**	0.11**	0.0059**	0.0061
Treatment	426.12**	6.64**	4700.99**	839.74**	2.12**	2.04**	4.47	0.48	0.35**	0.54**
Error	3.86	0.20	1.96	3.55	0.10	0.09	0.03	0.02	0.0057	0.01

* Significant at 5 percent probability level
** Significant at 1% probability level

(Table 1). Data further revealed that of the characters under study exhibited high degree of GCV revealing close relationship between phenotypic and genotypic and these characters are not influenced by environment hence improvement for these characters are difficult which is inconsance in the present finding.

With the help of GCV alone, it is not possible to determine the amount of variation that is heritable. Heritable variation can be finding out with greater degree of accuracy when heritability is studied in conjunction with genetic advance. The heritability estimates of fruit length and fruit width (0.86) to number of fruits per plant (0.99). High heritability accompanied with high genetic advance 152.36 for number of fruits per plant, 71.08per cent Avg. fruit wt. 69.02 per cent number of locules per fruit and 61.22 per cent acidity indicating that most likely the heritability is due to additive gene effects and selection may effective this confirm the findings of the Dudi et al. (1983) and Mittal et al. (1996). If heritability was mainly owing to non-additive gene action, the genetic advance could be expected. It was clear from table 1 that the characters like plant height, average fruit weight, fruit length, fruit width, pericarp thickness, locules per fruit, TSS %, acidity %, ascorbic acid possessing high GCV, heritability and genetic advance could be effectively used in selection as it has been suggested by Sahu and Mishra (1995) and Pujari et al., (2000) that characters with high heritability coupled with high genetic advance would respond to selection better than those with high heritability and low genetic advance values observed in other characters namely plant height 29.91 %, number of branches per plant 35.18 %, yield per plant 39.03 %, fruit length 36.09 %, fruit width 31.53 %, pericarp thickness 42.83 %, TSS 16.48 % and ascorbic acid 33.00 % indicated that the expression of these characters was governed by non – additive gene action. As suggested by Mittal et al. (1996) and Pujari et al. (1995), the high heritability is being estimated due to favorable influence of environment rather than genotype and selection for such traits may not be rewarding.

Genotypic and Phenotypic correlation studies are essential in evaluating the possibility of simultaneous improvement for many characters and also the impact of selection for one trait on the other related ones. In the present investigation, yield per plant was positively correlated with number of fruits, average fruit weight, number of branches and plant height. Positive correlation between yield per plant and average fruit weight was in accordance with the results of Singh and Mittal (1976), Sidhu and Singh (1989), Yadav and Singh (1998) and Prasad *et al.* (1998). It is revealed from the association studies that in addition to the direct selection pressure for yield, selection for more branches, taller plants will lead to a rapid genetic improvement for yield per plant. The TSS and ascorbic acid showed positive correlation while pericarp thickness and acidity percentage showed negative correlation with yield. Therefore, simultaneous improvement of yield and quality traits necessitates some sacrifices both in yield and biochemical constituents. Similar results were also reported by Bhattacharya (1977).

The direct and indirect effects of different traits on total yield are given by phenotypic path coefficient. Plant height contributed directly to yield and through number of branches per plant, width of fruits, pericarp thickness and TSS positive direct effect on yield have also been recorded for number of branches per plant, number of fruits per plant, average fruit weight, length of fruit, width of fruit, number of locules and acidity percentage whereas, negative indirect effect via plant height, number of fruits per plant, width of fruits, pericarp thickness and TSS did not show any considerable direct or indirect effect on yield. Residual variation left to be determined for yield was only 0.4521. Correlation studies reveal only the general relationship between any two variables without unfolding any possible cause of such associations. Path coefficient analysis allows partitioning the correlation

Table 2. Range, mean, variability, heritability and genetic advance

Characters	Range		(GM) Grand mean (x)	PCV (%)	GCV (%)	Broad sense heritability (%)	Genetic advance in percent of mean
	Min.	Max.					
Plant height (cm)	56.82	97.55	80.60	14.92	14.72	0.97	29.91
Branches/ plant	6.27	11.36	8.20	18.63	17.86	0.91	35.18
Fruits/ plant	24.88	199.75	53.47	74.05	74.00	0.99	152.36
Avg. fruit wt. (gm)	9.94	85.88	48.07	34.94	34.72	0.98	71.08
Fruit length (cm)	2.43	6.23	4.36	20.17	18.80	0.86	36.09
Fruit width (cm)	2.66	6.00	4.90	17.63	16.43	0.85	31.53
Locules / fruit	2.00	6.00	3.58	34.31	33.94	0.97	69.02
TSS %	2.78	7.73	5.30	22.75	21.75	0.91	42.83
Acidity %	0.28	1.55	1.11	31.19	30.44	0.95	61.22
Yield/ plant (kg)	1.45	2.92	2.12	20.75	19.83	0.91	39.03

Table 3. Estimates of genotypic and phenotypic correlation coefficients

Characters		Branches/ plant	Fruits/ plant	Avg.fruit wt. (gm)	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (mm)	Locules/ fruit	TSS %	Acidity %	Ascorbic acid (mg/ 100gm)
Plant height (cm)	P	0.43	0.45	-0.62**	-0.51*	0.16	-0.17	0.04	0.03	0.26	0.24
	G	0.44	0.45	-0.64	-0.55	0.15	-0.19	0.03	0.02	0.28	0.25
Branches/ plant	P		0.64**	-0.54	-0.51*	-0.34	-0.45	0.25	0.09	0.10	0.33
	G		0.67	-0.57	-0.56	-0.40	-0.52	0.27	0.10	0.12	0.37
Fruits/ plant	P			-0.72**	-0.65**	0.07	-0.17	-0.11	0.15	0.25	0.53*
	G			-0.73	-0.69	0.08	-0.18	-0.11	0.16	0.25	0.57
Avg. fruit wt. (gm)	P				0.61**	-0.15	0.13	0.30	0.02	-0.48*	-0.31
	G				0.66	-0.16	0.13	0.31	0.02	-0.50	-0.33
Fruit length (cm)	P					-0.05	0.29	-0.21	-0.10	-0.37	-0.12
	G					-0.04	0.36	-0.22	-0.10	-0.41	-0.13
Fruit width (cm)	P						0.62**	-0.49*	0.15	0.35	-0.05
	G						0.67	-0.55	0.20	0.41	-0.02
Pericarp thickness (mm)	P							-0.59*	0.36	0.01	0.02
	G							-0.63	0.44	0.014	0.010
Locules / fruit	P								0.08	-0.34	-0.25
	G								0.08	-0.35	-0.26
TSS %	P									-0.07	0.19
	G									-0.13	0.21
Acidity %	P										0.15
	G										0.17

* Significant at 5% probability level
** Significant at 1% probability level

coefficient into direct and indirect path effects. In the present investigation path-coefficient analysis of yield and yield components revealed that number of branches, number of fruit, average fruit weight, fruit length and width of fruits were the most important traits contributing to yield. Quality traits did not play any significant direct and indirect role. Further residual variation indicated that a little portion of the variation in yield remain unaccounted for in this path analysis. These findings are in the agreement with those of Bhattacharya (1977), Supe and Kale (1992) and Yadav and Singh (1998).

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Table 4. Direct (diagonal) and indifferent effects of different traits on yield (phenotypic & genotypic)

Characters		Plant height (cm)	Branches/ plant	Fruits/ plant	Avg. fruit wt. (gm)	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (mm)	Locules/ fruit	TSS %	Acidity %	Ascorbic acid (mg/ 100gm)
Plant height (cm)	P	0.645	0.136	0.069	–0.546	–0.063	0.005	0.095	–0.025	0.018	–0.059	–0.010
	G	0.800	0.145	0.004	–0.782	–0.037	0.022	0.281	–0.052	0.030	–0.079	–0.043
Branches/ plant	P	0.281	0.313	0.098	–0.473	–0.063	–0.010	0.246	–0.150	0.041	–0.023	–0.014
	G	0.353	0.329	0.006	–0.698	–0.038	–0.055	0.749	–0.371	0.104	–0.034	–0.065
Fruits/ plant	P	0.290	0.201	0.153	–0.632	–0.079	0.002	0.096	0.064	0.069	–0.055	–0.022
	G	0.366	0.221	0.009	–0.892	–0.047	0.011	0.270	0.151	0.169	–0.072	–0.092
Avg. fruit wt. (gm)	P	–0.405	–0.170	–0.111	0.870	0.075	–0.004	–0.073	–0.176	0.012	0.107	0.013
	G	–0.513	–0.189	–0.006	1.219	0.045	–0.022	–0.196	–0.425	0.027	0.138	0.057
Fruit length (cm)	P	–0.332	–0.161	–0.099	0.532	0.122	–0.001	–0.161	0.123	–0.045	0.082	0.005
	G	–0.446	–0.187	–0.006	0.815	0.067	–0.006	–0.527	0.308	–0.102	0.115	0.022
Fruit width (cm)	P	0.103	–0.109	0.012	–0.132	–0.006	0.029	–0.341	0.290	0.69	–0.079	0.002
	G	0.126	–0.132	0.001	–0.200	–0.003	0.137	–0.972	0.754	0.204	–0.113	0.004
Pericarp thickness (mm)	P	0.113	–0.142	–0.027	0.116	0.036	0.018	–0.543	0.347	0.166	–0.002	0.001
	G	–0.157	–0.172	–0.002	0.167	0.025	0.093	–1.432	0.866	0.450	–0.004	–0.002
Locules/ fruit	P	0.028	0.081	–0.017	0.264	–0.026	–0.015	0.324	–0.581	0.037	0.075	0.010
	G	0.030	0.090	–0.001	0.380	–0.015	–0.076	0.910	–1.363	0.090	0.098	0.046
TSS %	P	0.025	0.029	0.023	0.024	–0.012	0.005	–0.200	–0.048	0.451	0.017	–0.008
	G	0.024	0.034	0.001	0.033	–0.007	0.027	–0.633	–0.120	1.018	0.037	–0.037
Acidity %	P	0.173	0.033	0.039	–0.424	–0.046	0.011	0.006	0.198	–0.035	–0.222	–0.006
	G	0.229	0.040	0.002	–0.611	–0.028	0.056	–0.020	0.484	–0.136	–0.276	–0.029
Ascorbic acid	P	0.156	0.103	0.082	–0.273	–0.016	–0.002	0.001	0.146	0.088	–0.033	–0.042
(mg/100gm	G	0.124	0.124	0.005	–0.405	–0.009	–0.009	–0.014	0.366	0.220	–0.047	–0.173

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Studies on Genetic Variability of Pear Germplasm

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The pomological evaluation of 23 pear cultivars showed marked variation for all the morphological, fruit and quality parameter studied. The mean plant height ranged from 3.5 to 9.7 meters, tree girth 38 10 112 cm and plant spread from 3.0x3.2 to 6.8x6.2 meters. The cultivars expressed wide genetic variation. Cultivar Awal Number was early to attain full bloom on 22nd March whereas Bode Cappiament was late and full bloom was recorded on 23rd April. Cultivars Kala Hathi, Kashmiri Pear, Max Red Bartlett and Beurre Hardy were more productive in comparison to Novem Poitrum, Hengal, Seckel Yakumo, etc. Red Bartlett and Max Red Bartlett had better fruit weight (180.6 and 150 g) and size (78.3x75.2 mm and 73.5 x 68.4 mm); Basuiodse Favorite highest TSS (18.7°Brix) Anjou. Kashmiri Pear and Flemish Beauty were higher in fruit firmness.

Key words: Pear, Genetic variability, Germplasm, Selection, Trait, Adaptability

Pear (*Pyrus communis*) is considered to be the most popular and important temperate fruit after apple. It is a prehistoric crop and its cultivation in Europe started at an early time compared to that of apple. *Pyrus* genetically is diverse and its genepool is very well defined. Speciation through geographic isolation by mountain ranges and its adaptation to colder and drier areas provided man with variability from which to select desirable ones. The European pears for their soft buttery texture, distinct flavour, and with wide genetic variation both at species and variety level is regarded as the most delectable of all temperate fruits. Apple and pear though introduced almost at the same time in India, pear cultivation is far behind compared to that of apple, main reason being few cultivars introduced failed to adapt to varied agro-climatic conditions of Himachal Pradesh, low storage and transportation potential, non availability of suitable rootstocks, etc.

However, today marked changes in the germplasm have been brought about through introduction of diverse types varying in chill requirement, wide adaptability, colour, taste, storage and number of other characters. Temperate Horticultural Research Station, Kotkhai has been a centre for introduction and testing of pome and stone fruit. With the rapid changes in climatic conditions both apple production and productivity is sharply receding. To sustain this trend, production needs to be increased through diversification, and by way of cultivating other suitable crops. In this regard, pear is the most suitable alternative. With this in view, pear cultivars grown at the station were evaluated for various growth, yield and quality characters.

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Materials and Methods

The evaluation work on pear was undertaken at the experimental farm of Temperate Horticulture Research Station, Kotkhai during the year 2004 and 2005. The experimental material comprised 23 pear germplasm, which were introduced from different countries and through NBPGR Shimla. The cultivars were planted on seedling rootstock and each cultivar was replicated three times in a randomized block design. The data on characters like plant growth yield, physico-chemical traits of different cultivars was evaluated for two years of study i.e. 2004 and 2005 as per the standard methods. The data on various parameters was analyzed as per the method of Panse and Sukhatme (1985).

Results and Discussion

The tree growth characteristics recorded in terms of tree height, girth and spread of 23 pear cultivars is indicated in Table 1. The data shows marked inherent variation for tree height, which ranged from 3.5 to 9.7 meters. Minimum tree height was observed in cultivars Kiskusui and Luhimtra Kalapa (each 3.5 m) followed by Manning Elizabeth (4.5 m). Bodde Cappiament (4.6 m). All these cultivars were statistically similar to each other. Cultivar Kalahathi was the tallest growing (9.7 m), followed by Autumn of Yaklex (8.5 m) and Ishiwase (8.2 m). None of these cultivars differed for tree height character and were similar statistically. The other cultivar also depicted genetic variation amongst themselves.

The character tree girth also revealed variation (3.8 to 112 cms). Cultivar Beaurre Hardy had the maximum tree girth (112.0 cm), followed by Ishiwase (109.0 cm) and Autumn of Yaklex (91.0 cm) except for the last

cultivar. The other two were at par with each other. On the other hand, cultivars Manning Elizabeth had least tree girth (38.0 cm) followed by Luhimtsa Kalapa (44.0 cm) and William Bon Chratian (53.0 cm). All the three cultivars were statistically non-significant. Plant spread recorded in two directions, i.e. East-West and North-South also showed variation. Cultivar Kiskusui had least plant spread (2.5x2.3 m) followed by Luhimtsa Kalapa (3.0x3.2 m) and Bodde Cappiament (3.8x4.2 m) and all were similar statistically, whereas cv. Ishiwase had maximum spread (6.8x6.2 m) followed by Kalahathi (6.3x6.2 m) and Basuiodsc favourite (6.5x6 cm). Statistically these cultivars, were similar. The (lowering period of evaluated cultivars spread over to 33 days. Cultivar Awal Number was first to flower (22nd March), Flemish Beauty (30th March). The other cultivar, late to attain full bloom were Bode Cappiament (23rd April), Kiskusui and Lisnova Karavista (20th April) and Red Bartlett (19th April). The yield and fruit quality characters of various cultivars evaluated is presented in Table 2. The yield per tree varied from 5.0 to 90.0 kg. Cultivars Seckel (5.0 kg), Noveum Poitrum (7.0 kg). Kiskusui (12.0 kg), Yakumo (12.50 kg), Hengal (15.0 kg), were all low crop producing cultivars. All these cultivars were statistically similar to each other. The higher crop producing cultivars were Kalahathi (90.0 kg), Kashmiri Pear (77.0 kg) and Beurre Hardy (60.0 kg). The first two cultivars were statistically similar but differed from Beurre Hardy. The intermediate cultivars from yield point of view were Max Red Bartlett (63.0 kg), Starkrimson (42.0 kg), Bartlet (45.0 kg), whereby showing varietal variation in crop production.

The fruit size also showed substantial variation. Cultivar Yakumo had the most small sized fruits (41.3x45.0 mm), followed by Early China (44.2x47.4 mm) and Awal Number (45.0x53.3 mm), whereas Manning Elizabeth (67.3x65.0 mm). Williams Bon Chretien (66.0x65.0 mm) and Luhimtsa Kalapa (64.3x54.3 mm) recorded higher first size values, the cultivar with higher and lowers values were at par with each other. Fruit size ranged from 47.5 to 186.6 g per fruit. Higher fruit weight was observed in cultivars Red Bartlett (186.6g). William Bon Chretian (150.0 g) which differed statistically followed by Autumn of Yaklex (140.0 g). Starkrimson (126.2 g), Kashmiri Pear (110.0 g) Ishiwase and Lisnova Karavitsa (1 16.6 g).

The total soluble solid (TSS) contents of assessed cultivars was variable and ranged form 10.0 to 18.7°Brix. Cultivars Noveum Poitrum (10.0). Bode Cappiament,

Table 1. Growth character of different pear cultivar (2004 and 2005)

Cultivar	Tree height (m)	Tree girth (cm)	Tree spread (m)	
			NS	EW
Ishiwase	8.2	109	6.8	6.2'
Kiskusui	3.5	46	2.5	2.3
Yakumo	5.8	59	5.2	4.9
Seckel	6.2	86	5.4	5.0
Anjou	6.5	94	4.0	4.7
Beurre Hardy	7.2	112	5.4	4.8
William Bon Chretian	4.7	53	4.8	5.3
Lisnova Karasvitsa	6.0	79	5.0	5.1
Luhimtsa Kalapa	3.5	44	3.0	3.2
Jargo nelle	7.2	75	5.8	5.2
Kala Hathi	9.7	81	6.3	6.2
Autumn of Yaklex	8.5	91	5.8	6.2
Kashmir Pear	7.4	85	5.5	4.8
Manning Elizabeth	4.5	38	4.0	4.5
Hengal	6.0	63	5.9	6.1
Bodde Cappiament	4.6	82	3.8	4.2
Flemish Beauty	5.2	78	4.7	4.7
Noveum Poitrum	6.4	80	5.2	5.3
Awal Number	7.2	86	5.8	5.3
Basuiodsc Favourite	7.5	82	6.5	6.0
Red Bartlett	5.3	62	5.2	4.4
Max Red Bartlett	5.4	56	4.5	4.4
Starkrimson	4.9	59	4.3	4.6
$CD_{0.05}$	2.87	19.70	17.8	1.86

Yakumo (11.0), Kiskusui and Seckel (12.0) and William Bon Chretain (115.0 Brix) were similar for TSS contents whereas cvs. Basuiodsc Favourite (18.7), Early China (17.2), Max Red Bartlett (15.4) and Red Bartlet (14.8° Brix) had higher TSS contents. On the basis of TSS specific groups of cultivars can be established. The fruit firmness differed among the cultivars. Cultivar Kalahathi had least firmness (1.5), followed by Autumn of Yaklex. Basuiodsc Favourite and Starkrimson all had firmness of 17.0 lb/inch^2 and the cultivars were statistically similar compared to Flemish Beauty and Anjou (20.0), Hengal (19.5) and Red Bartlett (19.2), Seckel, Kiskusui and Manning Elizabeth (19.0 lb/inch^2), which recorded higher firmness.

Appropriate selection of diverse genotypes is the foundation of a successful orcharding system. Hence prior to recommendation of any genotype for cultivation at a particular place or region the germplasm needs to be systematically evaluated for different horticultural traits. Number of workers have evaluated pear germplasm in different parts of world and have recommended few which have performed exceptionally well over long period of time (Bernkoff, 1990; Bell, 1990; Coa Zong Fu, 1999; Blanchet *et al.*, 1997; Sharma and Sharma, 2002; Rachna, 2003; Bist and Yadav, 2004).

Table 2. Yield and fruit quality of pear cultivars (2004 & 2005)

Cultivar	Yield kg/tree	Fruit size		Fruit weight	TSS (°Brix)	Fruit firmness lb/inch²	Date of full bloom 04-05
		Length (mm)	Breadth (mm)				
Ishiwase	30.0	46.3	56.6	116.5	14.5	20.0	12-14/04
Kiskusui	12.0	37.3	40.3	50.0	12.0	19.0	20-23/04
Yakumo	12.5	41.3	45.0	63.3	11.0	18.0	8-10/04
Seckel	5.0	53.6	54.6	116.6	12.0	19.0	17-19/04
Anjou	30.0	52.3	56.6	100.0	12.5	20.0	7-9/04
Beurre Hardy	60.0	56.6	54.3	106.6	10.5	18.0	6-9/04
William Bon Chretian	5.5	66.0	60.0	150.0	11.5	18.5	11-14/04
Lisnova KLaravitsa	24.5	57.6	52.6	116.6	14.5	19.2	20-24/04
Luhimtsa Kalapa	25.0	64.3	54.3	103.0	13.5	17.0	18-21/04
Jargo nolle	32.5	50.6	45.0	70.0	12.5	18.0	12-15/04
Kala Hathi	90.0	58.3	47.3	76.6	13.5	16.5	12-16/04
Autumn of Yaklex	20.0	40.6	63.3	140.0	13.0	17.0	13-16/04
Kashmir Pear	77.0	54.0	54.3	110.0	14.0	20.0	31-34/04
Manning Elizabeth	35.0	67.3	65.0	186.6	14.5	19.0	5-8/04
Hengal	15.0	53.3	51.6	83.3	12.5	19.5	26-31/04
Bodde Cappiament	30.0	55.6	45.6	80.0	11.0	18.0	23-27/04
Flemish Beauty	25.0	52.0	54.3	136.6	13.0	20.0	30-34/04
Noxeum Poitrum	7.0	40.3	52.6	100.0	10.0	18.5	15-18/04
Awal Number	30.0	45.0	53.3	100.0	14.0	17.5	22-27/04
Basuiodse Favourite	25.0	48.5	43.5	56.6	18.7	17.0	1-4/04
Red Bartlett	45.0	78.3	75.2	186.6	14.8	19.2	19-22/04
Max Red Bartlett	63.0	73.5	68.4	150.0	15.4	18.4	3-6/04
Starkrimson	42.0	64.0	58.0	126.2	14.6	17.7	7-9/04
$CD_{0.05}$	12.46	8.32	8.63	13.6	2.24	1.23	

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Variability, Heritability and Genetic Advance Studies in Sweet Pepper (*Capsicum annuum* L.)

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The present investigation was conducted during *kharif*, 2003 at Hill Campus, Ranichauri, Tehri Garhwal, Uttarakhand with 45 sweet pepper genotypes. The experiment was laid out in randomized block design with three replications. Genetic variability was studied for characters viz., days to first picking, plant height, leaf area, fruit length, fruit diameter, flesh thickness, fruit weight, number of pickings, number of fruits per plant, yield per plant, TSS and ascorbic acid content. Data were analyzed statistically for phenotypic, genotypic and environmental coefficient of variation and heritability genetic advance/genetic gain. Analysis of variance revealed significant differences among the genotypes for ail the traits. Genotypes EC519610 and EC519611 were promising for further utilization in plant improvement programme as they possessed more than one desirable trails. Moderate to high PCV, GCV, heritability and genetic gain were observed for ascorbic acid content, number of fruits per plant, fruit yield per plant and fruit length.

Key words: Sweet pepper, Improvement, Variability, Heritability, Genetic advance

Sweet pepper or Shimla mirch (*Capsicum annuum* L.) is considered as one of the most important remunerative crops in Uttarakhand where it is mainly grown as off-season vegetable. The fruits are either sold in local markets or supplied to distant places as green vegetable. However, its popularity among the common mass is increasing. The farmers, thereby, fetch a good lucrative return through cultivating this crop. The net return from this crop was calculated to be as high as Rs. 1,58,607.45 per hectare. The commercially cultivated varieties in Uttarakhand are old introductions such as California Wonder and Yolo Wonder. In absence of suitable genotypes, expected growth in cultivation of this crop has not been accomplished till today. Identification of superior genotypes, therefore, becomes imperative for promoting its production, productivity and quality of the produce. Plant introduction has long been used to enrich our varietal stock. However, for their efficient use in breeding programme the introduced genotypes need to be classified into different groups based on the variability available for the best exploitation of heterosis as well as to ease in selection. Knowledge in terms of heritability, expected genetic advance, inter character relationship and relative contribution of individual characters to economic yield is needed for improvement of genotypes. In India, studies on sweet pepper have been very few because of the limited adaptability of crop. So to bridge the gap a study was undertaken under mid hill conditions of Ranichauri, Uttarakhand with 39 introduced and 6 locally adapted materials.

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Materials and Methods

The experimental material consisted of 39 sweet pepper genotypes obtained from AVRDC, Taiwan, five from Division of Vegetable Science, Ranichauri, Uttarakhand and one from DARL. Pithoragarh, Uttarakhand. The experiment was laid out in RBD with 3 replications each. The spacing followed was 45 x 45 cm. The net plot area was 2.025 m^2. Observation on different characters like days to first picking, leaf area, fruit length, fruit diameter, flesh thickness, fruit weight, number of pickings, number of fruits per plant, plant height, and yield per plant were taken. Parameters on variability were estimated as per formula given by Burton and Devane (1953).

Heritability in broad sense was calculated as per formula given by Burton and Devane (1953) and Allard (1960). The expected genetic advance resulting from selection of five percent superior individuals were worked out as suggested by Lush (1940) and further used by Burton and Devane (1953) and Johnson *et al.* (1955). Genetic gain expressed as percent of population mean was calculated by the method given by Johnson *et al.* (1955).

Results and Discussion

In the present investigation, the ANOVA revealed significant differences among the genotypes for all the traits (Table 1). These differences indicated the presence of considerable variability and good scope for further improvement. The variability in the fruit yield ranged from 153.66-464.33g per plant. The high variability in fruit yield of capsicum was also reported by Mishra *et al.*

(2001) and Dipendra *et al.* (2002). Maximum eight fruits per plant had been recorded in four genotypes which indicated that they posses greater potentiality to bear maximum number of fruits per plant and thus offer opportunity to breed variety having profuse bearing The range of fruit weight at edible maturity was 34.85-66.38 cm fruit length 4.66-8.53 cm, fruit diameter 3.86-6.06 cm. The highest flesh thickness 0.613 cm was also obtained, which indicated greater scope for long distance transport and long shelf life. Four genotypes recorded to be earliest producing marketable fruits in 56-58 days after transplanting which provide considerable for selection of early genotypes to catch the early market. The range of plant height was 29.66-49.03cm. Significant varietal differences were also observed by Sreelathkumary and Rajanomy (2002) for fruit yield and fruit length, Arya and Saini (1976 and 1977); for pericarp thickness, Choudhary *et al.* (2001) for plant height and days to 50 percent flowering. In this investigation maximum variability (55.2-318.55mg/100g) was recorded in ascorbic acid content. This indicated identification of suitable genotypes and its utilization as parent in a crossing programme may improve ascorbic acid content in sweet pepper. Simon (1966) obtained ascorbic acid content as high as 321 mg/100 g whereas Joshi and Singh, (1975) reported 175mg/100g vitamin C in *Capsicum.*

The magnitude of genetic and environmental effect involved in the expression of characters were determined by genotypic and phenotypic coefficient of variation which can precisely be used for making comparisons between populations for different matric traits. Maximum magnitude of PCV and GCV were recorded for ascorbic acid content. High PCV (31.43) was exhibited by yield per plant, number of fruits (29.4), and it has moderate value for leaf area (24.05), number of pickings (21.4). flesh thickness (20.73) and plant height (17.37), GCV estimate was high for yield per plant (29.66), lumber of fruits (28.64), and moderate for leaf area (16), number of pickings (15.48). Fruit length and fruit diameter exhibited low PCV and GCV. PCV and GCV estimates for various traits in sweet pepper have been compiled by several authors. Sreelathakumary and Rajanomy (2002) reported high PCV and GCV for fruits per plant, fruit weight, fruit length and fruit girth.

Study of genotypic coefficient of variation help to measure the range of genetic variation existed in a specific environmental site for a particular character and to compare the magnitude of variability existing in various characters. However, it cannot measure the heritable variation. GCV together with heritability estimates would give reliable indication of the expected amount of improvement through selection (Burton and Devane, 1953).

In the present investigation high heritability was found for ascorbic acid content, yield per plant, number of fruits, fruit length and days to 1st picking and moderate for TSS content, number of pickings, fruit weight, fruit diameter and plant height. High heritability for different traits indicated that large proportion of phenotypic variance has been attributed to genotypic variance and therefore, reliable selection could be made for these traits on the basis of phenotypic expression. Earlier work in this aspect revealed high heritability estimate for fruit yield per plant Kumar *et al.* (1993); number of fruits and fruit length Gogoi *et al.* (2002); Sreelathakumary and Rajanomy (2002) which are in conformity with the present study. Johnson *et al.* (1955) suggested that the estimates of heritability coupled with genetic advance provide better information rather than heritability alone.

High heritability along with high GCV and genetic gain was observed for ascorbic acid content, number of

Table 1. ANOVA for different trails in sweet pepper (*Capsicum annuum* L) genotypes

Traits	Range	General SE	Mean+/–	PCV	GCV	ECV	h^2	GA
Days to 1st harvest	56.33-77.33	65.22	1.34	9.59	8.89	3.58	86.06	11.09
Plant height (cm)	29.66-49.03	38.31	2.42	47.37	13.49	10.94	60.31	8.26
Leaf area (cm^2)	29.03-54.56	38.60	4.00	24.05	16.00	17.95	44.29	8.47
Fruit length (cm)	4.6-8.53	6.82	0.25	14.76	13.30	6.38	81.27	1.68
Fruit diameter (cm)	3.8-6.06	5.25	0.15	11.18	9.99	5.03	79.73	0.96
Flesh thick ness (cm)	0.33-0.613	0.41	0.04	20.73	12.24	16.73	34.88	0.06
Fruit weight (g)	34.85-66.38	55.87	2.65	14.36	11.74	8.23	67.17	11.11
No. of pickings	2.6-5.53	4.30	0.37	21.40	15.48	14.78	52.29	0.99
No. of fruits/plant	2.0-7.73	5.10	0.20	29.40	28.64	6.62	94.92	2.93
Yield/plant(g)	153.0-464.53	284.94	17.10	31.43	29.66	10.39	89.06	164.31
T.S.S. (Brix)	4.6-5.73	5.29	0.09	5.07	4.19	2.85	68.44	0.38
Ascorbic acid (mg/100g)	55.20-316.11	150.79	0.24	59.97	59.97	0.33	99.99	186.28

fruits per plant, fruit yield per plant, and fruit length, indicating that the traits were controlled by additive gene effect (Panse, 1957) and would respond very well to continuous selection so that considerable improvement of these traits, might be possible.

Moderate to high heritability, GCV and genetic gain for plant height and fruit weight at edible maturity and pericarp thickness suggested that these traits were controlled by non-additive gene effect. An improvement of these characters, therefore, can be achieved through exploiting the dominance effect.

High heritability and high genetic gain for fruit weight at edible maturity was reported by Vijaylakshmi *et al.* (1989) and Bhatt *et al.* (1996). These results were not in agreement with the present findings where high heritability but moderate genetic gain was observed. However, an identical result on high heritability and high genetic gain had reported in number of fruits per plant (Gupta and Yadav, 1984, Shah *et al.*, 1986), fruit length (Shah *et al.*, 1986, Meshram, 1987).

From the above study on mean performances and other genetic parameters of different plant characters, it was revealed that four characters *viz.* ascorbic acid content, number of fruits per plant and fruit yield per plant, fruit and fruit length were the most important traits for improving the genotypes while plant height, fruit weight at edible maturity and flesh thickness were considered as second most important characters for applying selection in sweet pepper genotypes.

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Genetic Variability, Heritability and Genetic Advance in French Marigold (*Tagetes patula* L.)

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Genetic variability, heritabality and genetic advance were estimated for various vegetative and floral characters in 30 genotypes of French marigold (*Tagetes patula*). The studies showed high range for total yield per plant (59.08-559.35g), weight per flower (0.96-8.59g) and number of flowers per plant (35.33-206.0). The coefficient of variation (PCV and GCV) was maximum for weight per flower (PCV=59.75, GCV=59.49) and minimum for duration of flowering (PCV=11.08, GCV=10.84). The phenotypic coefficients of variations were higher than those of genotypic coefficient of variation, which indicate greater GxE interaction. High estimates of heritability (broad sense) were obtained for all the characters studied. The highest value of heritability was obtained for weight of flower per plant (99.1), plant-spread (99.0), and plant height (98.9). Thus, these characters can be improved through direct selection. In the present study, flower yield showed maximum genetic gain (233.99). High heritability along with high genetic gain was observed for number of flowers per plant (h^2 = 97.4, GA = 77.53) and total flower yield per plant (h^2 =94.3, GA=233.99). High heritability with low genetic gain was observed for weight per flower (h^2 = 99.1, GA=4.02) and stalk length (h^2 = 96.6, GA=5.78). So, improvement in these characters could be brought about by practicing phenotypic selection.

Key words: Marigold, Variability, Heritability and Genetic advance

Marigold, a native of Central and South America is a member of Asteraceae family. It is one of the top five flowers grown widely for loose flower production in India. Mainly two species of marigold i.e. African marigold (*Tagetes erecta* L.) and French marigold (*Tagetes patula* L.) are grown for this purpose accounting for more than half of the nation's loose flower production. In French marigold, most of the varieties being local are poor flower yielders. Therefore, there is a scope to develop high yielding varieties in this species. Estimation of genetic variability in the germplasm of a particular crop is prerequisite for making any effective breeding programme. Selection of parents to be included in the hybridization programme should be based on genetic distance. Most of the important characters including yield are highly influenced by environment, since they are polygenically controlled, which make the selection process difficult. Heritability is an index for calculating the influence of environment on the expression of genotypes. Estimates of genetic advance together with heritability would be helpful in assessing the nature of gene action. Therefore, present investigation was carried out for estimating genetic variability, heritability and genetic advance for various vegetative and floral characters in 30 genotypes of French marigold (*Tagetes patula*).

Material and Methods

The experiment was undertaken in the Division of Floriculture and Landscaping, IARI, New Delhi with 30 genotypes of French marigold grown in RBD with three replications. Seeds of all the genotypes were sown on 15 cm raised seedbeds in the nursery and the seedlings were transplanted in the main field after one month at a spacing of 30 x 30 cm. Uniform cultural operations were followed regularly. Five plants per replication were selected randomly from each genotype and used for recording observations. Phenotypic and genotypic coefficient of variations (broad sense) were estimated according to Burton and Devane (1953). Genetic advance was calculated according to the formula given by Johnson *et al.* (1955). Heritability was estimated according to Allard (1960).

Results and Discussion

The data depicted in Table 1 reveals that there were significant differences among genotypes for various characters. High ranges for total yield of flower per plant (59.08-559.35g), weight per flower (0.96-8.59g) and number of flowers per plant (35.33-206.0) were observed. The higher phenotypic coefficient of variation than those of genotypic coefficient of variation indicated the predominant role of environment in the expression of the traits, which is in consonance with the results obtained by Ponnuswamy *et al.* (1985).

Phenotypic and genotypic coefficient of variation was maximum for weight per flower (PCV=59.75, GCV=59.49) followed by total yield per plant (PCV=49.80, GCV=48.36) and number of flowers per

Table 1. Range, mean, coefficient of variation, heritability (broad sense) and genetic advance for various characters in French marigold (*Tagetes patula*)

Characters	Range	Mean	PCV	GCV	h^2	GA
Plant height (cm)	31.33-85.50	49.02	36.29	36.09	98.9	36.25
Plant spread (cm)	32.83-110.17	54.36	36.83	36.63	99.0	40.81
Branch number	7.0-25.67	15.22	31.32	27.62	77.8	7.64
Leaf length (cm)	7.50-23.33	16.40	28.26	26.31	86.6	7.76
Leaflets per leaf	9.33-25.33	19.31	20.63	15.53	56.6	4.65
Leaflet length (cm)	2.33-7.33	4.34	27.84	23.22	69.56	1.73
Leaflet breadth (cm)	0.70-1.73	0.99	36.51	24.48	45.0	0.33
Stalk length (cm)	5.60-17.67	8.75	33.22	32.65	96.6	5.78
Flowers per plant	35.33-206.0	82.50	46.84	46.32	97.4	77.53
Flower size (cm)	2.57-5.93	4.63	19.13	17.37	82.5	1.51
Weight/flower (g)	0.96-8.59	3.29	59.75	59.49	99.1	4.02
Days to first flowering	56.67-120.0	76.89	23.93	23.70	98.2	37.20
Flowering duration (days)	78.67-119.33	94.91	11.08	10.84	95.6	20.72
Total yield/plant (g)	59.08-559.35	241.89	49.80	48.36	94.3	233.99

plant (PCV=46.84, GCV=46.32). These findings are in accordance with the observations recorded by Nandkishore and Raghava (2001) in African marigold and Raghava and Negi (1994) in China aster. Janakiram and Rao (1995) also reported high PCV and GCV for total yield per plant in African marigold. Similarly, Sirohi and Behera (2000), Chaugule (1985) and Chattopadhyay *et al.* (1992) also reported high PCV and GCV for number of flowers per plant but it was minimum for duration of flowering. Our results are in close conformity with the findings of Singh and Sen (2000) who worked on chrysanthemum. Narrow differences between GCV and PCV, gave evidence to the genotypes that the variability existing in them was mainly due to their genetic make up.

High estimates of heritability in broad sense were obtained for all the characters. According to Panse (1957), the magnitude of heritable value is the most important aspect of genetic constitution of breeding material, which has close bearing on the response to selection. The high values for heritability were obtained for weight per flower (99.1), plant spread (99.0), plant height (98.9), time taken for flowering (98.2) and number of flowers per plant (97.4). Janakiram and Rao (1995) also found similar results in African marigold for flower weight and number of flowers per plant. Ponnuswany *et al.* (1985) observed high heritability for number of flowers per plant and plant spread in chrysanthemum. Chaugule (1985) noted it for number and weight of flowers per plant in chrysanthemum. These findings suggest that there is scope for improvement in these characters through direct selection. In the present study total flower yield per plant showed maximum genetic gain (233.99), followed by number of flowers per plant (77.53) and plant spread (40.81). Singh and Sen (2000) and Janakiram and Rao (1995) reported high genetic advance for total flower yield per plant.

Heritability along with genetic gain are more useful criteria in predicting the resultant effect for selecting the best individual (Johnson *et al.* (1955). Burton (1952) suggested that characters with high heritability coupled with high genetic advance would respond to selection better than those with high heritability and low genetic advance. High heritability along with high genetic gain was observed for total flower yield per plant (h^2 = 97.4, GA = 77.53). These results are in accordance with the findings of Barad (1992) and Singh and Sen (2000). Here practicing phenotypic selection could bring about improvement in these characters. It is also suggested that variation for different characters in the genotypes studied were due to high additive gene effect. Similar observations have also been reported by Panse (1957).

High heritability and low genetic gain were observed for weight per flower (h^2 = 99.1, GA= 4.02), stalk length (h^2 = 96.6, GA= 5.78) and duration of flowering (h^2 = 95.6, GA=20.72). It reflects that high heritability is not always associated with genetic advance (Swarup and Chaugale, 1962). Hence, selection on the basis of these characters will be less effective as these are controlled by non-additive genes.

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Evaluation of Indigenous Landraces of Ricebean (*Vigna umbellata*) from Nagaland for Growth and Yield Attributing Characters

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Thirty landraces of ricebean collected from different localities of Nagaland were field evaluated for growth, development and yield attributing characteristics. The landraces exhibited significant variations particularly for yield attributing characteristics like 100 seed weight, number of pods per plant, number of seed per pod and pod length. The 100 seed weight character had highest heritability (0.984) followed by number of seeds per pod and number of pods per plant. The 100 seed weight also had maximum direct effect on yield (0.683) followed by seed per pod, pod length and pods per plant.

Key words: Ricebean, *Vigna umbellata*, Non conventional pulse, Yield attributing characters, Variability

Pulse grains and other leguminous plants are among the best sources of plant protein and were used as integral part of diet in India since time immemorial where majority of the population are vegetarian. In recent times emphasis on non-conventional pulses or legumes are gaining momentum due to perpetual stagnation in pulse production and growing demand for pulses. Non-conventional pulses can be defined as those legumes which are semi-wild or under-utilised or cultivated as backyard crop or in small areas in isolated and have great potentiality as a crop. With 35% of world area under pulse cultivation and 27% of world production; India is the world's leading producer of pulses but still India is the largest importer of pulses (Ashthana, 2000). Conventional pulses are basically recalcitrant crop, not amenable to genetic improvement and hence unlike cereals, pulses have very limited number of genotypes, cultivation of pulses are confined to northern India, which accounts for 78 per cent of country's pulse production, due to specific agro-climatic requirement and most experts are of the opinion that further expansion of pulse growing area is not possible (Ashthana, 2000). Pulse productivity is one area where green revolution did not have much impact. During pre-green revolution period pulse production in India varied from 10-11 million tons/year with a maximum of 15mt/year in 1958, which is comparable to post-green revolution period (Gadgil *et al.*, 1999). Against this stagnation in pulse production India's population has jumped from 36.1 crores in 1951 to 100 crores in 2001. As a consequence per capita availability of pulse dropped from 27 kg/year in 1958 to 13 kg/year in 1995. Considering the futuristic requirement it is estimated that India's pulse requirement will be 23 mt per year in 2020 AD (Kumar, 2000) which appears to be extremely difficult target, because India's pulse production never exceeded 14 mt/year in the last half century.

Against this alarming scenario of pulse productivity and pulse demand, a promising option is to evaluate the legume biodiversity, short listing the little-known but promising seed legumes and bringing the areas not covered by conventional pulses, under non-conventional pulses. North-Eastern and India is not a traditional pulse growing area because of its unsuitable climatic condition for cultivation of major pulses. But it is very rich in legume biodiversity. Among the North-Eastern states Arunachal Pradesh is richest in legume biodiversity (with 67 genera and 195 species) followed by Assam (with 68 genera and 171 species (Mao and Hynniewta, 2000). Among the non-conventional pulses, the most promising one is *Vigna umbellata* (Thunb.) Ohwi and Ohashi popularly known as ricebean. Unlike the conventional pulses in ricebean appreciably high genetic variation exist in rice bean and they can be grown in a wide range of agro-climatic conditions. Moreover, ricebean is generally resistant to most of the common leguminous diseases and pests (Chandel *et al,* 1980). In Nagaland, various ethnic tribes have been cultivating ricebean since time immemorial. However there is little or no record about the scientific scrutiny of the land races of ricebean from Nagaland. The present study was intended to collect and make preliminary evaluation of the landraces of ricebean from Nagaland.

Materials and Methods

Under field condition of Nagaland ricebean matures and becomes ready for harvest in November. Seed collection was done during the period of November

to February through visits to various villages of Nagaland. The sites of collection in Nagaland were shown in figure 1. The individual landraces were demarcated on the basis of seed size and seed colour. A total of 30 genotypes were collected and studied through field trial. Field trials were carried out in the experimental farm of the School of Agricultural Sciences and Rural Development, Nagaland University, Medziphema (altitude 305 m), Nagaland during 1998 and 1999. The climate is sub-tropical, predominantly humid with moderate temperature and medium to high rainfall. Field experiment was conducted in a randomised block design with three replications. Separate bamboo poles were provided to individual plants to ensure that they do not intermix. Seed sowing was done in the middle of June and observations were recorded on five plants selected randomly for each landrace in each replication. At maturity these plants were harvested and thrashed separately and data were recorded for the following - shoot length of the seedling, number of branches per plant, days to 50% flowering, days to maturity, number of pods per peduncle, number of pods per plant, number of seeds per pod, 100 seed weight. Analysis of variance was carried out as per the method outlined by Panse and Sukhatme (1978). Phenotypic and genotypic coefficients were calculated according to the formulation of Burton and Devane (1953). Phenotypic and genotypic correlation coefficient were worked out to study the inter-relationship between various pairs of characters as suggested by Al-Jibouri *et al,* (1958). Path coefficient analysis was carried out following the method of Dewey and Lu (1959).

Results and Discussion

Wide variations were observed for plant height 30 days after sowing. Highest growth rate in the range of 29.15 and 35.23 cm were recorded for a total of 13 cultivars, while lowest growth rate in the range of 19.83 to 23.0 cm were recorded for only 3 cultivars. As a whole mean growth rate was 28.22 cm with 18.51 per cent coefficient of variation. However, the number of primary branches exhibited limited variation in the range of 5.02 to 8.78 with a mean value of 7.05 and 16.34 per cent coefficient of variation. Considerable variations were observed in case of days to 50 per cent flowering. Twelve cultivars exhibited 50 per cent flowering in the time range of 99.0 to 109.75 days and these cultivars can be categorised as early flowering group. The remaining 18 cultivars took 110.8 to 122.0 days for 50 per cent flowering

Table 1. Growth and development data for plant height 30 days after sowing, primary branches per plant/days to 50 per cent flowering and days to maturity

Cultivar	Height at 30 (crn)	Primary branches per plant	Days to 50% flowering	Days to maturity
RB-1	26.87	8.26	108.30	145.92
RB-2	23.00	6.49	117.50	143.50
RB-3	28.26	7.54	110.80	146.95
RB-4	28.56	6.08	119.40	151.85
RB-5	19.83	8.04	119.40	146.10
RB-6	26.94	5.94	105.50	145.00
RB-7	35.23	7.53	113.00	147.50
RB-8	33.90	7.26	122.00	146.80
RB-9	26.31	5.02	112.50	146.50
RB-10	28.56	5.69	110.40	146.50
RB-11	29.27	8.78	112.50	146.50
RB-12	26.17	5.69	109.60	145.00
RB-13	29.94	6.77	99.00	144.50
RB-14	29.15	7.03	111.25	146.60
RB-15	31.75	6.54	108.70	146.75
RB-16	30.98	6.61	106.70	147.30
RB-17	29.84	7.08	107.00	146.50
RB-18	31.41	7.88	109.75	143.85
RB-19	25.53	8.39	111.00	149.50
RB-20	31.06	7.63	110.50	145.50
RB-21	27.77	6.40	112.70	150.18
RB-22	27.21	6.07	118.00	146.50
RB-23	25.17	6.36	116.35	146.75
RB-24	32.22	6.66	106.60	147.60
RB-25	26.64	7.82	110.10	146.00
RB-26	25.74	6.28	105.10	147.00
RB-27	28.33	8.43	108.40	147.31
RB-28	20.60	7 71	108.50	146.25
RB-29	30.56	8.60	112.60	146.00
RB-30	30.12	6.28	120.20	152.65

The values are mean for two successive years

Table 2. Data for yield attributing characters viz. pod per peduncle, pod length, pod per plant, seed per pod, 100 seed weight and grain yield per plant

Cultivar	Pod per Peduncle	Pod length	Pod/ plant	Seed/ pod	100 seed weight (gm)	Grain / plant(gm)
RB-1	2.41	8.64	44.72	3.87	8.29	20.18
RB-2	1.37	11.55	36.43	5.00	23.17	46.37
RB-3	1.77	9.99	30.42	4.25	19.81	35.98
RB-4	2.22	10.03	61.33	7.32	25.23	55.68
RB-5	1.10	7.24	68.28	5.17	9.15	36.97
RB-6	1.27	8.33	36.08	5.37	8.68	22.68
RB-7	1.79	9.00	35.97	6.98	13.23	30.26
RB-8	1.98	11.30	57.43	6.71	19.52	61.35
RB-9	1.35	8.46	36.37	5.39	19.38	37.35
RB-10	1.18	8.56	30.72	4.28	11.87	21.68
RB-11	1.40	8.81	29.45	4.58	11.82	22.10
RB- 12	1.33	9.21	38.61	5.35	13.73	30.93
RB-13	1.59	8.73	56.45	6.35	19.44	62.22
RB-14	2.28	9.57	48.44	4.47	14.45	32.72
RB-15	1.29	10.04	55.70	4.07	14.18	31.74
RB-16	1.14	8.48	46.78	4.49	12.26	30.96
RB-17	1.43	9.21	36.45	4.68	12.38	27.40
RB-18	1.32	9.07	52.48	6.98	19.04	54.64
RB-19	1.28	8.35	43.94	4.19	18.33	34.46
RB-20	2.28	8.56	40.71	4.69	19.83	32.40
RB-21	2.42	9.36	62.09	5.50	20.98	58.81
RB-22	1.96	7.70	32.54	4.35	20.76	22.46
RB-23	1.43	8.02	38.00	6.42	8.08	28.75
RB-24	1.59	9.65	55.31	4.44	25.98	61.68
RB-25	1.74	7.60	30.24	5.19	7.58	19.48
RB-26	1.59	7.78	35.34	5.44	7.24	23.00
RB-27	1.83	8.45	62.77	5.96	12.07	53.34
RB-28	2.19	7.84	58.66	5.55	7.38	34.12
RB-29	2.27	9.60	52.82	6.92	12.67	43.68
RB-30	1.20	9.10	58.28	4.70	18.17	40.46

The values are mean for two successive years

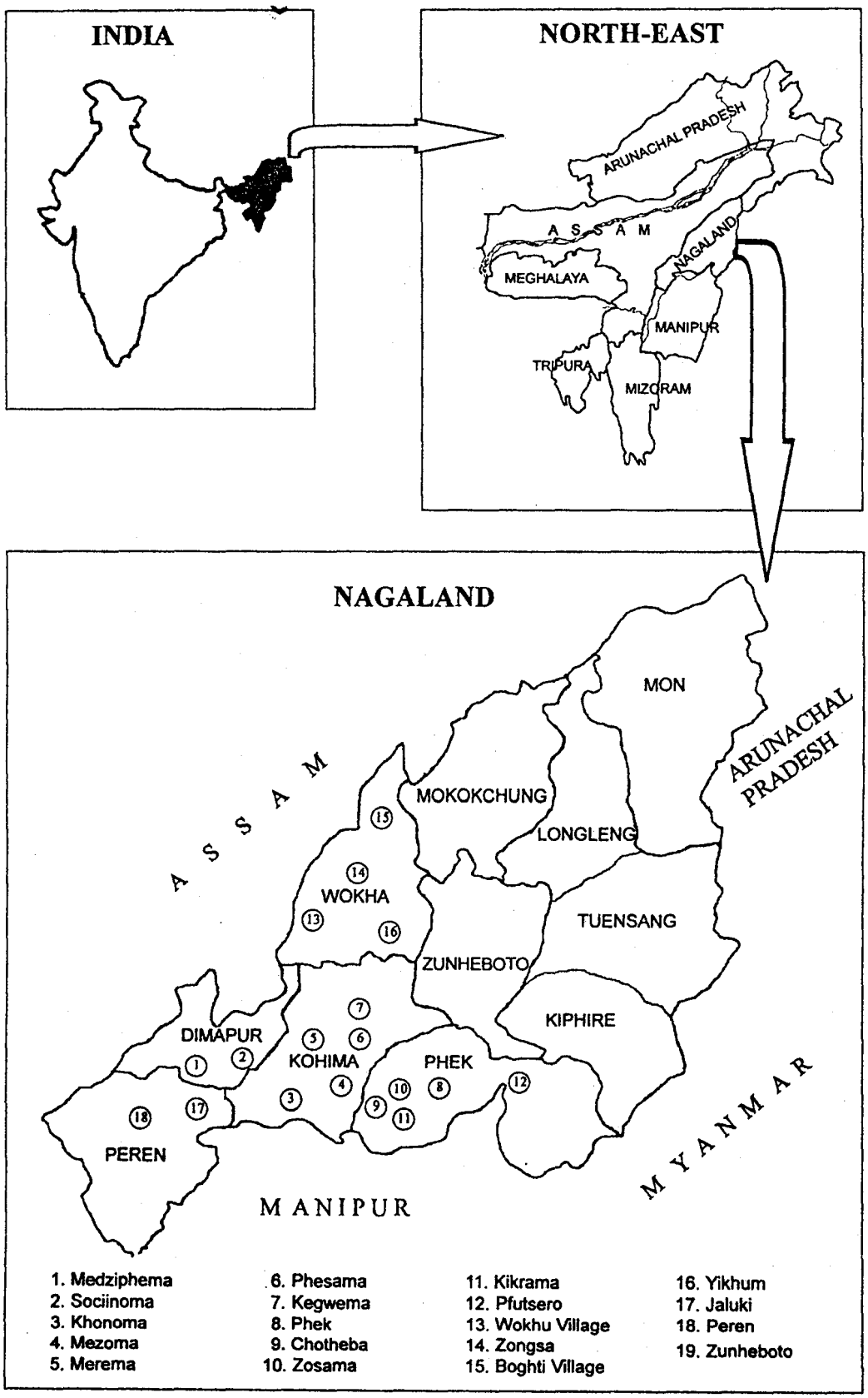

Fig. 1: *Localities of Nagaland from where indignous land races of ricebean were collected*

and can be considered as late flowering group. Time to maturity exhibited little variation as evident from the fact that coefficient of variation was 2.36 per cent with the range of variation being 143.5 to 152.65 days. Majority of the cultivars numbering 26, amounting to 86.6 per cent of all cultivars under study required 143.5 to 147.65 days for maturity.

Among the yield attributing characters number of pods per peduncle exhibited least variation which were in the range of 1.10 to 2.42 with a coefficient of variation 3.28 per cent and mean value of 1.59. On the other hand pod length exhibited considerable variation; the range being 7.24 to 11.55 cm with 14.67 per cent coefficient of variation. Half of the total cultivars had pod length in the range of 8.73 to 11.55 cm. Extensive variation was observed for pod per plant which is a foremost yield attributing character. The coefficient of variation was 59.77 per cent and the range of variation being 29.45 to 68-28 pods per plant. However half of the total cultivars had 29.45 to 44.72 pods per plant and only 8 cultivars had 56.45 to 68.28 pods per plant. Number of seeds per pod exhibited good deal of variation as evident from the fact that range of variation was 3.87 to 7.32 seeds per pod with 17.88 per cent coefficient of variation. Ten cultivars belonged to the group with relatively higher number of seeds per plant in the range of 5.50 to 7.32.

Of all the traits in the present study 100 seed weight exhibited very wide range of variation which was in the range of 7.24 to 25.98 gm with 38.18 per cent coefficient of variation. Cultivars RB-26 and RB-24 had 7.24 and 25.98 g weight for 100 seeds representing lowest and highest value implying that biggest seeds were 3.6 times bigger than the smallest seeds. Thirteen cultivars were characterised by relatively bigger seeds in the size range of 18.33 – 25.98 g/per 100 seed. Like 100 seed weight, grain yield per plant exhibited extensive variation which is evident from the fact that the range of variation was 19.48 to 62.22 g per plant and coefficient of variation was 62.78 per cent. RB-25 and RB-13 had 19.48 and 62.22 g grain yield per plant representing the lowest and highest value. Thus cultivar with highest yield per plant had 3.2 times more productivity than the cultivar with lowest yield which reflect the high degree of variability with respect to yield per plant. The range, mean, SE and coefficient of variation are shown in Table 3. Heritability estimate reveals that 100 seed weight had highest heritability (0.984) followed by number of seed per pod and number of pods per plant (Table 4). Genotypic and phenotypic path for different characters are shown in Table 5 and Table 6. The 100 seed weight contributed maximum direct effect on yield (0.683). Number of seeds per pod, pod length and number of pods per plant also contributed significantly to yield. Genotypic and phenotypic correlation for different character combination are shown in Table 7 and Table 8. Singh *et al.* (1998) evaluated 100 cultivars of ricebean collected from different ecogeographic origin for growth and yield attributing characteristics. The study revealed significant variability among the cultivars, particularly for yield attributing characters which is in conformity with the present study. Therefore unlike conventional pulses ricebean exhibited wide variability and can be exploited for breeding programmes. Although both the species have 2n = 22 (Kaur and Satij, 1988) interspecific hybridization between *V. umbellata* and *V. radiata* is not possible. Because of such limitations in interspecific hybridisation, the intraspecific variations observed in *V. umbellata* hold great promise for genetic improvement through hybridization.

Table 3. Range, mean, standard error (SE) and coefficient of variation (CV) for different characters of ricebean

Characters	Range	Mean	SE	CV (%)
Plant height at 30 days after sowing (cm)	19.83-35.23	28.22	0.48	18.51
Primary branches/plant	5.62-8.78	7.05	0.13	16.34
Days to 50% flowering	99.00-22.00	110.40	0.63	5.50
Days to maturity	143.50-152.65	146.37	0.36	2.36
Number of pods /peduncle	1.10-2.42	1.59	0.06	32.84
Pod length (cm)	7.24-11.55	8.97	0.14	14.67
Number of pods/plant	29.45-68.28	44.91	2.77	59.77
Number of seeds/pod	3.87-7.32	5.28	0.10	17.88
100 seed weight (gm)	7.25-25.98	15.47	0.61	38.18
Grain yield/plant	19.48-62.22	37.12	2.89	62.78

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Table 4. Estimate of genotypic and phenotypic variability, heritability, genetic advance, genetic advance as per cent of mean and genotypic and phenotypic coefficient of variability

Character	Genolypic Variability (GV)	Phenotypic variability (PV)	Heritability (h^2)	Genetic-Advance (GA)	Genetic Advance % of mean	Genotypic coefficient of variability (GCV)	Phenotypic coefficient of variability (PCV)
Plant height at 30 days of sowing (cm)	2.313	21.291	0.109	1.031	3.642	5.372	6.299
Primary branches per plant	0.550	1.719	0.319	0.857	12.156	10.519	18.598
Days to 50 % flowering	25.676	36.339	0.707	8.736	7.913	4.589	5.459
Days to maturity	7.129	11.338	0.629	4.342	2.966	1.824	2.301
Numbers pods per peduncle	0.112	0.292	0.384	0.425	25.086	19.754	31.895
Pod length in cm	0.570	1.158	0.492	1.085	12.115	8.430	12.016
Number of pod per plant	150.278	203.212	0.739	21.595	48.086	27.297	31.742
Number of seeds per pod	0.691	0.852	0.811	1.535	29.044	15.728	17.465
100 seed weight (gm)	34.627	35.207	0.984	11.969	74.541	37.503	37.816
Grain yield per plant	352.619	729.839	0.483	26.749	72.941	51.206	73.668

Table 5. Genotypic correlation for different character combination

	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	x_{10}
X_1	**0.0635**	–0.3793	0.1797	–0.1842	0.7623	0.9984	–0.1089	0.5766	0.9946	0.9165
X_2		**1.2039**	1.04X2	0.5902	0.7569	1.8053	–0.3179	1.7730	–0.5672	0.1207
X_3			**–0.2128**	–0.6434	0.8891	0.0515	1.1817	0.0839	–0.0400	0.4790
X_4				**0.4958**	–0.3267	0.2685	–0.2862	0.2739	0.2788	0.00254
X_5					**–0.2933**	0.0689	–1.0825	0.0207	0.0810	–0.5258
X_6						**–0.1299**	0.6284	0.1484	0.00119	0.3162
X_7							**–0.1122**	–0.0679	0.3942	0.2166
X_8								**0.1219**	0.0271	0.5986
X_9									**0.0866**	0.5484
X_{10}										**0.6966**

Table 6. Phenotypic correlation for different character combination

	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	x_{10}
X_1	**–0.0400**	0.1089	0.0333	–0.0266	0.05338	0.1495	0.2089	0.1999	0.3404	0.2971
X_2		**0.0110**	0.1547	0.0245	–0.0825	0.0597	–0.1204	0.1401	–0.0421	0.1171
X_3			**–0.0209**	–0.2520	0.0808	0.00254	0.3924	–0.0242	–0.0232	0.1610
X_4				**0.3569**	–0.1466	0.1186	–0.5106	0.2012	0.2449	0.0916
X_5					**–0.1887**	0.0641	–0.6378	0.0822	0.0470	–0.2027
X_6						**0.0251**	0.3745	0.10808	0.0170	0.1889
x_7							**0.0397**	0.0986	0.2592	0.1824
X_8								**0.0914**	0.000109	1.3396
X_9									**0.0866**	0.3753
X_{10}										**0.4677**

Table 7. Genotypic path for the different characters of ricebean in the present study

	1	2	3	4	5	6	7	8	9	10
1	0.007	0.000	–0.041	–0.037	0.029	–0.079	0.062	–0.0302	0.302	0.679
2	0.001	0.000	–0.043	–0.216	–0.095	–0.078	0.112	–0.099	0.927	–0.388
3	–0.003	0.000	0.036	0.044	0. 1 03	–0.092	0.003	0.370	0.044	–0.027
4	0.001	0.000	–0.008	–0.206	–0.079	0.034	0.017	–0.090	0.143	0.191
5	–0.001	0.000	–0.023	–0.102	–0.161	0.030	0.004	–0.340	0.011	0.055
6	0.006	0.000	0.032	0.067	0.047	–0.103	–0.008	0.197	0.078	0.001
7	0.007	0.000	0.002	–0.055	–0.011	0.013	0.062	–0.035	–0.035	0.269
8	–0.001	0.000	0.043	0.059	0.174	–0.065	–0.007	0.313	0.064	0.019
9	0.004	0.000	0.003	–0.056	–0.003	–0.015	–0.004	0.038	0.523	0.059
10	0.007	0.000	–0.001	–0.057	–0.013	–0.0001	0.024	0.008	0.045	0.683

Table 8. Phenotypic path for the different characters of ricebean in the present study

	1	2	3	4	5	6	7	8	9	10
1	–4.918	–0.001	1.419	–0.529	–0.143	–0.074	–0.082	–3.528	6.867	1.285
2	–0.211	–0.019	0.143	–2.456	–0.132	–0.114	–0.033	–2.033	4.813	0.159
3	–0.536	–0.001	13.029	–3.318	–1.356	–0.112	–0.001	–6.627	0.831	–0.088
4	–0.164	*–0.01)3*	–0.272	–15.874	–0.192	0.202	–0.065	8.623	6.912	0.925
5	0.131	–0.001	–3.283	–5.666	–5.382	0.260	–0.035	10.771	2.824	0.178
6	–0.265	0.002	1.053	2.327	1.016	–1.379	–0.014	–6.325	3.710	0.064
7	–0.735	–0.001	0.033	–1.883	–0.345	–0.035	–0.547	–0.670	3.387	0.978
8	–1.027	5.113	5.113	8.105	3.433	–0.517	–0.028	–16.888	3.139	0.001
9	–0.983	–0.315	–0.315	–3.194	–0.442	–0.149	–0.054	–1.544	34.353	0.327
10	–1.674	–0.302	–0.302	–3.888	–0.253	–0.024	–0.142	–0.002	2.975	3.776

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Genetic Divergence Analysis for Seed Yield and its Components in Chickpea *(Cicer arietinum* L.)

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Cluster analysis among 204 genotypes of chickpea excluding checks for nine quantitative traits revealed considerable genetic diversity in the material. Ten clusters for nine characters were obtained. Cluster III consisted of maximum 38 genotypes followed by cluster X which consisted of 35 genotypes whereas, cluster I consisted of two genotypes (as cluster I showed the maximum intra cluster distances with other clusters hence both genotypes) the maximum inter cluster distance was recorded between clusters I and IX followed by clusters I and V and I and VI, hence genotypes belonging to these clusters can be used as parents for hybridisation programme for the development of high yielding chickpea genotypes.

Key words: Chickpea, Cluster group, Cluster distance, Cluster means, Seed yield, Genetic divergence

Varieties from geographically diverse localities are generally included in hybridization programmes presuming genetic diversity and greater likelihood of recovering promising segregants. However, this being an inferential criterion, it can not be successfully utilized for discrimination between parents. The problem of selection may further be simplified if one could identify the characters responsible for discrimination between parents. The reports available on this aspect in chickpea are rather scanty. Therefore, the present investigation was aimed at ascertaining the nature and magnitude of genetic diversity among a set of chickpea genotypes. Genetic divergence analysis by using cluster statistics is a powerful tool in quantifying the degree of divergence between biological populations and to assess the relative contribution of different components to the total divergence.

Materials and Methods

The experimental material comprised 220 accessions of chickpea including four checks, *viz.* 2001-02, JG-74, Vaibhav and RG938 repeated five times. These accessions were evaluated in augmented design. Each entry was sown in two rows of 4 m length placed at 30 cm apart.

Observations on metric traits were recorded on single plant basis from five randomly selected competitive plants in each genotype from each plot for the traits. Observations on first flowering, days to 50% flowering, days to maturity, plant height, primary branches/ plant, pods/ plant, seeds/ pod, 100 seed weight and seed yield/ plant were subjected to multivariate analysis using Mahalanobis D^2 statistics suggested by Rao (1952).

Results and Discussion

Analysis of variance revealed that significant differences among the strains for all the characters studied indicating thereby the existence of genetic variability among the genotypes. Over all 204 accessions were grouped into ten clusters showing sufficient variability for selecting the genotypes for future breeding programmes. These cluster composition is presented in Table 1. The cluster III consisted of maximum 39 genotypes followed by cluster X consisted 35 genotypes. Whereas, cluster I consisted of minimum number of genotype i.e. two. Cluster IX consisted of 31 genotypes, cluster II consisted of 25 genotypes, cluster VII consisted of 23 genotypes, cluster VI consisted of 16 genotypes, cluster IV consisted of 13 genotypes, cluster VIII consisted of 10 genotypes and cluster V consisted of 10 genotypes. The different combination of different cluster distances are presented in Table 2.

Results of cluster analysis indicated that the highest intra-cluster distance was observed for cluster VI followed by cluster VII, cluster IX, cluster II and cluster V. Moreover, the highest inter-cluster distance was measured between cluster IX and I followed by V and I, VI and I and II and I. Whereas, the minimum distance was observed between X and IX followed by X and III, IV and II and VII and III.

Mean performance of individual cluster for different characters are presented in Table 3. For days to flower initiation cluster II possessed the highest mean value and lowest days to flower initiation was recorded for cluster IX. Days to 50% flowering exhibited the highest mean performance for the cluster number II, whereas, lowest days to 50 per cent flowering was observed for cluster IX. The cluster VI possessed the longest maturity and cluster I had the earliest maturity. Cluster VIII exhibited the highest plant height whereas, cluster IV possessed the lowest plant height, cluster VI had maximum number

Table 1. Cluster composition in chickpea

Clusters	Number of Accession	Accessions
I	2	ICC-11284, ICC-1923
II	25	ICC-6537, ICC-637, ICC-4872, ICC-9586, ICC-1356, ICC-1 437, ICC-7272, ICC-1 1198, ICC-8318, ICC-1398, ICC-9942, ICC-4841, ICC-13523, ICC-16524, ICC-12941, ICC8621, ICC-10885, ICC-13524, ICC-3512, ICC-3572, ICC-8350, ICC-5504, ICC-9137, ICC-3218, ICC-1 1627.
III	39	ICC-1397, RG-2001-02, Vaibhav, ICC-3776, ICC-14077, ICC-5639, ICC-15888, ICC-1098, ICC-8950, ICC-2507, ICC-16269, ICC-6816, ICC-16207, ICC-12824, ICC-1392, ICC-5383, ICC-16915, ICC-13124, ICC-1052, ICC-8058, ICC-10399, ICC-14098, ICC-14402, ICC-5613, ICC-12654, ICC-4918, ICC-3230, ICC-10341, ICC-10949, ICC-I083, ICC-13599, RG-2001-02, ICC-11584, ICC-7861, RG-2001-08, RG-2001-14, RG-9949, RG-9920.
IV	13	ICC-1161, ICC-14815, ICC-9755, ICC-15612, ICC-708, ICC-4567, ICC-2263, ICC-9420, ICC-14799, ICC-6874, ICC-1 2299, ICC-4657, ICC-5879
V	10	ICC-1180, ICC-2242, ICC-14669,"ICC-2720, ICC-11098, ICC-762, ICC-1510, ICC-1230, ICC-456, ICC-95
VI	16	ICC-15518, ICC-8855, ICC-6579, ICC-3325, ICC-9002, ICC-6816, ICC-13628, ICC-124-92, ICC-440, ICC-1205, ICC-3946, RG-938, ICC-11498, ICC-11944, ICC-506, ICC-3761
VII	23	ICC-8195, ICC-I2307, ICC-2277, ICC-9643, JG-74, ICC-13357, ICC-5337, ICC-7308, ICC-7554, ICC-13187, ICC-2919, ICC-10755, ICC-12037, ICC-8384, ICC-13461, KBL-12328, ICC-13764, ICC-2072, ICC-7571, ICC-12866, ICC-5845, ICC-8522, RG-2001-19
VIII	10	ICC-791, ICC-7184, ICC-15610, ICC-2629, ICC-6293, ICC-3421, ICC-2580, ICC-8740, ICC-15333, ICC-2990
IX	31	ICC-15510, ICC-1422, ICC-4463, ICC-12916, ICC-1715, ICC-13863, ICC-1194, ICC-11664, ICC-13219, ICC-15618, ICC-6571, ICC-6802, ICC-2210, ICC-I3077, ICC-7668, ICC-11121, ICC-14595, ICC-13283, ICC-867, ICC-11764, ICC-8151, ICC-1 6374, ICC-2065, ICC-15567, ICC-4495, RG-9903, RG-2001-03, RG-2001-18, RG-2001-20, RG-9930, RG-2001-08
X	35	ICC-12851, ICC-9862, ICC-1882, ICC-283, ICC-67, ICC-2884, ICC-2979, ICC-16487, ICC-12155, ICC-14778, ICC-14051, ICC-12928, ICC-7255, ICC-9895, ICC-4814, ICC-4593, ICC-1392, ICC-15435, ICC-15697, ICC-11378, ICC-15606, ICC-13892, ICC-4639, ICC-1915, ICC-10393, ICC-12537, ICC-4533, ICC-12726, ICC-5135, ICC-16261, ICC-9848, ICC-8607, ICC-11879, ICC-3637, ICC-6279.

Table 2. Inter- and intra-cluster distance of genotypes in chickpea genepool

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	1.657	–	–	–	–	–	–	–	–	–
II	6.278	1.899	–	–	–	–	–	–	–	–
III	5.332	3.526	1.835	–	–	–	–	–	–	–
IV	5.212	2.095	2.999	1.597	–	–	–	–	–	–
V	6.571	4.500	3.934	4.600	1.886	–	–	–	–	–
VI	6.412	3.144	3.975	3.699	2.938	2.588	–	–	–	–
VII	6.084	3.639	2.103	3.193	3.882	3.847	2.095	–	–	–
VIII	6.291	3.918	3.496	3.360	0.5307	5.018	2.598	1.899	–	–
IX	6.649	3.915	2.237	3.946	3.956	3.725	2.499	4.851	2.036	–
X	5.723	2.175	2.087	2.419	3.836	2.912	2.814	4.303	2.047	1.855

Table 3. Mean performance in individual cluster for different yield traits

Cluster	Days to flower initiation	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches/ plant	Pods/ plant	Seeds/ pod	100 seed weight	Seed yield/ plant
I	55.00	60.00	96.00	47.50	5.50	39.90	1.15	17.23	27.60
II	60.64	66.16	111.24	42.18	5.03	26.39	1.18	11.69	14.79
III	44.64	50.36	108.77	39.88	4.38	28.09	1.26	15.24	25.60
IV	58.69	65.62	108.38	36.79	4.07	30.80	1.20	19.42	21.65
V	47.00	52.00	110.20	44.42	6.38	84.12	1.28	16.25	11.13
VI	52.94	59.81	111.31	39.67	7.90	61.55	1.09	13.76	17.14
VII	46.13	52.70	110.96	48.59	4.79	30.00	1.21	23.36	25.07
VIII	55.40	62.10	111.10	50.34	4.26	27.78	1.32	22.91	40.38
IX	40.90	45.90	111.10	40.57	4.47	29.75	1.11	16.31	15.06
X	49.83	56.11	109.63	38.81	4.76	28.66	1.14	12.37	14.77

of branches per plant. The highest number of pods/ plant was observed for cluster V whereas, lowest number was observed for cluster II.

The maximum number of seeds/ pod was noted for cluster VIII, whereas lowest number of seeds/ pod was noted for cluster VI. Cluster VII exhibited the highest 100 seed weight whereas, cluster II showed lowest 100 seed weight. The highest seed yield/ plant was noted for cluster number VII whereas, lowest seed/plant was noted for cluster number V. The pattern of distribution of 204

genotypes in various clusters revealed that there was considerable genetic diversity in the material. In the present investigation, 204 genotypes were grouped into ten clusters. The highest intra-cluster distance was observed for cluster VI, which consisted of 16 genotypes. The maximum inter-cluster distance was recorded between clusters I and IX followed by clusters I and V and I and VI. As cluster I showed maximum intra-cluster distances with other clusters hence, both the genotypes belonging to cluster-1. (ICC-11284 and ICC-1923) could be utilized as parents in future breeding programme with the desirable genotypes belonging to clusters IX, V and VI. These results are in general agreement with the findings of Lal *et al.* (2001), Harisatyanarayana and Reddy (2001), Nimbalkar and Harer (2001), Gupta *et al.* (2003), Rao *et al.* (2003), Nanda (2003), Singh (2003), Billore *et al.* (2003), Kashyap *et al.* (2003), Dasgupta *et al.* (2003), Katiyar and Singh (1979), Adhikari and Pandey (1983) and Jain *et al.* (1981).

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Genetic Divergence of Exotic Germplasm Lines in Wheat (*Triticum aestivum* L.)

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One hundred fifty three exotic wheat genotypes were evaluated alongwith three checks for quantitative characters to study genetic divergence by employing D^2 analysis. The genotypes were grouped in to 13 diverse clusters. Clustering pattern of genotypes showed no definite relationship between genetic divergence and geographical distribution of genotypes. The highest genetic divergence was observed between cluster V and VIII, whereas, cluster I and II were closest one. On the basis of genetic divergence and mean performance, nine diverse and superior genotypes, being exceptionally good for one or more traits and reasonable for other, comparison to checks, were selected and these genotypes may be useful in multiple crossing or diallel selective mating system to recover transgressive segregants.

Key words: Wheat, Genetic divergence, Exotic lines

The success of any crop-breeding programme depends on the nature and amount of genetic variability available in the germplasm collections. Germplasm serves as the most valuable natural resources in providing needed attributes for engineering successful varieties (Hawkes, 1981). The indigenous as well as exotic materials obtained from other countries constitute the germplasm collections of a crop available to a breeder. The classification of germplasm collection is a prerequisite for distinguishing genetically close and divergent types for various plant breeding programme. By using advance biometrical techniques such as multivariate analysis based on Mahalanobis's D^2 statistics (Mahalanobis, 1936) it has now become possible to quantify the degree of genetic divergence amongst biological populations and assessing of relative contribution of various desirable attributes of breeding and agronomic value to the total divergence.

Materials and Methods

One hundred fifty three exotic lines of wheat germplasm alongwith three checks (HP 1731, PBW 343 and NW 2036) were evaluated in an augmented design at Main Experiment Station of ND University of Agriculture and Technology, Kumarganj, Faizabad during *rabi* 2003-04. Each genotype was accommodated in two rows plot of 2.5 m long with inter- and intra-row spacing of 25 cm and 5 cm, respectively. Recommended agronomic practices were followed to raise a good crop. Data were recorded on 5 randomly selected competitive plants from each plot on twelve quantitative characters namely, growth habit, days to heading, days to maturity, plant height, tillers per plant, ear length, spike weight, grains per spike, 1000 grain weight, biological yield per plant, harvest index and grain yield per plant. The data recorded on above characters were subjected to D^2 analysis of Mahalanobis (1936) and Rao, 1952.

Results and Discussion

Based on D^2 statistics, 153 genotypes were grouped in to 13 non-overlapped clusters (Table 1). Cluster I had maximum 24 genotypes, followed by cluster II, XI and VII having 23. 22 and 21 genotypes, respectively. These clusters having maximum number of genotypes, reflecting narrow genetic diversity.

The maximum inter cluster distance was observed between cluster VIII and V. Cluster VIII also recorded very high inter cluster distances from clusters indicating thereby, highly diverse nature of the members of cluster VIII with the members of cluster VI. VII, III, IX and XI. Therefore, hybridization of desirable genotypes belonging to cluster VIII in those of clusters VI VII, III, IX and XI may be recommended for isolating transgressive segregants. The minimum inter cluster distance was observed between clustery VII and VIII and followed by cluster III and VIII and cluster. VII and XI which showed existence of less diversity between these cluster pairs (Table 2).

The average intra cluster distance in cluster X was maximum suggesting that the genotypes in this cluster were relatively more diverse among themselves, however, in all cases, the inter-cluster distances were greater than the intra cluster distances implying presence of greater degree of genetic diversity between the genotypes of two cluster than the genotypes present within the cluster.

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Table 1. Clustering pattern of 153 genotypes on the basis of Non-hierarchical Euclidean Cluster analysis for 13 characters

Cluster No.	Number of Genotypes	Genotypes
I	24	35th IBWSN-5, 35th IBWSN-21, 35th IBWSN-42, 35th IBWSN-45, 35th IBWSN-162, 35th IBWSN-163, 35th IBWSN-170, 35th IBWSN-193, 35th IBWSN-210, 35th IBWSN-269, 35th IBWSN-301, 20th SAWSH-23, 20th SAWSH-202, 10th SAWYT-33, 23rd ESWYT-43, 10th HTWYT-14, 10th HTWYT-39, 10th HTWYT-50, 13th HRWSN-99, 13th HRWSN-124, 13th HRWSN-303, 35th IBWSN-416, 20th SAWSN-18, 13th HRWSN-147.
II	23	35th IBWSN-27, 35th IBWSN-37, 35th IBWSN-176, 35th TBWSN-410, 20th SAWSN-41, 20th SAWSN-227, 20th SAWSN-334, 20th SAWSN-338, 10th SAWYT-18, 13th HRWSN-36, 13th HRWSN-116, 13th HRWSN-211, 3rd IAT-24, RWCB 03-5, RWCB 03-20, RWCB 13-29, RWCB 03-33, 3rd RWYT-MR-9, 11th HMN-9, 23rd ESWYT-3, 23rd ESWYT-15, 13th HRWSN-141.
HI	9	35th IBWSN-375, 20th SAWSN-109, 10th SAWYT-15, 23rd ESWYT-48, 10th HTWYT-40, 6th EGPSN-3, 6th EGPSN-24, 6th EGPSN- 142, 11th HMN-6.
IV	15	35th IBWSN-294, 20th SAWSN-48, 13th HRWSN-7, 13th HRWSN-17, 13th HRWSN-21, 13th HRWSN-126, 13th HRWSN-168, 13th HRWSN-216, 10th HRWYT-23, 3rd IAT-78, 3rd IAT-80, RWCB-03-12, 13th HRWSN-127, 3rd IAT-31, HP- 1731.
V	5	10th HTWYT-8, 13th SRWSN-13, 6th EGPSN-45, 6th EGPSN-131, 6th EGPSN-133.
VI	8	35th IBWSN-415, 20th SAWSN-31, 20th SAWSN-70, 20th SAWSN-116, 10th HRWYT-19, 10th HRWYT-30, 6th EGPSN-147, RWCB 03-9.
VII	5	13th HRWSN-101, 10th HRWYT-19, 6th EGPSN-132, 3rd RWYT-MR-4, 11th HMN-22.
VIII	1	3rd IAT-9
IX	6	35th IBWSN-364, 35th IBWSN-367, 20th SAWSN-34, 6th EGPSN-41, 2nd HLWSN-182, 35th IBWSN-535.
X	5	20th SAWSN-43, 20th SAWSN-57, 10th HTWYT-42, 2nd HLWSN-18, 3rd IAT-44.
XI	22	35th IBWSN-39, 35th IBWSN-84, 35th IBWSN-85, 35th IBWSN-265, 20th SAWSN-71, 20th SAWSN-102, 20th SAWSN-108, 20th SAWSN-110, 20th SAWSN-111, 20th SAWSN-113, 20th SAWSN-117, 20th SAWSN-119, 20th SAWSN-138, 10th HTWYT-3, 13th HRWSN-149, 10th HRWYT-37, 6th EGPSN-30, 6th EGPSN-137, 6th EGPSN-143, 6th EGPSN-145, 3rd IAT-33, NW 2036.
XII	21	35th IBWSN-365, 35th IBWSN-366, 35th IBWSN-369, 35th IBWSN-374, 35th IBWSN-403, 20th SAWSN-45, 20th SAWSN-62, 23rd ESWYT-27, 10th HTWYT-15, 10th HTWYT-22, 10th HTWYT-30, 13th HRWSN-33, 13th HRWSN-108, 13th HRWSN-118, 13th HRWSN-119, 13th HRWSN-221, 13th HRWSN-307, 3rd IAT-54, RWCB 03-49, 3rd IAT-34, PBW -343
XIII	9	35th IBWSN-33, 20th SAWSN-225, 10th SAWYT-20, 10th SAWYT-48, 10th HTWYT-11, 13th HRWSN-125, 10th HRWYT-21, 3rd IAT-43, RWCB 03-10

Table 2. Estimates of average intra and inter cluster distances for the 13 cluster in wheat

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	**1.706**	2.272	2.604	2.820	3.998	3.310	5.568	9.403	4.359	4.326	2.465	1.879	3.685
II		**1.709**	3.808	2.114	3.857	4.372	4.278	8.468	5.729	5.385	2.435	2.345	4.528
HI			**2.229**	4.623	4.910	3.768	6.136	10.077	3.336	3.775	2.664	2.858	4.673
IV				**2.082**	2.803	3.669	3.865	8.936	6.423	5.739	3.001	2.533	4.286
V					**1.742**	3.938	3.435	11.129	7.167	7.061	3.009	4.267	5.584
VI						**2.612**	6.378	10.914	4.789	5.255	3.831	3.143	2.988
VII							**2.772**	10.095	8.774	7.533	3.941	5.177	7.665
VIII								**0.000**	10.068	9.292	10.053	8.596	9.332
IX									**2.749**	4.942	5.289	4.485	4.327
X										**3.194**	5.790	5.231	3.701
XI											**2.198**	3.689	2.583
XII												**1.951**	5.141
XIII													**1.923**

Bold figures represent intra-cluster distance

The cluster IX showed the highest cluster means for ear length, grains per spike, spike weight and grain yield along with second highest mean for biological yield per plant. Cluster VIII recorded highest mean for tillers per plant and biological yield per plant. The entries exhibited early flowering and maturity were concentrated in cluster V and VI, respectively. Plant height and harvest index resulted highest mean in cluster X. 1000 grain weight was exhibited higher mean in cluster III. The differential contribution to total divergence was observed in different yield attributes (Table 3). The germplasm lines were divergent mainly on the basis of ear length, grains per spike and spike weight as these traits contributed largely to divergence as compared to other traits.

Table 3. Cluster mean of different characters for 13 clusters in wheat

Cluster No./Characters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
Days to heading	84.62	87.83	82.47	87.00	79.92	83.07	83.96	106.00	85.30	88.88	81.93	86.90	87.53
Days to maturity	119.17	121.16	119.56	119.68	115.44	114.70	120.48	146.40	121.60	122.64	118.16	121.23	120.82
Tiller per plant	9.31	10.50	10.62	12.07	12.88	17.17	10.48	10.20	11.90	9.28	9.68	11.23	18.18
Plant height (cm)	84.85	82.91	92.56	82.40	75.99	92.24	79.26	86.08	101.50	106.96	90.67	94.68	83.88
Ear length (cm)	10.16	9.82	11.49	9.06	8.76	10.36	8.84	10.12	12.18	11.27	10.15	10.78	10.49
Grains per spike	56.32	50.00	58.82	42.76	39.28	52.93	29.88	48.60	63.24	61.32	48.70	50.88	56.53
Spike weight (g)	2.70	2.36	2.99	2.02	1.89	2.41	1.65	2.14	3.38	3.27	2.32	2.43	2.78
1000 grain weight	36.27	34.97	44.68	34.54	41.22	38.44	42.81	35.64	43.99	40.96	41.55	36.49	33.85
Biological yield (g)	31.93	22.85	29.49	29.77	28.37	38.27	12.35	30.48	42.33	31.61	23.03	30.87	45.71
Harvest index (%)	33.68	28.52	32.91	34.87	33.66	37.96	33.38	32.18	29.03	46.94	30.02	36.02	33.65
Grain yield per plant (g)	10.01	7.84	8.89	8.65	8.37	11.47	3.82	9.47	15.08	6.94	7.82	9.12	13.66

Table 4. Diverse and superior genotypes with desirable characters selected from different clusters

Genotype	Cluster number	Desirable characters
2nd HLWSN 182	IX	Plant height, ear length, grains per spike, spike weight and grain yield per plant
RWCB 03-9	VI	Days to maturity and tillers per plant
2nd HLWSN183	X	Ear length, grains per spike and harvest index
20th SAWSN34	IX	Spike weight, grains per spike and 1000 grain weight
20th SAWSN31	VI	Biological yield and grain yield per plant
35th IBWSN 415	VI	Grain yield per plant, harvest index and tillers per plant
20th SAWSN 225	XIII	Grain yield
RWCB 03-10	XIII	Tiller per plant, grain yield per plant and biological yield
10th HTWYTII	XIII	Grain yield and biological yield

The data on inter cluster distance and performance of the genotypes was used to select genetically diverse and agronomically superior genotypes among 153 genotypes. The genotypes, exceptionally good in respect to one or more characters and atleast comparable in respect to other to the checks, were deemed desirable. On the basis of nine genetically diverse genotypes, superior genotypes were selected (Table 4); they belong to different four clusters. Intermating of divergent groups would lead to greater opportunity for crossing over which release latent variability by breaking linkage and progenies derived from cross are expected to show broad spectrum of genetic variability providing a greater scope for isolating transgressive segregants in the advance generation. So, these genotypes may be used in a multiple crossing programme or in diallel selective mating system to recover transgressants.

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Genetic Divergence and Gene Source Studies in Cucumber (*Cucumis sativus* L.)

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Since there is an appreciable deficit between realized and potential crop yields in cucumber, so there is a strong need to develop hybrids having desirable horticultural traits. This necessitated the identification of suitable divergent parents to get high heterotic effect in terms of yield and quality. Thus, divergence analysis was carried out in 26 genotypes of cucumber. All the character under study showed a wide range of values except days to first picking and fruit circumference. Phenotypic variability was high for node at which first female flower appears, sex ratio, yield per plant, number of fruits and vine length. The genotypes could be grouped into 5 clusters. Cluster nos. I, II, III, IV and V contained 11, 3, 5, 2 and 5 genotypes, respectively which are independent of geographical distribution. The genotypes in cluster I had maximum intra-cluster distance closely followed by cluster nos. V and II. Inter-cluster distance was maximum between the clusters I and II followed by clusters II and III suggesting wide diversity between the groups.. Highest yield per plant was recorded in cluster no. IV followed by cluster no. III. Cluster nos. I and III may be employed for improvement programme in cucumber. Market Long was best gene source for yield, no. of fruits and TSS.

Key words: ***Cucumis sativus*, D^2 analysis, Cluster, Gene source**

Nature has endowed India with many precious gifts, wherein lies its immense potential for the vegetable sector. In the last three decades, India has witnessed a sea change in the scenario of vegetable production with the increasing popularity of hybrids in commercial cultivation. Cucumber (*Cucumis sativus* L.), a member of family Cucurbitaceae is one of the most important cucurbits grown in India for its tender fruits as summer vegetable and one of the oldest vegetable crop but little work has been done in hybridization programme. Thus, there is need to develop hybrids suitable for cultivation with high yield per unit area and quality. This necessitated the identification of suitable divergent parents to get high heterotic effect in terms of yield and quality.

To make an improvement in any crop species, the breeder is constantly engaged in effective choice of desireable parents of high genetic variation so that individuals with desirable character combination can be selected. Genetically diverse parents are likely to produce high heterotic effects and desirable segregants. Multivariate analysis by means of Mahalanobis's D^2 statistics is a powerful tool in quantifying the degree of divergence among the biological populations.

Divergence analysis in cucumber was employed by Prasad *et al.* (1993), Susic *et al.* (2000), Prasad *et al.* (2001) and Rao *et al.* (2003) in India and abroad. Thus, the present investigations are first attempt on divergence analysis in cucumber in Himachal Pradesh with the objective of ascertaining the nature and magnitude of genetic divergence present among twenty six genotypes of cucumber for further utilization in hybridization.

Materials and Methods

The present investigations on genetic divergence in cucumber (*Cucumis sativus* L.) were carried out on 26 genotypes at Nauni, Solan, Himachal Pradesh during *kharif*, 2005 at an altitude of 1270 m above mean sea level lying between latitude 30°52' North and longitude 77°11' East. It falls under the mid hill zone of Himachal Pradesh. The experiment was laid out in a Randomized Block Design with 3 replications. Direct sowing was done in the pits at a spacing of 1 x 1 m. Initially, 2-3 seed per pit were sown but only one healthy seedling per pit was retained. The standard cultural practices were followed for healthy crop.

The observations were recorded on ten randomly selected competitive plants from each treatment for the characters viz. days to first female flower appearance, node at which first female flower appears, sex ratio, days to first picking, harvest duration (days), yield per plant (g), number of fruits per plant, fruit weight (g), fruit length (cm), fruit circumference (cm), rind thickness (mm), flesh to seed cavity ratio, total soluble solids (°B), thousand

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seed weight (g), number of primary branches per plant and vine length (m).

For computing various statistical parameters like mean and standard deviation, the method suggested by Panse and Sukhatme (1985) was followed. Genetic divergence was determined using Mahalanobis D^2 statistics (Mahalanobis, 1936). Group constellation was formulated after computation of D^2 values by the method by Rao (1952)

Results and Discussion

It is axiomatic that for successful breeding programme, sufficient diversity should be present in the germplasm. The greater diversity of germplasm that a breeder handles, the better are the chances for selecting better genotypes (Vavilov, 1951). Now, F_1 hybrids are gaining momentum with high pace all over the world. Therefore, there is a strong need to isolate or to develop breeding lines which have high yielding potential, desirable horticultural traits and better quality. Selection of parents is the foundation stone of any hybridization programme. In context of this fact, the present investigations were undertaken to select horticulturally superior parent and to elicit information on divergence and clustering pattern in cucumber. The results obtained have been discussed below under the following sub-heads:

1. General Performance of the Genotypes

All the character under study showed a wide range of values except days to first picking and fruit circumference (Table 1). Phenotypic variability as revealed by coefficient of variation (%) was high for node at which first female flower appears, sex ratio, yield per plant, no. of fruits and vine length (also substantiated by wider range values) and moderate for harvest duration, fruit weight and fruit length. While, rest of the characters were of low variability. Coefficient of variation varied from 0.08% for fruit circumference to 53.45% for vine length. Coefficient of variation (%) was highest for vine length (53.45%) followed by sex ratio, node at which first female flower appears and yield per plant. Coefficient of variation depicted that differences among the genotypes were existing. The characters that exhibited high phenotypic variability had a wider range. Similar results on high phenotypic variability of vine length were reported by Solanki and Seth (1980) and Rastogi and Arya Deep (1990). Joshi *et al.* (1981) also observed a wide range of phenotypic variability in consonance with the present findings.

Phenotypic performance would be a good index for selection in cucumber for the characters like node at which first female flower appears, sex ratio, harvest duration, yield per plant, no. of fruits, fruit weight, fruit length and vine length as reported by Joshi *et al.* (1981).

2. Divergence Studies

Grouping pattern of genotypes under study into different clusters is given in Table 2. On the basis of D^2 analysis, the genotypes could be grouped into 5 clusters. Cluster no. I contained 11 genotypes *viz.* Henzil, SMR-58, Boston Pickling, Kakri, Sweet Delight, EC 381602, CHC-1, National, Yomaki, Hermaphrodite-61 and Poinsette which are of different geographical origin. Cluster no. II contained 3 genotypes namely LC-2, LC-7 and LC-12 which are of same geographical area i.e. these were collected from Hamirpur district of Himachal Pradesh. Cluster no. III contained 5 genotypes *viz.* Fazilka Coll.

Table 1. Range, mean, standard deviation and coefficient of variation of various characters in cucumber

Character	Range	Mean	Standard deviation	Coefficient of variation (%)
Days to first female flower appearance	38.27–59.73	47.28	6.29	13.30
Node number of first female flower	2.33–16.93	5.48	2.72	49.64
Sex ratio	1.00–22.79	11.30	5.97	52.83
Day to first picking	49.80–73.47	58.98	5.99	10.16
Harvest duration (days)	6.53–21.07	14.38	4.11	28.58
Yield (g)	392.00–2201.00	1081.13	484.77	44.84
No. of fruits	1.60–8.13	4.42	1.62	36.65
Fruit weight (g)	207.33–440.33	293.59	70.43	23.99
Fruit length (cm)	8.96–32.65	18.42	4.41	23.94
Fruit circumference (mm)	13.91–19.44	17.16	1.35	0.08
Rind thickness (mm)	0.86–1.88	1.40	0.30	21.43
Flesh to seed cavity ratio	0.17–0.42	0.24	0.06	0.25
TSS (°B)	1.97–3.47	2.26	0.40	14.87
1000–seed weight (g)	14.88–36.07	24.10	4.60	19.09
No. of primary branches per plant	2.00–4.50	3.47	0.53	15.27
Vine length (cm)	39.50–604.17	204.89	109.51	53.27

Table 2. Grouping pattern of different genotypes based on D^2 analysis

Cluster No.	No. of genotype	Genotype
I	11	Henzil, SMR-58, Boston Pickling, Kakri, Sweet Delight, EC 381602, CHC-1, National, Yomaki, Hermaphrodite-61, Poinsette
II	3	LC-2, LC-7, LC-12
III	5	Fazilka Coll. 94, CHC-2, Market-76, Market More-76, Market Long
IV	2	Khira-75, Khira-90
V	5	Sel. 75-2-10, Sel. 20-3-2-1, Shogain 1-48, Long Green, EC 381606

94, CHC-2, Market-76, Market More-76 and Market Long. There were only 2 genotypes namely Khira-75 and Khira-90 in cluster no. IV. Both these genotypes are from Solan (H.P.). Cluster no. V contained 5 genotypes viz. Sel. 75-2-10, Sel. 20-3-2-1, Shogain 1-48, Long Green and EC 381606 which are also from different geographical areas.

Genotypes from different locations/ countries are accommodated in the same cluster (Table 2). This indicates their close affinity. On the other hand, genotypes from same location/ country were distributed into different clusters indicating the geographical diversity may not necessarily be related to genetic diversity. These findings were in general agreement with Prasad *et al.* (1993), Prasad *et al.* (2001) and Rao *et al.*(2003) in cucumber.

Table 3 indicated inter and intra-cluster distances between the 5 clusters. Intra-cluster distance ranged from 0.761 (cluster no. IV) to 2.826 (cluster no. I). The genotypes in cluster I had maximum distance closely followed by cluster nos. V and II. As for as inter-cluster distance is concerned, maximum distance was observed between the clusters I and II followed by clusters II and III suggesting wide diversity between the groups. The crosses made between the genotypes from the above clusters may give transgressive segregants. On the other hand, minimum distance (3.380) was recorded between clusters I and V indicating minimal diversity between these clusters.

On the basis of inter- and intra-cluster distance, cluster nos. I, II and III may be considered as most diverse and can be utilized for hybridization when selecting genotypes for breeding purposes.

Besides high genetic divergence, the performance of genotypes for characters with maximum contribution towards genetic divergence should also be given due consideration. Mean performance of the clusters with respect to different character (Table 4) indicated that

Table 3. Inter- and intra-cluster distances between the clusters

Cluster	I	II	III	IV	V
I	**2.826**				
II	7.035	**2.520**			
III	3.445	6.807	**2.311**		
IV	4.740	5.301	4.217	**0.761**	
V	3.380	5.804	3.513	4.414	**2.773**

Bold figures are the intracusters distances

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

Character	Cluster					Percent contribution towards diversity
	1	2	3	4	5	
Days to first female flower appearance	42.85	58.87	47.65	55.33	46.48	38.18
Node number of first female flower	4.27	11.49	4.89	5.53	5.12	14.19
Sex ratio	9.17	22.36	9.14	13.97	10.44	13.64
Day to first picking	55.12	70.11	59.67	65.50	57.49	8.91
Harvest duration (days)	16.51	11.11	18.24	7.70	10.48	6.08
Yield (g)	1020.82	495.44	1641.87	1756.00	734.53	5.04
No. of fruits	4.84	1.82	6.28	4.40	3.19	4.32
Fruit weight (g)	258.61	357.11	307.67	404.83	273.87	3.22
Fruit length (cm)	15.96	18.55	20.61	18.48	21.55	2.21
Fruit circumference (mm)	17.15	18.91	16.70	18.79	15.94	1.37
Rind thickness (mm)	1.15	1.69	1.54	1.37	1.64	1.21
Flesh to seed cavity ratio	0.26	0.20	0.24	0.22	0.22	0.76
TSS (°B)	2.47	2.67	3.05	2.60	2.88	0.53
1000-seed weight (g)	22.57	29.80	24.03	22.28	24.86	0.19
No. of primary branches per plant	3.17	3.50	3.97	3.58	3.57	0.11
Vine length (cm)	163.89	457.00	189.43	178.42	169.87	0.05

Table 5. Gene sources for some important characters in cucumber genotypes under study

Sr. No.	Character	Potential	Genotype
1	Days to first female flower appearance	38.27 days	Hermaphrodite-61
2	Node number of first female flower	2.33	Hermaphrodite-61
3	Sex ratio	1.00	Hermaphrodite-61
4	Day to first picking	49.80 days	SMR-58
5	Harvest duration (days)	21.07 days	Fazilka Coll. 94
6	Yield (g)	2201.00 g	Market Long
7	No. of fruits	8.13	Market Long
8	Rind thickness (mm)	1.88 mm	Fazilka Coll. 94
9	TSS (°B)	3.47	Market Long

minimum number of days to first female flower appearance and lowest node of first female flower exhibited by cluster no I. However, minimum sex ratio was recorded in cluster no III closely followed by cluster no I. Cluster no. I also recorded minimum days to first picking. Cluster no. II recorded maximum days to first female flower appearance, highest node of first female flower, highest sex ratio and maximum days to fruit picking. Longest harvest duration was found in cluster no. III followed by cluster I. However, highest yield per plant was recorded in cluster no. IV followed by cluster no. III. Cluster II recorded lowest yield per plant which might be due to the fact that it took maximum no. of days to first female flower appearance, bore female flower on higher nodes and exhibited high sex ratio. No. of fruits per plant were highest in case of cluster no. III. Fruit weight was highest in cluster no. IV which might be a reason for highest yield per plant in this cluster.

Cluster no. V had longest fruits while cluster no. II showed highest fruit circumference and thickest fruit rind. Flesh to seed cavity ratio and TSS were highest in cluster no. I and III, respectively. Maximum thousand seed weight and no. of primary branches were observed in cluster II and III, respectively. Vine length was minimum in cluster no. I and maximum in cluster no. II. Comparison of cluster means for all the sixteen characters indicated that different characters showed considerable differences between the clusters.

Relative contribution of different characters towards genetic divergence in the cucumber germplasm (Table 4) indicated that first 9 characters explained more than 95 % variation in cucumber germplasm under study. Days to first female flower appearance gave maximum contribution (38.18%) followed by node of first female flower (14.19%) and sex ratio (13.64%). Considering the cluster distances and cluster means, cluster nos. I and III may be employed for improvement programme in cucumber.

3. Gene Source Studies

Gene sources for some important character are given in Table 5. It is evident from the data in the Table that gene source for minimum days to first female flower, node of first female flower appearance and sex ratio was Hermaphrodite-61. Gene source for minimum days to first picking was SMR-58. Fazilka Coll. 94 was found best gene source in the germplasm for longest harvest duration and thickest fruit rind. Thick fruit rind is important for fruit fly resistance breeding. Gene source with high potential in terms of yield per plant, no. of fruits and TSS was Market Long. These gene sources can be employed according to the need of improvement programme.

In the light of present findings, it may be concluded that on the basis of the cluster distances and cluster means, cluster nos. I and III may be employed for improvement programme in cucumber. Gene source Hermaphrodite-61 was found best for earliness and Market Long for yield and quality.

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Studies on Genetic Divergence in Upland Cotton (*Gossypium hirsutum* L.)

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Genetic divergence in twenty nine upland cotton (*Gossypium hirsutum* L.) genotypes were studied for nineteen yield attributes and quality characters. The pattern of grouping of genotypes reveled that the genetic diversity is not fully related to the geographical diversity. The inter-cluster distances were found to be greater than intra-cluster distances, revealing considerable amount of genetic diversity among genotype studied. Intra-cluster distances, inter-cluster distances, cluster mean for all the characters studied and cluster-wise performance of all the genotypes suggest that the genotypes selected for improvement of yield and quality components are JK-54, Khandwa-2, CNH-120MB, LRA-5166, CAT-834, C-1084, C-YG-2859 and JBWR-13-1. The hybridization programme with the selected genotypes by considering inter-cluster distances may produce high magnitude of heterosis or desirable segregants, which would be meaningful for improvement in yield and quality attributes of cotton.

Key words: Cluster, Genetic Divergence, Upland cotton, Intra-cluster distance, Inter-cluster distance

Cotton is the most important fibre crop and backbone of textile industry of India. It alone accounts 70 per cent of total fibre consumption in textile sector with approximately 38 per cent of the country's export. India ranks first in area under cotton cultivation as compared to the other major cotton growing countries of the world with unique distinction for growing all the four linted cotton species.

Among four linted cotton species, upland cotton (*Gossypium hirsutum* L.) is a predominant species of cotton in world as well as in India. It alone contributes about 90 per cent to the global production. By virtue of its wider adaptability, higher yield and good fibre quality, it gradually replaced Asiatic diploid cottons and grown under irrigated as well as rainfed conditions. Varieties and hybrids of *Gossypium hirsutum* L. occupies about 75 per cent area and 85 per cent cotton production of country (Singh, 2004), and have played a significant role in achieving self-sufficiency in cotton production of India. However, Indian cotton productivity is quite low (403 kg lint/ha) as against the worlds productivity (600 kg lint/ha) (Singh and Ramasundaram, 2005). It is experiencing a plateau which needs to be rectified urgently.

Genetic diversity plays a key role in analyzing the general distance among the genotypes selected as parent. Within a certain limit, hybridization of more diverged parents is expected to enhance the level of heterosis in hybrids and generate wide range of variability in segregating generations (Joshi and Dhawan, 1966). Therefore, the present investigation was undertaken to study the nature and magnitude of genetic divergence in twenty nine upland cotton (*G. hirsutum* L.) genotypes evaluated in Chhattisgarh state under rainfed conditions.

Materials and Methods

The study was conducted in the Instructional Farm, College of Agriculture, Indira Gandhi Agricultural University, Raipur (Chhattisgarh), India. Twenty nine upland cotton genotypes obtained from Central Institute for Cotton Research (CICR), Nagpur (Maharashtra), India, were planted in Randomized Complete Block Design with three replications. Uniform spacing of 90 x 45 cm and all standard manorial and cultural treatments were adopted. In each replication, five plants were randomly selected and observations were recorded for nineteen characters *viz.*, seed cotton yield/plant, days to 50 per cent flowering days to 50 per cent boll opening, plant height, number of sympodial branches as well as monopodial branches plant/ha, lint weight and seed weight boll/ha, number of seeds boll/ha, boll weight, lint and seed index, lint per cent, boll length and girth, 2.5 per cent span length elongation per cent, fibre fineness and fibre strength. The lint quality parameters were studied in Ginning Training Center (GTC), Central Institute for Research on Cotton Technology (CIRCOT), Nagpur (Maharashtra). The genetic divergence was worked out by using Mahalanobnis D^2 statistic as described by Rao (1952). On the basis of D^2 values, investigated genotypes were grouped into different clusters by employing Tochers's method as outlined by Rao (1952).

Results and Discussion

The analysis of variance indicated significant differences among all the genotypes for all the characters studied

and specified existence of considerable genetic diversity among genotypes. Hence, further analysis was carried out for relative magnitude of D^2 values for all the characters and all the genotypes and groped them into five clusters (Table 1).

The maximum number of germplasm accessions (7) were included each in clusters I and III followed by cluster V (5), cluster IV (4) and the lowest in cluster II (4). Generally, geographical diversity has been considered as a measure of genetic diversity. However, this is an inferential criterion and it may not be so effective in quantifying or differentiating different populations. The present pattern of grouping of genotypes in study indicates that the genetic diversity is not fully related to the geographical diversity. This was in accordance with the results of Singh and Bains (1968), Singh *et al.* (1971), Singh and Gill (1994), Sumathi and Nadarajan (1994) and Pushpam *et al.* (2004). Hence, it indicated that the geographic diversity though important might not be the only factor in determining genetic divergence. It may be the outcome of several other factors such as genetic drift, natural selection forces and diverse environmental conditions within the country. Therefore, choice of the parents for hybridization should be decided on the basis of genetic diversity rather than geographical diversity.

Table 1. Group constellation

Cluster no.	Number of genotypes	Genotypes
I	7	SB-166, JBWR-25, BW-28, BBR-310, CAT-834, C-1084 and LRA-5166
II	4	JBWR-36, JBWR-14, JK-54 and C-YG-2859
III	7	Mahalaxmi Narmada, C-YG-1830, C-2076, C-2889, C-2625 and EC 11 0788
IV	5	CAT-2923 C-1857,C-3718, C-1489and JBWR-13-1
V	6	Bikaneri Narma, Khandwa-2, JBWR-13-2, EG-2932 Buri0394, and CNH 120mb

Table 2. Inter- and intra-cluster distances

Cluster number	1	2	3	4	5
I	(3.825)				
II	4.574	(3.176)			
III	3.455	5.121	(3.164)		
IV	4.066	3.891	4.124	(2.934)	
V	3.603	5.236	3.469	5.457	(3.410)

Note: Values in parenthesis are of intra-cluster distance

In the present study intercluster distances were found to be greater than intracluster distances, revealing considerable amount of genetic diversity among genotypes studied (Table 2). The highest intracluster distance was observed in cluster V (3.410) followed by cluster II (3.176), cluster III (3.164) and cluster IV (2.934). Whereas, the highest intercluster distance was observed in between the clusters V and IV (5.457) followed by clusters V and II (5.236), clusters III and II (5.121), clusters 11 and I (4.574), clusters IV and 111 (4.124), clusters IV and I (4.066), clusters IV and II (3.89), clusters V and III (3.469), clusters I and III (3.455) and the lowest in between clusters V and I (3.603). Maximum genetic divergence between the cluster points to the fact that hybridization among the genotypes included with them would produce potential and meaningful hybrids and desirable segregants too. Use of genetically distant genotypes as parents to get the most promising breeding material had also been suggested by Singh and Singh (1984), Sambamurthy *et al.* (1995a), Sambamurthy *et al.* (1995b) and Pushpam *et al.* (2004). However Arunachalam and Bandopadhyay (1984) and Altaher and Singh (2003) experimentally proved that more number of heterotic combinations with higher level of heterosis were from the parents grouped into moderate divergent groups like cluster II and I in this study. The results obtained from clustering pattern are in agreement with hypothesis of moderate divergence for the best heterotic combinations.

Divergence reflecting in the material was also evidenced by an appreciable amount of desirable variation among cluster means for different characters as shown in Table 3. The component of cluster means for seed cotton yield plant^{-1} was the highest for cluster II (126.15 g) and the lowest for cluster III (81.3 g). Minimum days to 50 per cent flowering and days to 50 per cent boll opening were observed for cluster II (77.42 and 107.58 days, respectively) and maximum for cluster III (81.90 and 113.86 days, respectively). For plant height, the highest cluster mean was recorded in cluster IV (129 cm) followed by cluster III (126.88 cm), cluster II (123.97 cm) and cluster I (116.77 cm), while it was the lowest in cluster V (109.43 cm).

For number of sympodia and monopodia plant^{-1} cluster II (22.45 and 2.38, respectively) exhibited the highest cluster mean, while cluster I (16.51 and 0.93, respectively) had minimum cluster mean. The cluster IV had the highest cluster mean (1.93 g) for lint weight

Table 3. Components of intracluster D^2 of cotton

Cluster no.	Number of genotypes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
I	7	78.33	108.9	116.77	16.51	0.93	1.68	2.36	26.96	5.44	5.23	7.56	39.87	5.73	10.23	28.16	4.96	4.29	23.02	68.37
II	4	77.42	107.58	123.97	22.45	2.38	1.57	2.79	30.58	5.83	5.37	9.02	39.64	5.65	10.07	29.97	4.43	4.43	22.89	126.15
III	7	81.9	113.86	126.88	18.18	1.36	1.59	2.23	28.28	4.94	5.61	8.76	38.66	5.6	10.21	24.79	5	3.54	20.91	81.3
IV	5	79.67	108.53	129	19.19	1.42	1.93	2.87	30.24	5.9	6.9	9.42	40.29	5.81	10.47	27.12	4.84	4.36	21.72	102.52
V	6	78.72	111.83	109.43	17.27	1	1.39	2.18	31.22	4.18	5.12	8.9	40.29	5.41	9.36	26.6	4.75	4.1	21.92	61.43

Note: 1: Days to 50% flowering; 2: days to 50% boll opening; 3: plant height; 4: no. of sympodia plant^{-1}; 5: no. of sympodia plant^{-1}; 6: lint weight boll^{-1}; 7: seed weight boll^{-1}; 8: Number of seeds boll^{-1}; 9: Boll weight (g); 10: Lint index (g); 11: Seed index (g); 12: Lint per cent; 13: Boll length (cm); 14: Boll girth (cm); 15: 2.5 per cent span length (mm); 16: Elongation (%); 17: Fibre fineness; 18: Fibre strength (g tex^{-1}); 19: Seed cotton yield plant^{-1} (g)

boll^{-1}and the lowest value was recorded for cluster V (1.39 g). For character seed weight/boll cluster IV showed the highest mean value (2.87 g) and it was the lowest in cluster V (2.18g).

The highest cluster mean for number of seeds/boll was exhibited by cluster V (31.22) followed by cluster II (30.58), cluster TV (30.24), and cluster III (28.28), while it was the lowest in cluster I (26.96). The cluster IV had the highest cluster mean for boll weight (5.9 g) followed by cluster II (5.83 g), cluster 1 (5.44 g), cluster III (4.94 g) and the lowest in cluster V (4.18 g). For characters namely lint index, seed index, boll length and boll girth cluster IV possessed the highest cluster mean (6.9 g, 9.42 g, 5.81 cm and 10.47 cm, respectively) and the lowest cluster mean was observed for cluster V (5.12 g, 8.9 g, 5.41 cm and 9.36 cm, respectively).

For character lint per cent, cluster IV and V exhibited the highest cluster mean (40.29 % each) and was lowest in cluster III (38.66 %). However, for the character 2.5 per cent span length cluster II possessed the highest cluster mean (29.97 mm) followed by cluster I (28.16 mm), cluster IV (27.12 mm), cluster V (26.6 mm) and cluster III (24.79 mm). For character elongation per cent cluster III had the highest cluster mean (5.00 %), whereas it was lowest in cluster II (4.43 %). For character fibre fineness cluster II possessed the highest cluster mean (4.43 micronaire) and was lowest in cluster III (3.54 micronaire). For fibre strength the highest cluster mean was exhibited by cluster I (23.02 g per tex) followed by cluster II (22.89 g per tex), cluster V (21.92 g per tex), cluster IV (21.72 g per tex) and it was lowest in cluster III (20.91 g per tex).

The better genotypes selected for all the characters under consideration are presented in table 4. Among them JK-54 included in cluster II possessed the highest seed cotton yield/plant (157.33 g). Similarly, genotype LRA-5166 of cluster I and CAT-2923 of cluster IV showed minimum days to 50 per cent flowering (76.67) and days to 50 per cent boll opening (103), respectively. Similarly for the traits namely plant height, number of sympodia as well as monopodia per plant and seed weight per boll the genotype JK-54 included in cluster II was recorded the highest mean value (148.73 cm, 26.73, 3.33 and 3.25 g, respectively) for these traits. The genotype CAT-834 of cluster I exhibited the highest mean value for lint weight per boll (2.25 g), lint per cent (44.92 %), boll weight (6.64 g) and fibre fineness (5.40 micronaire). The highest mean performance for number of seeds per boll

Table 4. Desirable genotypes for the important traits of cotton

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Days to 50 per cent flowering	LRA-5166	JBWR-36	Narmada	C-1489	CNH-120MB
Days to 50 per cent boll opening	BW-28	JBWR-14	C-2625	CAT-2923	JBWR-13-2
Plant height (cm)	LRA-5166	JBWR-36	C-YG-1830	C-1489	Buri0394
Number of sympodia plant^{-1}	BW-28	JK-54	C-2625	JBWR-13-1	EG-2932
Number of monopodia plant^{-1}	BBR-310	JK-54	C-YG-1830	C-1857	CNH-120MB
Lint weight boll^{-1} (g)	CAT-834	JK-54	Narmada	C-1857	Bikaneri Narma
Seed weight boll^{-1} (g)	BBR-310	JK-54	C-YG-1830	JBWR-13-1	JBWR-13-2
Number of seeds boll^{-1}	SB-166	JBWR-36	EC-110788	JBWR-13-1	Khandwa-2
Boll weight (g)	CAT-834	JBWR-36	Narmada	JBWR-13-1	Khandwa-2
Lint index (g)	BBR-310	JK-54	EC-11 0788	JBWR-13-1	Bikaneri Narma
Seed index (g)	JBWR-25	JK-54	C-2625	JBWR-13-1	CNH-120MB
Lint per cent	CAT-834	JBWR-14	Narmada	C-3718	CNH-120MB
Boll length (cm)	C-1084	JBWR-14	C-YG-1830	C-1489	Bikaneri Narma
Boll girth (cm)	C-1084	JBWR-14	EC-11 0788	C-1489	EG-2932
2.5 per cent span length (mm)	JBWR-25	C-YG-2859	C-2889	JBWR-13-1	JBWR-13-2
Elongation (%)	LRA-5166	C-YG-2859	Mahalaxmi	JBWR-13-1	EG-2932
Fibre fineness (micronaire)	CAT-834	JBWR-36	C-2076	CAT-2923	CNH-120MB
Fibre strength (g tex^{-1})	LRA-5166	C-YG-2859	C-2076	JBWR-13-1	Khandwa-2
Seed cotton yield plant^{-1} (g)	BW-28	JK-54	C-2625	JBWR-13-1	Khandwa-2

(38.25) was exhibited by the genotype Khandwa-2 included in cluster V. Likewise the genotype CNH-120MB grouped in cluster V showed the highest seed index (11.28 g). For character lint index, the highest mean value was exhibited by the genotype JBWR-13-1 (7.60 g) of cluster IV. The highest mean for boll length and girth was recorded in genotype C-1084 of cluster I. However, the genotypes C-YG-2859 of cluster II found superior for 2.5 per cent span length (33.40 mm) and genotype LRA-5166 of cluster I for elongation (5.70 %) and fibre strength (26.20 g per tex).

Based on the present findings of genetic divergence and its component analysis it can be concluded that intercrossing among the genotypes of genetically diverse clusters showing superior mean performance may be helpful for obtaining desirable segregants with higher yield and better lint quality. In view of this, genotypes namely Khandwa-2, CNH-120 MB of cluster V; JBWR-13-1 of cluster IV; JK-54 and C-YG-2859 of cluster II and LRA-5166, CAT-834 of cluster I possessing superiority for more than two characters may be utilized as parents in hybridization programme for obtaining desirable combinations. It is also evident that cross combinations between the genotypes falling in cluster V and IV; V and II and II and I may be most compatible considering the high inter cluster distances among them.

Intracluster distances, intercluster distances, cluster mean for all the characters studied and cluster-wise performance of all the genotypes suggested the selected genotypes improvement of yield and quality components-JK-54, Khandwa-2, CNH-120MB, LRA-5166, CAT-834, C-1084, C-YG-2859 and JBWR-13-1. The hybridization programme with the selected genotypes by considering intercluster distances may produce high magnitude of heterosis or desirable segregants, which would be meaningful for improvement in yield and quality attributes of cotton.

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Evaluation of Exotic Germplasm of Ethiopian Mustard and Rocket

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The exotic germplasm of crop plants is one of the important sources of some of the agronomical traits for the development of improved cultivars. In the present study, 35 and 26 exotic accessions of *Eruca sativa* (rocket) and *Brassica carinata* (Ethiopian mustard), respectively, were evaluated for various 14 agro-morphological and quality traits. Both these annual species are among the seven cultivated oilseeds of India, belonging to family Brassicaceae. These accessions were acquired from Germany. Among the 14 traits studied, the maximum variability was observed, for seed yield per plant and the least variability is observed for oil content in both the crop species. In rocket genotypes EC 447079 was identified as a useful donor for 1000 seed weight, harvest index and seed yield per plant. However, EC 447092 and EC 447123 were identified as donors for main shoot length and siliquae on main shoot in rocket and Ethiopian mustard, respectively. Identified promising donors for various economic traits can be further used for future breeding programme.

Key words: *Eruca sativa, Brassica carinata*, Exotic germplasm, Evaluation, Variability, Donors

Germplasm plays an important role in any breeding programme (Kumar *et al.*, 2004). A wider genetic base thus assumes priority in breeding research aimed at developing new varieties with desired traits. The exotic germplasm of crop plants are one of the important sources of some of the agronomical traits for the development of improved cultivars. Keeping these considerations, in the present study, 35 and 26 accessions exotic accessions of *Eruca sativa* (rocket/taramira) and *Brassica carinata* (Ethiopian mustard/karan rai), respectively, were evaluated. Both these annual species are among the seven cultivated oilseeds of India, belonging to family Brassicaceae and are limited to the drought prone/ drier areas of Haryana, Himachal Pradesh, Punjab and Rajasthan in India.

Materials and Methods

The exotic accessions of *Eruca sativa* and *Brassica carinata* were acquired from Federal Research Centre of Agriculture, Braunschweig, Germany through NBPGR, New Delhi. Seeds of 61 elite germplasm accessions were grown on 30 cmx10 cm spacing under augmented design with checks (RTM 314, T 27 for *E. sativa* and PC 5, PBC 9902 for *B. carinata*) during *rabi* of 2002-2003 at National Research Centre on Rapeseed–Mustard, Bharatpur-321 303 (Rajasthan). These germplasm accessions were evaluated for various agro-morphological and quality traits including initiation of flowering, 50% flowering, maturity, plant height, primary branches, secondary branches, main shoot length, siliquae on main shoot, siliqua length, siliqua beak length, seeds per siliqua, seed yield per plant, 1000-seed weight, harvest index, oil and protein content.

The observations were recorded on five randomly tagged five plants for different traits at appropriate growth stages. 1000-seed was counted by electronic seed counter (The Old Mill Company, USA) and weighed by electronic balance. Further, protein and oil content were analyzed by NMR (Dickey-John, USA). Range, mean, and coefficient of variation were computed using standard statistical methods (Gomez and Gomez 1984).

Results and Discussion

Among the traits studied, the maximum variability was observed for seed yield per plant (CV 58.1%) followed by harvest index (CV 37.1 %) and the least variability is observed for days to maturity (CV 2.5 %) followed by initial flowering (CV 5.4 %)in *B. carinata* (Table 1). The maximum variability in *E. sativa*, is observed for seed yield per plant (CV 42.3%) followed by secondary branches per plant (CV 39.8%), however, the least variability is observed for days to maturity (CV 1.3 %) followed by oil content (CV 2.6%) and protein content showing CV 3.7% (Table 2).

In *B. carinata* all the exotic accessions were late flowering as compared to best check PC 5, however, accessions EC447104, EC 447199 and EC447130 mature early than the best check PBC 9902. All these accession were dwarf in comparison of checks and showed more number of primary or secondary branches except two accessions. Accession EC447103 and

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Table 1. Range, mean and coefficient of variation (cv) for different agro-morphological traits in Karan rai (*Brassica carinata*) germplasm

Character	Range	Mean ± Sem	CV (%)	Mean values of checks	
				PC 5	PBC 9902
Initial flowering (days)	84-104	97.6±1.03	5.4	71.00	89.50
50% flowering (days)	95-120	108.7±1.60	7.5	85.50	109.00
Plant height (cm)	73-156	121.08±4.32	17.1	180.70	178.30
Primary branches (No.)	12-24	16.52±0.71	20.5	12.60	12.80
Secondary branches (No.)	5 - 41.7	26.51±1.94	35.1	15.20	16.30
Main shoot length (cm)	11.7-38.3	23.07±1.52	31.5	26.50	30.50
Siliquae on main shoot (No.)	11.3-26.3	16.54±0.81	23.5	18.70	14.40
Maturity (days)	146-158	152.7±0.75	2.5	154.00	153.50
Siliqua beak length (cm)	0.3-0.7	0.42±0.02	24.1	0.50	0.83
Siliqua length (cm)	2.9-4.9	3.90±0.13	15.7	4.90	4.99
Seed yield/ plant (g)	1.39-14.3	6.67±0.81	58.1	9.50	9.00
Harvest index (%)	6.4-23.8	11.86±0.92	37.1	16.40	16.25
1000-seed weight (g)	2.0-4.0	3.04±0.11	17.3	4.20	3.94
Seeds/ siliqua (No.)	8.3-25.4	19.09±1.10	23.8	15.20	15.55

Table 2. Range, mean and coefficient of variation (cv) for different agro-morphological traits in taramira (*Eruca sativa*) germplasm

Character	Range	Mean ± Sem	CV (%)	Mean values of checks	
				RTM 314	T 27
Initial flowering (days)	55-71	64.9±0.63	5.8	44.7	48.7
50% flowering (days)	67-77	73.9±0.36	2.9	58.7	64.0
Maturity (days)	123-130	126.2±0.27	1.3	134.0	134.0
Plant height (cm)	56-102	75.9±1.85	14.0	122.1	126.7
Primary branches (No.)	4.3-11	7.4±0.31	24.2	6.6	5.8
Secondary branches (No.)	3.7-26.3	13.6±0.94	39.8	8.1	6.6
Main shoot length (cm)	34.7-73.7	47.5±1.39	16.8	30.1	34.7
Siliquae on main shoot (No.)	16-37	24.6±0.78	18.1	19.9	21.1
Seed yield/ plant (g)	2.8-9.4	5.0±0.61	42.3	8.0	7.7
1000-seed weight (g)	2.0-4.0	2.7±0.12	19.4	2.8	2.7
Harvest index (%)	16.7-37.3	24.2±1.92	27.5	16.4	16.2
Protein content (%)	21.5-24.4	22.7±0.14	3.5	23.3	23.1
Oil content (%)	34.6-37.9	36.1±0.17	2.6	34.4	34.2

Table 3. List of promising donors identified

Character	DONORS	
	E. sativa	*B. carinata*
Plant height (cm)	–	≤ 91.0 : EC447109, EC447115, EC447121
Primary branches	≥ 10.7 : EC447085, EC447090	≥ 20.0 : EC447113, EC447117, EC447124, EC447128
Main shoot length (cm)	≥ 55.0 : EC447064, EC447073, EC447081, EC447092	≥ 30.0 : EC447101, EC447103, EC447122, EC447123
Siliquae on main shoot	≥ 31.3 : EC447064, EC447076, EC447075, EC447092	≥ 20.0 : EC447103, EC447111, EC447123, EC447128
Days to maturity (DAS)	≥ 124.0 : EC447061, EC447075, EC447080, , EC447085	≥ 147.0 : EC447130, EC447184
Seed weight per plant (g)	≥ 8.7 : EC447057, EC447079	≥ 12.1: EC447110, EC447117, EC447129, EC447133
Seeds per siliquae	–	≥ 23.0 : EC447101, EC447109, EC447124, EC447136
1000-seed weight (g)	≥ 4.1 : EC447079	–
Harvest index (%)	≥ 31.33 : EC447058, EC447057, EC447079	≥ 20.3 : EC447115, EC447129
Protein content (%)	≥ 24.1 : EC447067, EC447071	–
Oil content (%)	≥ 37.6 : EC447057, EC447061, EC447092	–

EC447123 had long main shoot as well as number of siliquae on main shoot in comparison with best check. Accept four accessions all showed high number of seeds per siliqua, but all had less test weight in comparison of checks.

The exotic accessions of *E. sativa* are dwarf and early maturing in comparison of checks. The main shoot length and siliquae on main shoot were recorded higher in genotype EC447092, EC447064 and EC447075. Besides these, genotype EC447075 was also early maturing. Seed

weight and seed per siliqua and harvest index were observed higher in genotypes EC447079 and EC 447057. Further, genotypes EC447079 and EC447057 were recorded for higher 1000-seed weight and oil content, respectively. Genotype EC447085 was observed for higher primary branches per plant and early maturity. Genotype EC447058 recorded higher harvest index and seeds per siliqua.

Similar trends of genetic variation have also been reported by various other workers in oilseed *Brassica* (Meena *et al.*, 2000; Misra *et al.*, 2004; Sharma *et al.*, 1991; Yadav *et al.*,1997).

Promising donors were identified (Table 3) for various economic traits which can be further used for future breeding programme. There has been wide variability for primary and secondary branches per plant, seed yield per plant number of siliquae on main shoot and seeds per silique. Some of these promising lines are being utilizing in the breeding programme.

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Genetic Analysis of Seed Yield and its Components in some Cultivars of Linseed (*Linum usitatissimum* L.)

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The combining ability and gene action revealed contribution of both additive and non-additive gene effects playing an important role for the characters studied. Parents Kiran, NL 93, LCK 9312 and EC596A were found to be good general combiners, while the crosses LCK9312 x Kiran, NL 93 x LCK 9312, NL 93 x Kiran and EC596A x Kiran appeared to be some of the promising combinations for most the yield related traits. Since, significant genotypic variation was generated in majority of the crosses involving six divergent parents, it appears worthwhile to intermate the selects in segregating generations, enabling in the accumulation of more number of favourable genes for seed yield and its important attributes.

Key words: Linseed, *Linum usitatissimum*, Additive, Dominance gene action, GCV, SCV

Linseed (*Linum usitatissimum* L.) is basically an industrial oilseed crop occuping an important place among oilseeds having several commercial uses. The development of varieties for high seed and oil yield than the existing varieties is the main aim of linseed breeding. Since, selection of parents and genetic diversity in crop improvement programme is of immense significance, there is a need to augment the germplasm production by developing high yielding genotypes with sufficient variability in linseed crop. Therefore, knowledge of genetic control of character under improvement and combining ability of parents will help in developing better genotypes of linseed. The combining ability studies provide valuable information regarding selection of appropriate parents for hybridization programme as well as to assess the ability of parents. It also elucidates the nature and magnitude of different types of gene actions involved in the inheritance of various traits. The present study was undertaken to estimate the general and specific combining ability effects through diallel cross analysis in twenty one diverse genotypes of linseed comprising of six diverse parents and fifteen hybrids.

Materials and Methods

Six genetically divergent parents were selected, crossed in all possible combinations and analysed following half-diallel method excluding reciprocals. The material for the study comprises of 6 parents *viz.* NL 93, LCK 9312, EC596A, ICAR 3, R 552 and Kiran with 15 F_1's which were planted in a Randomized Block Design with four replications at research farm of Indira Gandhi Agricultural University, Raipur (Chhattisgarh) during *rabi* season. Row to row and plant to plant distances were kept 30cm and10 cm respectively. Observations on five randomly selected plants were recorded for ten characters *viz.* days to flower initiation, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, number of seeds per capsule, hundred seed weight, number of seeds per plant and seed yield per plant. The combining ability analysis was carried out by using method 2, model II (Griffing's 1956).

Results and Discussion

The combining ability and gene effects revealed contribution of both additive and non- additive gene action playing an important role for the characters studied. Predominance of additive gene effect was indicated in the expression of days to flower initiation, days to maturity and plant height. Dominance gene effect was noticed for number of secondary branches per plant, number of capsules per plant, seeds per capsule and seed yield per plant. Parents Kiran, NL 93, LCK 9312 and EC 596A were found to be good general combiners, while the crosses LCK9312 x Kiran, NL 93 x LCK 9312, NL 93 x Kiran and EC596A x Kiran appeared to be some of the promising combinations for most of the yield related traits.

Analysis of variance revealed significant differences for majority of the characters studied, indicating wider genetic variability among genotypes. The mean squares (Table 1) due to general combining ability (gca) and specific combining ability (sca) were significant for most of the traits like days to flower initiation, days to maturity, plant height, number of secondary branches per plant, number of capsules per plant and hundred seed weight.

Table 1. Analysis of variance for combining ability analysis of 6 parent half diallel in linseed

Name of the Character	Mean squares (F generation) GCA df=5	SCA Df=15	Error Df=60
Days to flower initiation	23.17**	2.57**	1.070
Days to maturity	57.02**	4.39**	0.640
Plant height (cm)	260.91**	12.35**	1.490
Number of primary branches per plant	0.66	0.51	0.088
Number of sec. branches per plant	19.19**	35.28**	5.410
Number of capsules per plant	921.77**	2079.58**	202.700
Number of seeds per capsule	0.93	0.46	0.038
Number of seed per plant	0.06	0.002	0.004
100 seed weight (g)	76938.98**	76801.49**	11007.220
Seed yield per plant	0.83	5.49**	0.360

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

This indicated that both additive and non-additive types of gene actions were equally important in the expression of these characters. The predictability ratio (Table 4), derived from equivalent component of variance, indicated that the gene actions were predominantly of the non-additive type for characters like number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, number of seeds per capsule, hundred seed-weight and seed yield per plant and additive gene effect for characters like days to flower initiation, days to maturity, plant height and number of seeds per plant. The earlier results of Kumar and Chauhan (1980) and Khorgade *et al.* (1990) for plant height and Singh (2000) and Patel *et al.* (1999) for non-additive effects for seed yield per plant were in agreement with earlier findings of the study.

The gca effects (Table 2) showed that parent Kiran was found to be good general combiner for number of secondary branches per plant, number of capsules per plant, number of seeds per plant and seed yield per plant. The parent NL 93 was identified as good general combiner for days to flower initiation, days to maturity and plant height. The parent LCK 9312 was found to be a good general combiner for number of primary branches per plant. Parent EC596A appeared to be good general combiner for number of seeds per capsule whereas, ICAR 3 proves to be good general combiner for hundred seed weight followed by NL 93.

Table 2. Estimates of gca effects in six parent half diallel in linseed

Character	NL 93	LCK 9312	EC596A	ICAR 3	R 552	Kiran
Days to flower initiation	-2.72**	0.17	2.56**	0.54	-0.69*	1.20
Days to maturity	-4.36**	-0.41	2.84**	2.17**	1.23**	-1.47**
Plant height (cm)	-7.17**	-4.80**	8.36**	4.05**	0.84*	-1.27**
Number of prim. branches/ plant	0.10	0.31**	-0.38**	-0.93**	0.07	0.24*
Number of sec. branches/ plant	-0.65	1.12	0.39	-2.35**	-0.59	2.08**
Number of capsules/plant	2.12	-6.83	3.60	-14.18**	-2.19	17.48**
Number of seeds/capsule	-0.35**	-0.29**	0.56**	-0.03	-0.11	0.22**
Number of seeds/plant	-22.61	-64.34	97.43**	-110.96**	-40.81	141.29**
100 seed weight (g)	0.07**	0.05**	-0.12**	0.08**	-0.01	-0.06**
Seed yield/ plant	0.35	0.02	-0.36	-0.18	-0.25	0.42*

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

These parents also exhibited significant mean performances for these characters.

The sca effects (Table 3) revealed that cross LCK 9312 x Kiran involving average and high general combiner has high sca effects with high mean performance for days to maturity.

The cross EC596A X R 552 had significant sca effects for plant height. The best cross for number of tillers per plant was found to be LCK 9312 x Kiran involving high general combiner, followed by NL 93 x LCK 9312 and EC596A x Kiran. The cross LCK 9312 x Kiran showed the highest positive significant sca effect. For number of secondary branches per plant, the cross NL 93 x EC596A was found to be promising followed by NL 93 x Kiran. The cross LCK 9312 x Kiran was adjudged as the best cross for number of capsules per plant followed by R 552 x Kiran and EC596A x Kiran involving significant mean performance with average and high general combiner parents. For number of seeds per plant, cross EC596A x Kiran appears to be promising. The cross NL 93 x LCK 9312 observed to be the best combination for seed yield per plant. Other prominent crosses with significant sca effects for number of seeds per plant and seed yield per plant were ICAR 3 x R 552, NL 93 x Kiran and EC596A x Kiran. Though the parents ICAR 3 and R 552 were poor

Table 3. Estimates of sca effects of six half diallel in linseed

Parent combination	Days to flower initiation	Days to maturity	Plant height (cm)	Number of prim-branches plant^{-1}	Number of sec-branches plant^{-1}	Number of capsule plant^{-1}	Number of seed capsule^{-1}	Number of seeds plant^{-1}	100-seed weight(g)	Seed yield plant^{-1}(g)
P1 x P2	1.16	1.23	2.53*	0.77*	5.17*	36.69**	-0.77**	321.08**	0.03	3.42**
P1 x P3	2.17*	0.47	3.48**	0.60*	6.10*	34.05**	-0.17	105.67	-0.04*	0.38
P1 x P4	1.19	0.77	1.13	0.01	0.08	12.64	0.17	90.76	0.0001	0.97
P1 x P5	1.22	0.65	-0.91	0.37	-1.08	7.82	-0.22	53.43	0.001	0.29
P1 x P6	1.88*	2.53**	1.05	0.44	5.76**	28.62**	-0.40*	200.60**	0.04*	1.92**
P2 x P3	-1.36	-0.72	1.50	-0.66	0.83	16.26	-0.31	63.85	0.06*	1.02
P2 x P4	-0.10	-1.95**	-1.44	0.25	2.42	12.84	-0.87**	73.69	0.01	1.20*
P2 x P5	-0.34	-1.79*	1.42	-0.06	1.40	-4.95	-0.22	-59.91	0.04*	-0.40
P2 x P6	-1.70	-1.71*	0.18	0.78**	4.79*	54.07**	-0.19**	199.36*	0.03	1.74**
P3 x P4	0.17	1.24	0.40	0.18	-0.60	9.12	-0.91	140.08	0.001	-0.53
P3 x P5	-0.15	0.48	-3.09**	0.53*	4.13*	42.49	-0.92**	-5.94	0.02	0.22
P3 x P6	-1.64	0.58	3.52**	0.71**	4.72*	35.49**	0.29	436.06**	0.01	2.29**
P4 x P5	0.36	2.25	4.12**	0.63*	5.07*	35.00**	0.21	340.50**	0.01	2.56**
P4 x P6	-0.48	-4.04**	1.18	-0.13	-0.54	-6.23	-0.26	-19.45	0.04*	-0.22
P5 x P6	-0.39	-1.56*	5.89**	0.61*	3.95*	44.08**	-0.47**	122.15	0.01	0.014

*,** Significant at 5% and 1% levels respectively
(P1=NL 93, P2=LCK 9312, P3=EC 596A, P4=ICAR 3, P5=R 552, P6=Kiran)

Table 4. Components of gca and sca and their predictability ratios in linseed

Character	Type of gene action σ^2g	σ^2s	Predictability ratio $2\sigma^2g/2\sigma^2g+\sigma^2s$
Days to flower initiation	2.58	1.50	0.77
Days to maturity	6.58	3.75	0.78
Plant height (cm)	31.07	10.86	0.85
No. of primary branches / plant	0.02	0.42	0.08
No. of secondary branches / plant	2.01	29.87	0.16
No. of capsules / plant	144.73	1876.88	0.18
No. of seeds / capsule	0.06	0.42	0.22
No. of seeds / plant	0.01	0.001	0.92
100 seed weight (g)	17.19	65794.27	0.005
Seed yield / plant(g)	0.583	5.13	0.30

general combiner, but their cross combination proves significant for seed yield per plant. This may be due to complementary genes. Therefore, superior combination may occur even from poor combiners as well. The cross NL 93 x Kiran followed by ICAR 3 x Kiran was observed to be the good cross combination for hundred seed weight.

Thus, it appears worthwhile to exploit these crosses in hybrid breeding programmes and in fixing more number of favourable genes for seed yield and its important attributes. Also, further advancement of such crosses by using diallel selective mating or biparental matings of superior segregants in the early segregating generations would be effective in varietal improvement.

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Evaluation and Genetical Studies of Yellow Seeded Germplasm of Linseed (*Linum usitatissimum* L.)

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Yellow seeded linseed (*Linum usitatissimum* L.) germplasm was evaluated for 10 agro-morphological and quality characters using two checks, namely Surabhi and KL-223 at Crop Research Farm, Nawabganj, CSAUA & T, Kanpur during *rabi* 2003-04 and 2004-05. Among 10 traits studied maximum variation was observed for branches per plant (9.85%) followed by seed yield per plant (7.44%). The least variability was observed for plant height (0.23%) followed by oil content (0.61%). Promising donors were identified for various economic traits which can be further use for future breeding programme. Genotype EC41583 was found to be one of the useful donor for branches/ plant, capsules per plant and seed yield per paint. The genotype BSL-4 was observed to be good donor for oil content. The positive and significant values of correlation were observed for branches per plant, test weight and capsules per plant with seed yield per plant. Hence, selection for the highest values of these traits will be desirable to increase seed yield. The positive and significant correlation indicated that bold seeded types are having high oil content. Characterization of promising donors for high oil content was also studied.

Key words: Yellow seeded linseed, Agro-morphological traits, Coefficient of variations, Donor, Correlation

Linseed (*Linum usitatissimum* L.) is second largest oilseed crop of *rabi* after rapeseed-mustard grown in India. It has unique feature for its oil and fibre. Linseed is basically an industrial oilseed crop and its each and every part is endowed with commercial and medicinal properties. It is also unique that each part of linseed plant is commercially utilized either directly or after processing. At national level yield productivity of linseed is 403 kg/ ha as against the world production of 851 kg/ha (2003-04). Thus, there is wide gap between India and World productivity which gives a pace for enhancement of production.

The present study was undertaken to study the variability among quantitative and qualitative traits of yellow seeded germplasm which have greater oil concentration than brown seeded (Saeidi and Rowland, 1999), available at Project Coordinating Unit (Linseed). This study also aimed to characterize the germplasm for certain useful agro-morphological traits. The identified accessions may prove to be an important genepool for different traits and may be exploited in the term of breeding programmes.

Material and Method

A total number of fifty yellow seeded elite germplasm of linseed were grown in 40 cm row to row space with row length of 3m, under augmented design with two checks i.e. Surabhi and KL-223, in three blocks at Crop Research Farm, Nawabganj, CSAUA&T, Kanpur during *rabi* 2003-04 and 2004-05. These germplasm lines were evaluated for 10 traits including yield, its component and quality traits. The traits selected included branches per plant, capsules per plant, seeds per capsule, days to flowering (50%), days to maturity, test weight (g), plant height (cm), technical plant height (cm), seed yield per plant (g) and oil content (%). The observation each entry was based upon five randomly selected plants for all traits at appropriate stage of growth. The test weight was observed with weighing 1000 randomly selected seeds by electronic balance. Oil content was estimated from dry seed having less than 10 per cent moisture by NMR (MQO-07, USA), range of variation, mean, coefficient of variation, simple correlation coefficient were compiled using standard statistical methods (Gomez and Gomez, 1984).

Table 1. Variability in some agro-morphological traits in yellow seeded linseed

Characters	Range of variation	CV%	Mean value of checks	
			Surabhi	KL-223
Branches/plant	9-4	9.85	6.5	6.0
Capsules/plant	125-38	2.29	5.9	125
Seeds/capsule	9-6	6.95	8.0	8.0
Test weight (g)	9.4-4.49	0.65	4.49	7.05
Seed yield/plant (g)	8.72-2.14	7.44	2.89	7.61
50% flowering (Days)	135-55	0.68	102	92
Maturity days	157- 138	2.48	141	148
Plant height (cm)	110-51	0.23	58	58
Tech. plant height (cm)	71 -26	0.86	42	39
Oil content	46.21-31.97	0.61	37.15	40.57

Table 2. Promising cultures for different traits

Characters		Yellow seeded lines
Branches/plant	≥8	EC23269, EC322652, ECJ41583, NP(hyb)-47, Omega-2
Capsules/plant	≥90	EC41583, EC-588 A-388, Ajgan-1 1, NP(RR)- 405
Seeds/capsule	≥9	Poona-10, Omega- 1, NP(hyb)-47, LCK-9414, LCK-9411, EC322652
Test weight (g)	≥8	FRW-1, BSL-4, EC-568, A-388, KYS-15
Seed yield/plant (g)	≥7	KL-178, EC/41583, NP(hyb)-47, A-388, NP(RR)-60, KYS-15
50% flowering (Days)	≤83	NP(RR)-463, NP(RR)-405, EC/41662, EC41579, EC22781, KYS-15, CI-1574
Maturity days	≤141	GLC-1, NP(RR)-463, T-56, Ajgan-10, NP-125, Ajgan-11, EC41662
Plant height (cm)	≤60	KL-223, NP(RR)-463, EC23269, NP(RR)-405, EC41662, KYS-2
Technical plant height (cm)	≥60	LCK-9414, R-10, Poona-10, LCK-87311, L-23, Omega-2
Oil content	≥42	BSL-4, FRW-1, KYS-1, KYS-7, EC422781, EC22784, EC41579

Results and Discussion

The seeds of linseed are generally brown but some yellow colour seeds are also available in germplasm pool in limited number. Table 1 revealed great genetic variability in yellow seeded types particularly for the traits such as branches per plant, seeds per capsule and seed yield per plant as their coefficient of variations were observed to be high. Green and Marshall (1981) also observed variation in seed weight and oil content while studying diverse collection of 201 linseed and thirteen flax accessions. Among ten studied traits, maximum variability was observed for branches per plant (9.85%) followed by seed yield per plant (7.44%). However, least variability was observed for plant height (0.23%) followed by oil content (0.61%). Promising donors identified for various economic traits presented in Table 2 can be further used for further breeding programme. Genotype EC41583 was found to be one of the useful donor for branches per plant, capsules per plant as well as seed yield per plant. Genotypes BSL-4 and FRW-1 was found for higher test weight and oil content. Genotype A-388 was observed for higher number of capsule, 1000 seed weight and high yield per plant.

Correlation of metric traits (Table 3) revealed that seed yield had positive and significant correlation with capsules per plant, test weight and branches per plant. Pal *et al.* (2000) also observed positive correlation among these traits. Test weight had the positive and significant correlation with seed yield and oil content, thereby, revealing that bold seeded genotypes directly reflect seed yield and ultimately oil yield in positive direction. Technical plant height is major criteria for deciding double

Table 3. Correlation among the different traits of yellow seeded linseed

Characters	Branches/ plant	Capsules/ plant	Seeds/ capsule	Days to flowering	Days to maturity	Seed yield	Test weight	Oil content	Plant height	Technical plant height
Branches/plant	–	–	–	–	–	–	–	–	–	–
Capsules/plant	0.197	–	–	–	–	–	–	–	–	–
Seeds/capsule	–0.012	–0.181	–	–	–	–	–	–	–	–
Days to –flowering	0.199	–0.356*	0.149	–	–	–	–	–	–	–
Days to maturity	0.183	–0.023	0.151	0.302*	–	–	–	–	–	–
Seed yield	0.291*	0.500*	0.041	–0.158	–0.001	–	–	–	–	–
Test weight	–0.118	0.249	–0.112	–0.071	0.239	0.389*	–	–	–	–
Oil content	–0.100	0.119	0.058	–0.380*	–0.149	0.063	0.378*	–	–	–
Plant height	0.049	0.241	0.049	0.110	0.249	–0.131	0.236	0.006	–	–
Technical plant height	0.069	–0.323*	0.069	0.594*	0.370*	–0.184	0.007	–0.575*	0.309*	–

Table 4. Characterization of promising cultures of yellow seeded linseed having high oil content (> 42%)

Cultures name	Oil content	Branches/ plant	Capsules/ plant	Seeds/ capsule	Days to flowering	Days to maturity	Seed yield/ plant (g)	Test weight (g)	Plant height (cm)	Technical plant height (cm)
BSL-4	45.21	7.5	89	8.5	86.5	146	5.75	9,39	64.5	30.5
KYS-1	44.32	4.5	55	8.5	84	147	4.95	7.19	65.5	34.5
FRW-1	43.17	4.5	59	8.5	86.5	147	5.59	9.40	68.5	38.5
EC/41579	42.76	6.0	74	8.5	84	150	5.56	6.65	66.0	31.0
EC/22781	42.73	4.0	64	8.0	83	142	5.04	6.29	61.0	32.0
ECJ22784	42.53	5.5	84	8.5	89	147	5.39	6.65	65.0	33.0
KYS-7	42.47	6.0	54	6.5	89	153	4.57	7.47	67.5	37.5

Table 5. Characterization of promising cultures of yellow seeded linseed having high seed yield/plant (> 7 g)

Cultures name	Seed yield/plant (g)	Branches/ plant	Capsules/ plant	Seeds/ capsule	Days to flowering	Days to maturity	Test weight (g)	Oil content	Plant height (cm)	Technical plant height (cm)
KL-178	8.72	7	91	7	91	144	6.635	38.30	71	50
NP(hyb)-47	7.59	8	75	9	104	150	6.335	38.46	68	41
A-388	7.31	6	102	7	101	152	8.305	38.03	72	51
NP(RR)-60	7.23	7	69	8	103	148	7.025	40.18	78.5	50

purpose linseed, observed positive and significant correlation with days to flowering, days to maturity and plant height indicated that taller the plants take more days to flower as well as to mature. Technical plant height had shown negative and significant correlation with the traits capsules per plant and oil content and also negative and poor association with seed yield which ultimately reflected that the technical plant height had poor number of capsules bearing branches resulted in poor seed yield. Plant height had the negative correlation with number of branches and capsules per plant (Pal *et al.*, 2000). Froment *et al.* (2000) also observed that seed yield of the fibre flax types were less than for industrial oil.

The oil content had less variation as its coefficient of variation was observed less (0.61%). The maximum oil content *Le,* 45.2% was observed in BSL-4.The promising yellow seeded types having more than 42% oil along with their agro-morphological traits were presented in Table 4. Similarly, promising donors like A-388, NP(Hyb)-47, NP(RR)-60 and KL-178 for seed yield among yellow seeded of linseed alongwith their agromorphological features are presented in Table 5, which can be exploited in future breeding programme and yield improvement. High seed yield has been reported by selecting high seed number per plant and a medium 1000 seed weight (Hemker, 1989). These high seed yield and oil containing germplasm may be utilized for improving target yield.

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Selection Parameters for Yield, its Components and Oil Content in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]

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Thirty six F_1s, 36F_2s hybrid combinations obtained from nine parents crossed in a dial lei fashion in Indian mustard (*Brassica juncea* (L.) Czern & Coss) were grown in complete randomized block design. Data were recorded on nine quantitative and one qualitative characters. Wide range of means was observed for all the ten characters. High value of phenotypic coefficient of variation (PCV) with their respective genotypic coefficient of variation (GCV) in both F_1 and F_2 analysis suggest that phenotypic selection may be useful. Parameteres of heritability, genetic advance, correlation and path analysis revealed that for enhancing seed yield/plant by selection in segregating hybrid populations major emphasis should be stressed largely upon five characters namely, test weight, secondary branches, plant height, primary branches and number of siliquae on main raceme.

Key words: Indian mustard, Diallel, Heritability, Genetic advance, Correlation, Path analysis

Indian mustard or rai (*Brassica juncea* (L.) Czern & Coss) is an important *rabi* oilseed crop. Every part of mustard plant is utilized commercially either directly or after processing. Since 2001, mustard cultivationn has gained more economic importance as compared to *rabi* cereals, pulses or even vegetables, because after threshing seeds for extracting edible mustard oil and cake the remaining plant part called *'turi'* has been purchased as fuel by brick furnace owners in Uttar Pradesh at profitable cost. Mustard is cultivated mostly in sub-marginal lands under unirrigated and rainfed confitions in different states of our country. Uttar Pradesh is one of the important mustard growing states of India. This accounts for nearly 35 per cent area and 40 per cent production of country. In Uttar Pradesh Indian mustard has occupied 2200.00 thousand hectare area with a productivity of 1000 Kg/ha. Average productivity of this crop in India is quite low (1013 Kg/ha) as compared to the world average of 1333 Kg/ha. So there is a much scope of enhancing the productivity level of mustard or *rai* in Uttar Pradesh. Many times breeders greatly depend upon the nature and magnitude of genetic variance of the characters under consideration and interrelationship them before taking up hybridization programme. Therefore in the present investigation diallel analysis was done to evaluate the nature and magnitude of genetic variances, heritability, genetic advance, association and path analysis for yield and its variables in Indian mustard.

Materials and Methods

The present investigation was conducted at Agricultural Research Farm, Narain College, Shikohabad affiliated to Dr BRA University (formerly Agra University), Agra during *rabi* season 2003-2004. The experimental material comprised of 36 F_1s and 36 F_2s cross combinations of nine divergent genotypes of Indian mustard *viz.* T-59, RH-30, Pusa Bold, RL-1359, RW-351, JGM-01-15, CS-52, RK-1418 and Pant Rai-16. All the above genotypes were choosen from rapeseed-mustard seed material collected in October, 2000 from National Research Centre for Rapeseed-Mustard, Sewar, Bharatpur, Rajasthan. The crosses were developed by adopting the diallel mating system in earlier years. F_1 and F_2 generations were grown in randomized complete block design with three replications. F_1s and F_2s were grown in single and three rows plots of 4 m long, spaced at 45 cm apart. The distance of 15 cm between plants within rows was maintained by thinning of densely grown plants after 15-20 days of sowing. One non-experimental row was sown on both sides of each replication to avoid border effect. A basal dose of NPK@40:20:20 Kg/ha was given just before seeding. Recommended cultural practices and plant protection measures were adopted as and when needed to raise a good and healthy crop under irrigated condition. The observations were recorded on ten (parents and (F_1s) and twenty (F_2s) randomly selected competitive plants in each plot and also from each replication for the following ten Characters *viz.*, days to first flowering (mean in days on row basis), plant height (cm), main raceme lingth (cm), primary branches/plant, secondary branches/plant, number of siliquae on main raceme, siliqua length (cm), 1000-seed weight (g), seed yield/plant (g) and oil content/

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plant (%). The oil content/plant in percent was measured by using official methods of analysis of the Association of Official Analytical Chemists (AOAC, 1985). Range, mean, coefficient of variability were computed using standard statistical methods (Gomez and Gomez, 1984). Heritability, genetic advance, correlation and path analysis were analysed as proposed by Johnson *et al.* (1955) and Dewey and Lu (1959). All these biometrical calculations were performed form F_1 and F_2 population's mean only.

Results and Discussion

The genetic parameters of variability in F_1 and F_2 diallel progenies for different characters studied are presented in Table 1. The genotypic variance (GCV) in general were observed to be lower in magnitude than the corresponding phenotypic coefficient of variances, indicating environment masking influence on the expression of genetic variability. Comparison of relative magnitude of genotypic coefficient of variation for F_1 and F_2 diallel population revealed that maximum amount of genetic variability was present for seed yield/plant in both (42.76%) F_1 and F_2 (41.28%). High amount of genotypic coefficient of variation in F_1 generation was possessed by number of secondary branches per plant (22.26%), 1000-seed weight (20.73%), number of siliquae on main raceme (18.78%), number of primary branches per plant (16.81%) and length of main raceme (15.47%) comparatively parallel but higher magnitude of GCV was also exhibited in F_2 for all the characters studied except length of main raceme. This indicates good scope for the genetic improvement of these traits. Similar findings were also reported by Mahla *et al.* (2003) in Indian mustard. In the present study minimum genetic variation was recorded for oil content per plant in the study material with overall mean 39.33 per cent in F_1 and 39.26 per cent in F_2.

Narrow sense heritability estimates in per cent ranged from 7.28 per cent (seed yield per plant in F_1) to 66.70 per cent (days to first flower in F_2). The magnitudes of heritability in F_2s were found higher than those of F_1s for all the characters except siliqua length (36.55%). The genetic advance computed as per cent of mean ranged from 0.87 per cent (siliqua length) to 28.26 per cent (plant height) in F_1 and from 0.73 per cent (siliqua length) to 23.00 per cent (plant height) in F_2. The estimates of genetic advance in F_1 were recorded higher than in F_2. High heritability coupled with high genetic advance was observed for days to flower, plant height and main raceme length, while 1000-seed weight and siliqua length exhibited high heritability coupled with extremely low genetic advance in F_1 as well as F_2. Low heritability was observed for primary branches, secondary branches and siliquae on main raceme in F_1. Since heritability in narrow sense is a ratio of additive genetic variance to phenotypic variance, relative higher proportion of dominant component for

Table 1. Genetic parameters of variation for 10 traits in diallel populations of Indian mustard

Populations	Parameters		Days to flower	Plant height	Main raceme length	Primary branches	Secondary branches	Siliquae on main raceme	Siliqua length	Test weight	Seed yield/plant	Oil content
F_1	Mean		38.22	184.05	71.42	7.20	22.25	44.50	4.60	3.40	14.10	39.33
	Range	Min	35.00	140.00	41.25	5.00	10.00	25.00	3.70	2.10	5.26	34.55
		Max.	46.25	224.00	101.38	12.00	50.25	76.25	5.00	5.22	33.76	41.62
	PCV		4.20	9.33	16.69	22.75	25.21	20.16	11.26	22.26	45.82	5.14
	GCV		3.72	8.77	15.47	16.81	22.26	18.78	10.35	20.73	42.76	3.45
	h^2(ns)		60.09	30.66	40.33	8.59	11.36	13.01	38.26	51.93	7.28	15.75
	GA* (as % of mean)		8.36	28.26	17.11	2.82	7.36	11.86	0.87	0.99	5.32	4.65
F_2	Mean		36.25	181.25	66.25	7.60	22.15	44.00	4.5	3.3	12.15	39.26
	Range	Min.	33.21	141.25	42.35	5.00	9.25	23.00	3.6	2.00	5.25	35.25
		Max.	48.25	216.75	96.25	13.50	47.35	78.65	5.9	5.15	30.45	41.45
	PCV		4.51	9.78	16.21	23.66	26.45	21.35	10.77	24.16	44.05	5.21
	GCV		3.92	8.56	15.32	17.28	24.15	19.23	10.26	22.67	41.28	4.32
	hzjns)		66.70	58.39	60.03	40.19	40.71	23.03	36.55	54.00	28.41	21.25
	GA* (as % of mean)		6.71	23.00	10.74	1.17	2.33	8.35	0.73	0.85	2.39	3.72

PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, h^2 = Heritability, GA = Genetic advance
* The selection differential used was 2.06 at 5% selection intensity.

Table 2. Genotypic (upper values) and phenotypic (lower values) correlations among nine character in Fi (above the diagonal) and F2 (below the diagonal) of Indian mustard

Characters	Days to flower	Plant height	Main raceme length	Primary branches	Secondary branches	Siliquae on main raceme	Siliqua length (cm)	Test weight (g)	Seed yield/plant (g)	Oil content (%)
Days to	Fi→ G	0.710**	0.053	0.295	0.159	0.268	-0.379*	-0.403**	-0.234	0.085
flower	F_2↓ P	0.665**	0.048	0.277	0.152	0.258	-0.352*	-0.376**	-0.220	0.072
Plant	G0.712**		0.326*	0.415**	0.450**	0.638**	-0.112	-0.216	0.172	0.105
height	P 0.643**		0.321*	0.407**	0.443**	0.634**	-0.112	-0.215	0.162	0.095
Main raceme	0.297	0.054		0.198	0.223	0.589**	0.386*	0.352*	0.289	-0.162
length	0.241	0.040		0.196	0.222	0.581**	0.384*	0.351*	0.286	-0.155
Primary	0.264	0.396**	-0.388*		0.581**	0.330*	0.191	0.270	0.503**	-0.045
branches	0.233	0.357*	0.322*		0.573**	0.322*	0.189	0.266	0.493**	-0.031
Secondary	-0.183	0.017	-0.512**	0.189		0.414**	0.244	0.195	0.652**	-0.378*
branches	-0.171	0.017	-0.468**	0.183		0.407**	0.241	0.195	0.643**	-0.365*
Siliquae on	-0.628**	0.605**	0.280	0.162	-0.462**		0.327*	0.246	0.396**	-0.210
main raceme	0.55**	0.58**	0.262	0.155	-0.425"		0.320*	0.241	0.387*	-0.202
Siliqua	-0.318**	-0.301	-0.046	-0.254	0.033	0.043		0.782**	0.543**	0.115
length	-0.293	-0.292	-0.039	-0.230	0.030	0.043		0.765**	0.535**	0.112
Test	-0.542**	-0.571**	-0.402**	-0.128	0.306*	-0.573**	0.267		0.585**	-0.055
weight	-0.496**	-0.544**	-0.360*	-0.115	0.286	-0.547**	0.299		0.535**	-0.050
Seed yield/	-0.271*	-0.037	-0.174	-0.163	0.221	-0.082	0.109	0.302		-0.295
plant	-0.259	-0.038	-0.163	-0.153	0.204	-0.076	0.108	0.310		-0.283
Oil content	0.088	0.091	-0.155	-0.033	-0.295	-0.198	0.101	-0.050	-0.188	-
	0.070	0.090	0.141	-0.026	-0.271	-0.190	0.086	-0.038	-0.181	-

*, ** Significant at 5% and 1% level of probability; G = Genotypic; P = phenotypic

primary and secondary branches may have resulted into lower estimates of narrow sense heritability for these characters as compared to other component characters of yield. The major character seed yield per plant (g) and important trait oil content per cent both expressed low heritability with low genetic advance in F_1s and F_2s, indicating prevalence of non-fixable type of genetic variation for the expression of these traits. Earlier findings of Trivedi and Mukherjee (1986) and Sikarwar *et al.* (2000) were in agreement with present study.

The genotypic and phenotypic correlation coefficients analysed for the ten characters in the F_1s and F_2s are summarized in Table 2. The computed data showed that genotypic coefficients of correlation in general, were higher in magnitude than the corresponding phenotypic coefficient of correlation in F_1s as well F_2s, indicating that there was an inherent association among the various characters and the phenotypic expression of correlation was lessened under the influence of environment. Correlation study also revealed that highly significant positive correlation of seed yield per plant existed with number of primary branches (0.503 G and 0.493 P), number of secondary branches (0.652 G and 0.643 P), number of siliquae on main raceme (0.396 G and 0.387 P), siliqua length (0.543 G and 0.535 P) and 1000-seed weight (0.585 G and 0.576 P) whereas, it was negative with oil content (-0.295 G and - 0.283 P) and days to flower (-0.234 G and -0.220 P) which promote early maturity in F_1 population. These results corroborated the earlier findings of Rawat and Anand (1977) and Satyavathi *et al.* (2000).

In F_2 population the results regarding correlation of seed yield with its component characters was completely different than F_1s, because positive but non-significant correlation of seed yield per plant was recorded with only secondary branches (0.0221 G and 0.204 P) siliqua length (0.109 G and 0.108 P) and test weight (0.302 G and 0.310 P) and correlation of days to flower (-0.271 G and -0.259 P) and oil content (-0.188 G and -0.181 P) with seed yield were negative at both genatypic and phenotypic levels in F_2 hybrids. These results were concordant with those of Anand *et al.* (1975).

The estimates of direct and indirect effects of different characters on seed yield per plant are presented in Table 3. The path coefficient analysis revealed that yield contributing characters like secondary branches per plant (0.421 F_1 and 0.267 F_2) number of siliquae on main raceme (0.038 F_1 and 0.472 F_2) and 1000-seed weight (0.346 F_1 and 0.457 F_2) had highest direct positive effect on seed yield per plant in both F_1s and

Table 3. Path coefficient at genotypic levels of nine characters on seed yield per plant in India mustard

Characters	Populations	Days to first flower	Plant height (cm)	Main raceme length (cm)	Primary branches	Secondary branches	Siliquae on main raceme	Siliqua length (cm)	Test weight (9)	Oil content (%)	Genotypic correlation (seed yield / plant)
Days to	F_1	**–0.394**	–0.270	–0.021	–0.117	–0.063	–0.105	0.148	0.157	–0.183	–0.234
flower	F_2	**–0.625**	0.301	0.019	–0.069	–0.049	0.295	0.063	–0.249	–0.115	–0.271
Plant	F_1	0.186	**0.263**	0.086	0.110	0.119	0.171	–0.030	–0.057	0.152	0.172
height	F_2	–0.45	**0.421**	0.004	–0.104	0.005	0.289	0.059	–0.261	0.144	–0.037
Main	F_1	–0323	–0.020	**–0.061**	–0.012	–0.014	–0.037	–0.024	–0.022	0.185	0.289
raceme	F_2	–0.176	0.023	**–0.064**	0.101	–0.135	0.132	0.009	–0.182	–0.095	–0.174
length											
Primary	F_1	0.049	–0.067	0.033	**0.165**	0.097	0.055	0.031	0.045	0.132	0.503**
branches	F_2	–0.165	0.167	–0.025	**–0.026**	0.052	0.077	0.050	–0.058	–0.041	–0.163
Secondary	F_1	0.067	0.193	0.095	0.248	**0.421**	0.176	0.104	0.083	–0.110	0.652**
branches	F_2	0.114	0.007	–0.033	–0.048	**0.267**	–0.220	–0.007	0.140	–0.231	0.221
Siliquae on	F_1	0.011	0.026	0.024	0.013	0.016	**0.038**	0.013	0.010	0.086	0.396**
main raceme	F_2	–0.394	0.251	0.018	–0.042	–0.124	**–0.472**	–0009	–0.263	0.201	–0.082
Siliqua	F_1	–0.011	–0.003	0.011	0.005	0.007	0009	**0.028**	0.022	0115	0.543**
length	F_2	0.199	–0.124	–0.003	–0.042	0.009	0.021	**–0.192**	0.141	–0100	0.109
Test	F_1	–0.140	–0.075	0.123	0.005	0.068	0.085	0.271	**0.346**	–0.153	0.585**
weight	F_2	0.332	–0.241	–0.026	0.066	0.082	–0.272	–0.060	**0.457**	0.121	0.302*
Oil content	F_1	–0.136	0.080	0.096	0.175	0.236	0.137	0.125	0.165	**–0.435**	–0295
	F_2	0.101	0.155	–0.072	–0.211	–0.210	0.225	0.116	0.098	**–0.336**	–0118

*, ** Significant at 5% and 1% levels of probability, respectively. The bold diagonals are direct effects and the remaining indirect effects. The genotypic residual effects were 0.2813 in F_1 and 0.1421 in F_2.

well as F_2s and growth character like plant height (0.263 F_1 and 0.421 F_2) and primary branches only in F_1 (0.165) follow them for direct positive effect. Similar results had earlier been obtained by Singh and Chaudhary (1983).

The negative direct effect on seed yield was observed in oil content (-0.435 F_1 and 0.336 F_2) and days to flower (-0394 F_1 and -0.625 F_2), followed by main raceme length (-0.031 F_1), primary branches (-0.026 F_2) and siliqua length (-0.060 F_2). As a matter of fact, plant height was the only character whose correlation with seed yield was non-significant but it was one of the top three direct contributors to seed yield. However, this was offset due to strongly negative indirect effect through days to flower and test weight in F_2. The estimates of character association in a sizable case were changed not only in magnitude but in direction also from F_1 to F_2, which may be attributed to the recombination and breaking of linkages at the time of segregation. Similar trend in path-analysis was also recorded. Thus, in order to increase seed yield, attributes like test weight, secondary branches, siliquae on main raceme and plant height were indentified as important components of yield. Emphasis must also be given for traitses, having negative, direct association like main raceme length, primary branches and siliqua length.

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Winter Wheats as Donors of Higher Productivity Traits

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With the growing population pressure and expected 20% increase in per capita availability of wheat, India now faces a challenge of producing extra 40 million tonnes, which requires a growth rate of 1.8% per year as against the current 1%. Research efforts are in progress to increase yield levels by developing hybrid wheats, breeding cultivars with durable resistance to newly emerged diseases and pests, introgressing the higher yielding alien genes in the background of present cultivars, etc. but nothing seems to bring in the desired impetus since national average of production has been stalemating for the last few years. At this juncture, it has been envisaged to derive the genes offering promise of higher yields and robust disease resistance from various sources on a hit and trial basis and the winter wheats are the most revealing in this context. Winter wheats have already served this cause by donating *Norin 10* dwarfing gene to spring wheat cultivars which harbingered green revolution in the late sixties. Pace of higher productivity of wheat was further maintained through nineties and till date by Veery cultivars adapted for spring cultivation also find their origin in winter wheat sources. Therefore why not to tap the available winter wheat germplasm again through attempting winter x spring crosses for identifying cultivars with significantly higher yield potential as compared to the present ones. Growing winter wheats in a crossing block in Indian plains during normal wheat season *(rabi)* is an arduous task involving huge investments for artificial fulfillment of vernalisation, a prerequisite for flowering. However, the winter wheats sown in the month of October at ICAR's regional station at Lahaul-Spiti situated in temperate Himalaya of Himachal Pradesh flower in the ensuing month of July and synchronize for crossing with the spring wheat cultivars sown at the same location in the month of May. Therefore, transfer of superior traits from winter wheats to spring wheat cultivars or vice versa can be achieved economically with more feasibility.

Key words: Winter wheat, Spring wheat, Vernalisation, Photoperiod, Wheat production

Winter and spring wheats are the two groups of the same *T. aestivum* species isolated geographically by space and time. As a result of long agro-ecological isolation, they have remained as two separate diverse gene pools. Winter wheats need minimum 270 days of crop period as well as being obligate to vernalisation and photoperiod can be grown naturally in temperate areas receiving snowfall after seed germination leading to seedling burial under snow for 3-4 months before tillering sets in. On the contrary, spring wheats do not require freezing temperatures at seedling stages and being photoinsensitive require only 140 days or even lesser crop period. The agro-climatic conditions of *rabi* part of the two cropping sequences followed in India match for cultivation of spring wheats only. It is expected that by crossing between these gene pools it will be possible to create new genetic variability for selection and development of superior genotypes. These two distinct gene pools offered very good dividends earlier in the form of contribution of *Rht* dwarfing genes as well as 1B/1R translocations of winter wheat parents in spring wheat background known as "Veery" lines. Role of cultivars with dwarfing gene ushering green revolution in India is well known. The Veery cultivars played a vital role in sustaining wheat production in India after dwarf cultivars of green revolution fell prey to new pathogenic races.

Winter Wheats: Vernalisation and Photoperiodism are Critical for Growth and Flowering

Both winter and spring types of wheat may manifest sensitivity or insensitivity to photoperiod. Winter wheats have a considerable vernalization requirement but spring wheats may be insensitive or only partially sensitive to vernalisation. Between these groups, intermediate wheats (semi winter, alternative, facultative) also exist. Out of 12 global wheat growing mega environments (ME), the ME 1 to ME 6 are classified as spring wheat areas and ME 7 to ME 12 as winter and facultative wheat (WFW) areas (Rajaram, 1995). Of the 220 million ha of wheat in the world, roughly 75 million ha are sown to WFW. The stages and sub-stages of winter wheat are similar to spring wheat except that in the former, the tillering stage is interrupted. Plants normally emerge and tiller in the autumn, but the growth is arrested or delayed during the winter and tillering resumed in the spring. When wheats having the full winter growth–habit are sown in the spring,

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they do not normally head, flower, and produce seed in the same growing season (Fig. 1), if not vernalised (Crocker and Barton, 1953). Accomplishing artificial vernalisation calls for heavy investments on raising infrastructure to build low temperature regimes for two months continuously. However, natural vernalisation takes place in areas ME 7–ME 12 (Rajaram, 1995) and high altitude Himalayan location such as Lahaul-Spiti, (Himachal Pradesh), India also falls in this category.

The concepts of the genetic control of flowering in wheat as expressed by vernalisation requirement and photoperiod response as well as on other regional adaptation traits have been described in detail (Ferrara *et al.*, 1998).Qualitative differences in growth habit due to vernalisation requirement are controlled by a system of *Vrn* genes (Pugsley, 1968, 1971). The major *Vrn* genes are *Vrn1*, *Vrn2*, *vrn3* or respectively *VrnA1*, *Vrn–B1*, *Vrn–D1* according to the latest wheat gene catalogue (Mc Intosh *et al.*, 1998). Fully recessive genotypes (to *Vrn*) respond to vernalisation, while dominant alleles fully or partially inhibit this requirement. Typical alternative wheats often carry dominant *Vrn2* in a photosensitive background (Stelamakh, 1986). The genetic control of photoperiod sensitivity is complex, determined primarily by a non homoeologous series or genes *Ppd1*, *Ppd2* and *Ppd3* located on group 2 chromosomes 2D, 2B and 2A respectively (Welsch *et al.*,1973 and Law *et al.*,1978). Genes on other chromosomes particularly 3D (Miura and Worland, 1994), 4B (Halloran and Boydell, 1967) and 6B (Faridi, 1988) have also been implicated in determining photoperiod response.

Methods of *Vrn* gene manipulation including methods for winter genotype selection from spring x spring crosses have been described in detail (Stelamakh, 1998) wherein influence of *Vrn* genes was extremely studied and it was revealed that dominant allele of *Vrn* genes inhibit the vernalisation requirement. The *Vrn* genes (growth habit), the *Ppd* genes (response to photoperiod) and the genes controlling earliness per se, contribute to differences in the rate of development (early emergence and ripening time) for cultivars of common wheat (*T. aestivum* L.) making them widely adaptable. The *Vrn* genes contribute upto 70–75 % of differences in the total length of the wheat life cycle (Stelamakh, 1981). A detailed account of growth habit (spring x winter) as influenced by *Vrn 1–vrn4* genes in global set of commercial cvs. is available in a catalogue (Stelamakh *et al.*, 1987). The dominant gene *Vrn1* and/or *Vrn2* controls spring growth habit in European varieties of common wheat (Akerman and MacKey,1949 and Stelamakh, 1990), macaroni wheat (*T. durum*) (Dzhalpakova *et al.*,1995) and *T. dicoccum* (Rigin *et al.*,1994). Introgression of the *Vrn* genes from related species into cultivated wheats offer new opportunities for altering ear emergence and ripening time.

***Fig.1:** Growth disparity between winter and spring wheats after 110 days of simultaneous sowing at Dalang Maidan, Lahaul-Spiti in summer*

Strong photosensitivity is under the control of recessive alleles in the ppd gene system, while dominant *Ppd* alleles inhibit this sensitivity fully or partially (Piech, 1969 and Law *et al.*, 1978). It has been demonstrated that photoperiod response genes play a major role in determining the climatic adaptability of European wheat varieties (Worland *et al.*, 1998). Photoperiod insensitivity in majority of European wheats is probably determined by a *Ppd1* allele originally derived from the old Japanese variety Akakomugi. Analysis of the pleiotropic effects of a *Ppd1* allele from the Italian variety Mara shows that besides accelerating ear emergence time, *Ppd1* also reduces plant height, tillering and spikelet number, but increases spikelet fertilization more than compensating for reduced spikelet numbers, thus producing increased number of grains per ear. In southern Europe, early flowering *Ppd1* genotypes produce larger grain and greater yields. Alternatively weaker gene for photoperiod insensitivity *Ppd2* similar but less significant pleiotropic effects as compared to *Ppd1*.

Earlier Contributions of Winter Wheats towards Improvement of Spring Wheats

Green revolution liberated India from distressing ship to mouth situation of sixties and heralded a pride era of food self sufficiency. Major credit for bringing the success of green revolution in India can be largely attributed to *Rht1* and *Rht2* dwarfing genes obtained from a winter wheat source, the *Norin–10* (Kronstad, 1996) present in wheat cultivars introduced to India from CIMMYT in late sixties. The utilization and exploitation of *Norin–10* gene for dwarfness in wheat has resulted in tremendous increase in the productivity of wheat in other south Asian sub tropical countries also. It is well known that high yielding varieties owe their superior productivity to their dwarf stature; which gives mechanical strength and keep them erect under conditions of high fertility and irrigation in which traditional tall types would normally lodge (Kulshrestha *et al.*, 1977). Cultivars possessing dwarfing genes increased production and productivity of wheat by six folds in India. This miracle gene has its origin in a winter wheat source revealing thereby the indirect role of winter wheats played in bringing prosperity to our country.

The potential of winter x spring wheat crosses has also been widely demonstrated by the release of Veery lines which were indigenized after dwarf cultivars of green revolution era lost their charm due to susceptibility to various diseases. The Veery cultivars resulted from the cross (Kavkaz/Buho's//Kalyansona/Blue Bird) where winter wheat Kavkaz also contributed among other factors the 1B/1R translocation. These lines in common carry the 1B/1R translocated segment from rye, but otherwise differ markedly in plant height, leaf size, maturity, head size, grain size, grain color etc. (Rajaram and van Ginkel, 1996). Other agronomic characters such as many grains/m^2 and in some cases, many heads / m^2 contributing to the high yielding lines were derived from these spring x winter veery lines. The most famous Indian cultivars PBW 343 and WH 542 ruling the entire North West plain zone of India also belong to this category. Veery lines are being grown on estimated 5 million hectares under a number of different cultivar names as represented by Kauz, Attila, Pastor, Baviacora in different parts of the world. It has been estimated that 80% of the advanced spring wheat lines at CIMMYT carry some degree of winter parentage (Kronstad, 1996).

Based on the pattern of expansion and an increase of 8% yield attributed to the use of winter wheat from winter x spring crosses, a return in excess of 10 million US dollars each year in the 1980s was realized (Mitchell *et al.*, 1988). These gene pools of winter and spring wheats have remained genetically isolated due to their different growth requirements and this variability needs to be harnessed more in Indian wheat programme. There are centres available in Himalaya where winter wheats flower under natural conditions. These centres can attempt crosses between elite winter and spring wheats and segregating materials can be supplied to other centres for selection in their respective agroclimates (Rao, 2001). Spring x winter wheat crosses need to be subjected to screening both in drought prone areas as well as Kashmir and the Himalayan region (Swaminathan, 1977).

Promising Traits of Winter Wheats for Further Exploitation

Discussion on how to increase the yield potential of wheat often centers around winter wheat traits that contributed to the success of the green revolution cultivars more than 30 years ago, e.g. photoperiod and dwarfing genes (Worland *et al.*,1998 and Sears, 1998). A study by Slafer *et al.* (2001) revealed that sensitivity to photoperiod may actually be used as a tool to further rise wheat yields. This opens the possibility to attempt to manipulate the sensitivity to photoperiod during stem elongation as an alternative avenue for raising yield potential. Winter x spring genepools have provided enhanced genetic variability to several abiotic factors such as aluminium

tolerance, winter hardiness, frost and sprouting tolerance. Morso possessing, durable and broad spectrum resistance to diseases and insects has also been derived from winter wheat stocks. The winter germplasm has also contributed the larger and more fertile spikes, stiffer straw, shorter plant stature etc. to spring wheat cultivars (Kronstad, 1996). The winter x spring crossing approach may prove interesting for breeders developing hybrid wheats. In limited studies where comparisons were made with winter x spring F1s and those resulting from winter x winter or spring x spring crosses, the former gave a greater expression of hybrid vigor, perhaps reflecting a greater degree of diversity between these two genepools (Kronstad, 1996)

The spring x winter gene pool recombination has transmitted a higher number of grains either through higher number of heads/m^2 or through bigger heads (Villareal *et al.*, 1991; Villareal, *et al.*, 1994; Villareal, *et al.*, 1995). It was also noted that the resulting lines keep their canopies cooler than the surrounding environment, show higher stomatal conductance and are photosynthetically more efficient (Rees *et al.*, 1993). The spring x winter wheat populations also produce vigorous progenies, tiller profusely, have more surviving spikes, are robust in appearance and keep their leaves healthy for a longer period (Rajaram and van Ginkel, 1996). Crosses between spring and winter wheats have also been successfully used to improve germplasm of both types of wheat (Dorofeev and Udachin, 1987). At CIMMYT, photoperiod insensitive spring wheat germplasm is used to transfer short stature, high yield potential and disease resistance into winter/facultative germplasm. However, there is also a possibility to select vernalisation sensitive genotypes (winter or facultative type) directly from crosses between two vernalisation insensitive genotypes (spring type) as reported in case of phoenix variety in California, USA (Pugsley *et al.*, 1985).

Winter wheats have ability to tiller profusely after vernalisation of seedlings is successfully completed. This particular trait can find usage in popularizing these wheats as fodder crop in Himalayan deserts confronting dire scarcity of grasses in the pasteurs immediately after passage of severe winters. Forage usage of winter wheats as additional advantage has already been reported elsewhere (Epplin and Peeper, 1998)

Winter Wheat Exploitation in India–Need of the Hour

It is expected that the population of India would rise at the growth rate of 1.6% and estimated to reach a figure of 1.3 billion by 2020 AD. The per capita availability of wheat has more than doubled in the last 30 years, from 79.1g/day to 185.4g/day. Assuming a 20 per cent increase in per capita availability of wheat, India has to produce over 109 million by 2020 AD (Rao, 2001). This poses a challenge of producing extra 40 million ton, which requires a growth rate of 1.8% per year as against the current 1%. To achieve this, the national average productivity of wheat has to increase from 2700 Kg/ha to 4200 Kg/ha (Nagarajan, 1998).

It is a matter of great concern that for the last several years plateau in wheat production (Fig. 2) is being

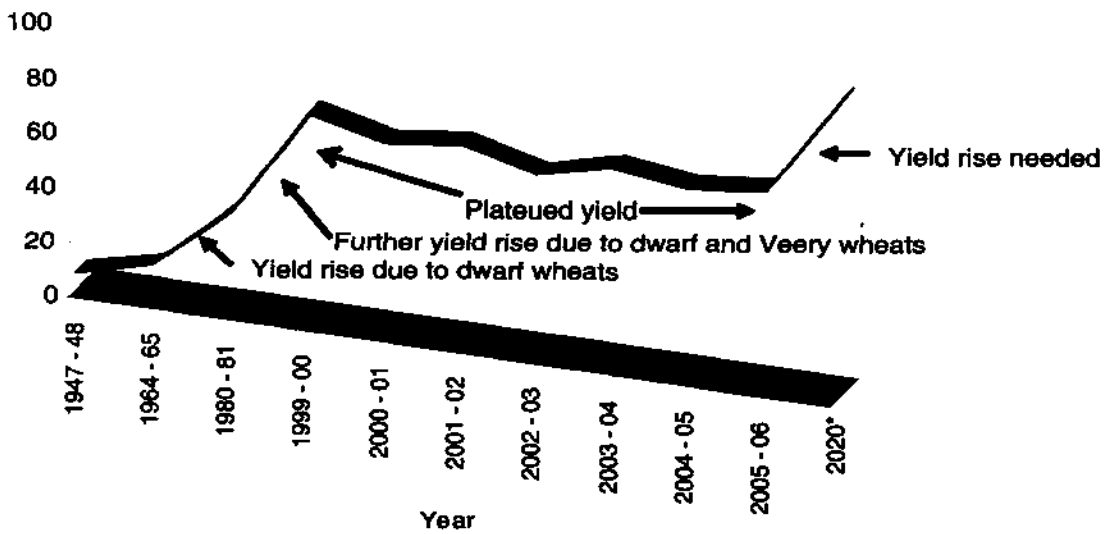

Fig. 2: Past, present and required future of wheat production (mt) in India

observed (Mishra, 2006). The major challenge is to break yield barriers. There is a very little scope for increasing the area under wheat cultivation due to growing urbanization, crop diversification, dwindling water resources, micronutrient deficiencies and soil health deterioration. It has also been realized that there is not much scope for increasing the productivity in favourable environments, because maximum exploitation, has already taken place. Various strategies based on novel and innovative approaches such as hybrid wheat, breeding for durable resistance, wide hybridisation, breeding for photosynthetically efficient genotypes and molecular marker assisted selection though show promise, yet, could not exhibit satisfactory results as yield levels remain plateued despite intensive efforts made on all these aspects in the last decade. The high yielding genotypes, which India used to get previously from international sources mainly CIMMYT through various international nurseries may be stopped in future as regulations and legalities of plant cultivar protection (PVP) and plant or gene patents will restrict access to alien germplasm.

At this juncture, hope is still upheld by realizing a fact that last 35 years of breeding work has not been successful in making any headway in improving the yield levels in the rainfed and warm climates, particularly in central and peninsular India where genotypes have to be bred with tolerance to heat and short growing period to fit in this situation. Similarly, in a large area of Indo–Gangetic plains, wheat is sown as late as middle of December. For this area, effort should be focused on developing short duration varieties which can germinate and establish at low temperature, produce effective tillers profusely, have more number of spikelets/spike and increased grain weight, have early growth vigour and heat tolerance at maturity. In prime, genotypes proposed for these situations must possess ability to germinate and establish at low temperature (December sowing) as well as yield higher and such traits can be possibly imparted by winter wheats. Genotypes identified holding capacity to survive after germination at extreme temperature may also adapt for the cold region in the upper reaches of Himalayas. Such genotypes may emerge as cultivars suitable to grow in Himalayan areas that are covered with snow during winters.

Previous Indian Work on Winter Wheats – A Review

Earlier researches carried out on winter wheats in India Joshi and Tandon (1977) have revealed that the winter x spring crosses may look unpromising in early generations yet there are great possibilities that in latter generation these will throw out desirable segregates. Several of undesirable traits like a high proportion of ineffective tillers (can be explored for fodder quality) will get eliminated either by the process of natural selection or conscious selection against the sensitive loci. It was thus recommended that winter x spring type of crosses should either be advanced as bulks or selections restricted to only against the sensitivity genes in early generations and selections for desirable combinations should be started in later generations. This conclusion was made on the basis of a trial conducted with (i) F2 and F3 of a 4x4 diallel between winter types Tadorna, Holfast and Mariswinger and a spring type VL 404; (ii) F2s of a 5x5 diallel between winter types namely Victor, Maldova and Bezostaya and two spring types VL 404 and HB 117–107; and (iii) 14 miscellaneous F2s involving crosses between winter types Heines VII, Holdfast, Rossulka, Yeoman, Gassner, NS 879/4, Laberator, Canus, Tadorna, Gaines and Mariswinger and spring types S 308, S 227 and VL 404. Among the winter types NS 879/4 and Victor are intermediate types while Maldova and Rossulka have a low chilling requirement as compared to the other varieties. A specific combining ability analysis was conducted using fixed effects model for the design which includes the crosses and their parents without the reciprocals (Griffing, 1956). In a bid to improve wheat through crossing between winter x spring types (Saini and Tandon, 1977), it was concluded that it may not produce expected results in case the desirable features of the winter types are attributable to the genes controlling photo - thermo sensitivity which is the most distinguishing feature differentiating the winter from spring wheats. The gene prolongs the life cycle of winter types and a requirement of chilling before entry into reproduction phase. Selfed population of a heterozygote Kiran (spring) x Favina (winter) for association of photo-thermo sensitivity with physiological and agronomical characters was studied. This study revealed that sensitive type was significantly superior to the non-sensitive type for flag leaf area, volume and thickness, plant height and spikelets/spike. The non-sensitive type was superior to the sensitive type in total grain yield, 1000 grain weight, harvest index and mean ear grain weight. It also matured significantly early and produced significantly less number of unproductive tillers as compared to the sensitive types.

Winter x Spring Wheat Crossing in India– A New Initiative

The Regional Station at Dalang Maidan in the district of Lahaul & Spiti, Himachal Pradesh, provides the Summer Nursery facility for the Indian wheat programme. The station is located at an altitude of 10,000 feet. It has twelve hectares of land, of which only six hectares is cultivable. The office cum laboratory and guest-house facilities has been created for the benefit of research workers. Many centres of All India Coordinated Wheat and Barley Improvement Programme (AICW&BIP) funded by Indian Council of Agricultural Research are using this facility for raising wheat between May to October when temperature in the plains exceed 45°C. This research station popularly known as Wheat summer Nursery (WSN) or Wheat off-season nursery has the following mandate:

- Advancement of the generation (growing two crops in a year, during winter in the plains and at WSN in the following summer) to reduce the time lag in the development of a variety.
- Multiplication of important selected stocks/varieties to raise seed for distribution or bulk use in the ensuing season.
- Attempting most important/corrective crosses with the view to speed up the process of developing superior lines.
- Screening the important wheat and barley material against rusts and powdery mildew diseases.
- Organise high altitude wheat and barley varietal identification trials.
- Serve as a natural repository for wheat and barley germplasm for long-term storage.

To harness the maximum potential of this station, it has been envisaged to initiate research on winter wheats at this station. As described earlier, the winter wheat stocks require vernalisation as well as longer crop period of minimum 9 months. Therefore growing winter wheats would be possible in the suitable temperate climate of this regional station. So far this facility has not been put to use for exploring winter wheat traits in Indian wheat improvement programmes. Directorate of Wheat Research, Karnal has taken an initiative for the first time in this direction by keeping the station functional even during winter months (October to April) also. Earlier, station operated only for a brief period of April to September for growing spring wheats only.

The winter x spring single crosses will be made at this station where high elevation provides crop environment that meets the vernalization requirement of the winter parents. The resulting F_1 populations will be divided with a portion staying at head office, DWR, Karnal for top and backcrossing to spring material. Following selection, the superior lines will be sent to cooperators throughout the country for evaluation in respective agro ecological situations.

The regional station will thus address the following objectives:

- Collection of winter wheat and alien species from national and international sources.
- Sowing of winter wheats in the month of September/ October every year (flowering will occur in July next year).
- Sowing of spring wheats after melting of snow in the month of May which attain flowering during July next year in synchrony with winter wheats.
- To generate database of agronomic, resistance and quality traits of various winter wheat stocks and prepare an information manual for the ready use of breeders.
- To attempt desired spring x winter or vice versa crosses.
- To keep on enriching the donor block of winter wheats with new entries every year.
- To test potential of winter wheats as fodder (owing to inherent profuse tillering ability) in temperate hilly areas.

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Studies on Variability in Seed Longevity of Castor (*Ricinus communis* L.) in Relation to Seed Morphological Characters

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The castor seeds under the present investigation showed wide variation in the seed morphological characteristics *viz.*, seed size, length and breadth ratio, caruncle size, mottling, colour and thickness of the seed coat and seed surface. Presence of caruncle did not show any additive effect on seed germination. Based on the size, the seeds were classified into three categories viz. small, medium and bold. Different sized seeds showed significant differences in their seed viability and vigour pattern during storage. The desiccated seeds of medium size at 4.0 % moisture on fresh weight basis showed maximum survival of 65- 70 percent after storage of five years at ambient temperature.

Key words: Castor, *Ricinus communis* L, Variability, Storage behaviour, Seed morphological characters, Oilseed

Ex-situ seed storage is a complementary strategy for preserving crop genetic resources. Seeds can remain viable for extended periods if kept under low temperature and moisture conditions. However, experiments using a number of different species have shown that longevity may be improved if seeds are dried to less than the recommended value with altered storage conditions (Ellis *et al.*, 1990, 1995), Castor *(Ricinus communis* L.) is an important oilseed crop of India and is widely grown in tropical, sub-tropical and temperate parts of the world, it is extremely variable in habit, colour, amount of waxy bloom, flowering habit, inflorescence type, fruit and seed characters (Singh, 1976). The medium and small are the two groups to which most of the cultivated varieties of the Indian castor belong. There is a great range of variation in seed size (Kulkarni and Ramanamurthy, 1977) and oil contents (45-57 %). The large fruits usually contain big seeds and have low oil content. The seed viability also varies in different accessions, which decreased gradually during storage. However, the extent of loss in viability varies from crop to crop, and even amongst the accessions of the same crop, depending on the seed morphology and its composition.

In castor, the domestication trend is not well defined. Even today most of the seed is collected from wild population. The semi- wild plants with taller habit and few racemes are available very frequently in different areas of the country. Long-term human selections from wild types have tended towards an annual, dwarf, herbaceous, indehiscence and less spiny capsules with synchronized maturing (Singh, 1976; The Wealth of India, 1972). The only representative in this genus is probably originated as dump heap-camp following species has come up as an oilseed crop, a drug and an ornamental plant (Anderson, 1952). Besides its use in manufacture of lubricants, soaps and paints, the oil has great industrial and medicinal value (Watt, 1892, The Wealth of India, 1972).

The present investigation was undertaken to study the morphological variation in the castor seeds of different sizes and the impact of seed size on the their storage pattern.

Materials and Methods

Indigenous variability in castor was assembled from Himalayan region and Trans-gangetic plains. The diversity from these regions has been least represented in the Genebank collections of National Bureau of Plant Genetic Resources (NBPGR), New Delhi. The diversity collected represented wild and cultivated forms from diverse habitat as road side, riverside, garbage land, around farmers field and courtyard/backyard cultivation located in Western Himalaya (Himachal Pradesh, Jammu and Kashmir) and Trans-gangetic plains (Punjab and Haryana) (Duhoon *et al.*, 1996). The variability was recorded and data was analysed using Non-Hierarchical Euclidean Cluster Analysis.

Seed morphological diversity of 73 accessions was studied for seven seed morphological characters (hundred seed weight, length/breadth ratio (L/B ratio), caruncle size, seed mottling, seed coat colour, seed coat thickness and seed coat surface) in relation to storability under ambient conditions. All the accessions were tested for viability by germinating the seeds. The standard germination test was conducted by placing the seeds in replicates of 50 seeds each in between the moist rolled

paper towel (BP) and kept at 27 ± 2°C with 80-90 per cent relative humidity (RH) in the seed germinator. The moisture content was determined by low constant temperature oven method. The seeds were assessed from 10-15 days after plating for the germination when both radical and plumule emerged completely to form a seedling. The normal and the abnormal seedlings were also counted separately for calculating the viability percentage (ISTA, 1985). All the seeds meeting the Gene Bank Standards (> 80% viability) were selected and desiccated to low moisture levels (4 % on fresh weight basis). The seeds were made into three subsets and were hermetically sealed and stored at three different temperatures, *viz.*–20°C, +10°C and ambient temperature. The samples were monitored at regular intervals for viability. The seed viability pattern in the sub-samples stored at ambient temperature was correlated with the seed morphological characters to find out if any correlation existed. Two accessions representing each category were used for detailed investigations and all the experiments were carried in replications of three with block design and the results were analyzed by ANOVA.

Results and Discussion

Total seed collections (73 accessions) comprised of small seeded types, medium size and bold seeds (Fig. 1). The small seeded types were mainly collected from wild or abandoned, disturbed habitats and roadsides. The capsules were smaller with more spiny fruits and shattering type with narrow spikes. The medium seeded types were largely from the abandoned areas near human habitations, farmer's fields, representing semi-spreading habit and smooth spiny fruits but long spike. The bold seeded types on the other hand had non-spiny (smooth) fruits and compact large and showy spikes. They were mainly fetched from fence or borders of fields mainly under the rainfed conditions.

Enormous variability was observed in hundred seed weight (9.40- 63.30 g), length/ breadth ratio (0.04-1.82), caruncle size (1.95-4.90 mm), mottling (dull-whitish grey-darkly mottled), seed coat colour (light, medium, dark), seed coat thickness (thin, medium, thick), seed surface (shiny-dull). Using Non Hierarchical Euclidean Cluster Analysis they were grouped into ten clusters. Cluster I contained 5 genotypes; cluster II contained 6 genotypes; cluster III contained 8 genotypes; cluster IV contained 6 genotypes; cluster V contained 7 genotypes; cluster VI contained 10 genotypes ; cluster VII contained 7 genotypes; cluster VIII contained 9 genotypes; cluster IX contained 5 genotypes; and cluster X contained 10 genotypes. Inter-cluster distances were highest between cluster I and VIII (5.148), followed by cluster V and VIII (4.307) and cluster 1 and IX (4.172). Inter-cluster distance was lowest between cluster III and VII (2.299) followed by clusters II and IV (2.305) and X and VII (2.305).

Generally on an average the castor seeds weigh about 300g/100 seeds but the samples under the present investigation showed a wide range of variation starting from as low as 20 g/100 seeds to as high as 70g/100 seed weight. Seeds of medium size category weighed about 30-50 g/100 seeds. Based on their size and weight the seeds were mainly categorized as small, medium and bold.

The study conducted on the diversity of seed morphological characters showed the maximum representation of small sizes seed type (less than 30 g/ 100 seed) in clusters I, II III, V, VII and IX where the seeds had mixed mottling on seed coat, medium thick seed coat, with both dull and shiny type of seed surface. This category was followed by medium sized seeds represented in cluster IV, X seeds having seed weight 30-45 g/100 seeds of longer size, medium seed coat and wide variation in seed mottling, thickness of seed coat and surface. The third category comprised of bold seeded types represented by cluster VI and VIII with more than 45 g/ 100 seeds and big caruncle size and wide variation in seed coat characters. Amongst the 73 accessions taken for present investigation, 38 (52.5%) were of small size, 16 (21.9%) were of medium size and 19 (26.02%) were in the range of medium to big category (Table 1).

Within the clusters maximum variability was observed in cluster VI representing large-medium seeded types, longer-broader seed ratio, big caruncle, mix mottling, medium colour of seed coat, medium thickness

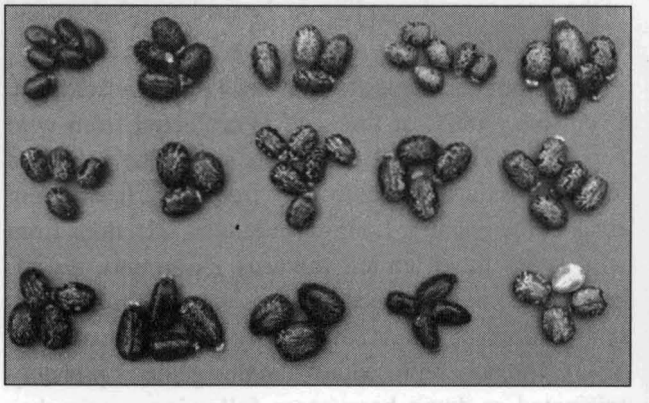

Plate I: Variability in castor seeds

and dull seed surface. This represented most heterogeneous group of accessions collected from Trans-Gangetic Plains of India.

Among the morphological characters positive correlation was observed in seed weight and mottling (0.452), mottling and seed coat (0.341), caruncle and L/B ratio; negative correlation was observed in seed characters, seed colour and seed surface (–0.423), mottling and seed surface (–0.348), seed coat thickness and 100 seed weight (–0.324) (Table 2). In the present investigation, the caruncle was well developed in most of the seeds irrespective of size. However, in bigger size seeds the shape of the caruncle varied from flat to a conical shape while in smaller seeds it was pointed-small and conical in shape (Table 1).

The seed length and breadth varied from 0.82-1.85 cms and 0.47-1.47 cms respectively. Similar trends in seed variability has been reported earlier (Anjani *et al.* 1993, Atsmon 1989, Duhoon *et al.* 1996). The seed structure plays a major role for classification of different *Ricinus* genotypes (Singh, 1954)

In the Indian types generally the caruncle is present. The absence of the caruncle was found to be due to mechanical damage. The seeds without caruncle did not show any significant difference in germination compared to the seeds with caruncle (data not shown). Therefore the role of the caruncle, which protrudes at the tapering side of the seed, might be in attracting insects (mostly ants), and helping in seed dispersal (Kulkarni and Ramanamurthy, 1977). The wild castor seeds with a small caruncle usually shatter and germinate in clusters directly beneath the mother plant.

Thus the diversity rich areas in India *viz.* Indo-gangetic plains which are the centres of botanical variability in castor (Stuhlmann, 1909, Kulkarni and Ramanamurthy, 1977, Moshkin, 1986) needs to be fully explored for assemblage of additional genetic variability available in castor. Targeted explorations, characterization and utilization of genetic resources are required to develop this important crop to its full potential for the benefit of mankind.

Table 3 depicts the seed viability, vigour and oil content in three different categories of castor seeds. All category seeds differed significantly in their 100 seed weight but there was no significant difference in their oil content, which showed an average value of 45.7, 46.7 and 47.1 per cent in small, medium and bold seeds. The viability in all the accessions was found to be in the range of 88-98 per cent, whereas the bolder seeds recorded maximum viability compared to the small and medium size seeds. The viability was directly proportional to the vigour index. Higher the viability, more was the vigour index (Table 3).

Table 1. variation in seed morphological characters of castor

Cluster (no. of genotypes)	100 seed weight (g)	L/B ratio	Caruncle size (mm)	Seed mottling	Seed coat colour	Seed coat thickness	Seed surface
I(5)	Small	Broader	Small-medium	Light-mix	Light	Thick	Dull
II(6)	Small	Longer	Small	Light	Medium-dark	Medium	Shiny
III(8)	Small	Longer	Small	Light-mix	Dark	Medium-thick	Dull
IV(6)	Medium	Longer	Medium	Mix	Medium-Dark	Thin-medium	Dull
V(7)	Small	Longer	Big	Light	Medium	Thick	Dull
VI(10)	Bold	Longer-	Big	Mix	Medium	Medium	Dull
VII(7)	Small	Longer	Big	Mix	Medium	Medium-Thick	Shiny
VIII(9)	Bold	Longer	Big	Dark	Dark	Thick-Medium	Shiny
IX(5)	Small	Longer-Broader	Big	Mix-	Dark	Medium-thick	Shiny
X(10)	Medium	Longer	Big	Dark	Medium	Thick	Shiny

Table 2. Correlation matrix for seven seed morphological characters of castor

100 seed weight (g)	L/B ratio	Caruncle size (mm)	Seed mottling	Seed coat colour	Seed coat thickness	Seed surface
1.0000						
–0.0654	1 .0000					
–0.0597	0.3173	1.0000				
0.4517	0.0842	0.1510	1.0000			
0.0742	0.2537	0.0267	0.3405	1. 0000		
–0.3241	–0.1756	0.0836	–0.1063	–0.1651	1.0000	
0.0360	–O.S098	–0.1146	–0.3484	–0.4237	–0.0980	1.0000

Table 3. Characteristics and viability pattern in different sizes of castor seeds

Seed type	National Identity	100 Seed wt (g)	Oil content	Viability (%)	Vigour index
Small	IC240528	13.0	44.0	90	270
	IC240536	15.0	45.0	89	268
	IC240538	16.5	44.5	90	294
	IC240577	15.3	47.0	90	310
	IC240590	17.0	48.2	88	340
	CD (0.05%)	**0.82**	**1.65**	**2.55**	**5.97**

Seed Type	National Identity	100 Seed wt (g)	Oil content	Viability (%)	Vigour index
Medium	IC240519	37.9	42.5	92	370
	IC240523	38.0	46.0	94	460
	IC240524	43.8	47.0	98	420
	IC240525	36.4	46.5	90	390
	IC240532	38.0	46.8	96	480
	CD (0.05%)	**1.00**	**1.16**	**1.78**	**15.33**

Seed type	National identity	100 Seed 1M	Oil content	Viability(%)	Vigour index
Bold	IC240513	54.6	46.0	92	520
	IC240520	56.8	50.0	98	580
	IC240521	54.6	46.0	95	542
	IC240591	53.9	46.8	96	563
	IC240592	54.8	46.7	92	520
	CD (0.05%)	**2.49**	**2.49**	**1.98**	**8.63**

Table 4. The effect of storage temperature on seed viability of different sized seeds

Seed size	Storage temperature	Accession No.	0 M	12M	24 M	36M	48M	60 M
Small	-20°C	IC240577	90	90	89	88	89	88
	10° C	IC240577	80	80	78	76	72	65
	Ambient	IC240577	78	60	30	12	0	0
	-20°C	IC240590	89	88	88	86	85	85
	10° C	IC240590	88	85	80	70	70	50
	Ambient	IC240590	80	05	41	20	15	0
Medium	-20°C	IC240523	98	98	98	98	98	98
	10° C	IC240523	94	90	90	90	90	80
	Ambient	IC240523	92	90	90	80	72	65
	-20°C	IC240525	98	98	98	98	96	97
	10° C	IC240525	98	95	90	90	85	80
	Ambient	IC240525	96	90	85	80	75	70
Bold	-20°C	IC240521	98	97	96	96	95	94
	10° C	IC240521	98	95	90	90	86	70
	Ambient	IC240521	98	90	84	70	65	49
	-20°C	IC240592	98	98	98	96	96	96
	10°C	IC240592	96	95	86	82	80	70
	Ambient	IC240592	95	90	89	75	62	50

M: months after storage

CD at 0.05%		
Size	0.79	0.70
Time	1.12	0.99
Size x Time	1.95	1.71
Temperature	0.79	0.70
Temp x Size	1.38	1.21
Temp, x Time	1.95	1.71
Size x Time x Temp.	3.38	2.97

The freshly harvested seeds in all the accessions were kept directly for drying for a period of 15-20 days for good germination which is in agreement with the earlier report made by Atsmon (1958). The freshly harvested seeds showed moisture content of 15 to 18 per cent on fresh weight basis which could be easily lowered down to 5 per cent without any effect on the seed viability and vigour (ISTA, 1985, 1993, Heit, 1949) thereby showing a typical orthodox nature. The germination of the seeds in case of fresh lot was found to be 90-98 per cent (Table 3).

Table 4 depicted the effect of storage time on the seed viability of all three categories. The seed viability was maintained well under the long-term storage conditions of –20°C in all the accessions whereas the seeds lost viability significantly with storage time at 10°C and ambient temperature. A significant decline in seed viability of 78 and 80 per cent was recorded in the small seeds stored at ambient temperature followed by 49 and 45 per cent in bold seeds .The medium size seeds showed the best survival at ambient temperature where the decline was minimum of only 32 and 26 per cent even after storage for a period of five years (Table 4). A similar trend was observed at 10° C but the extent of deterioration was less as compared to the ambient temperature. Viability declined at a much faster rate at ambient temperature, wherein the decline was observed at the third year itself and at 10° C the decline started at 4^{th} year of storage. The smaller seeds lost viability earlier followed by larger size and bold seeds whereas the medium size seeds showed a significant level of higher germination percentage in all the treatments.

Not only the viability but also the rate of growth was affected with storage period at ambient temperature. In the experimental lot, seed size had a good correlation with the storability. The medium size seeds survived longer than the smaller and the bold seeds (Table 4) which is in contradiction with the earlier studies made by Singh and Rai (1988) where large seeds showed better germinability, field emergence and productivity as compared to the medium and small size seeds in cowpea.

Genetically inhibited germination, associated with small seed size and low lipase activity, has been reported in isolated cases (Varier *et al.*1999). Germinability drops drastically after 2 to 3 years unless the seeds are stored under cool and dry conditions. Germination does not occur at temperatures below 15°C (Atsmon, 1989). Castor seed is very hard and does not require much care during storage. Under ordinary storage conditions in jute /gunny bags the oil and free fatty acid content of the seeds are not affected even after three years of storage. In warehouses, castor seed is generally stored in gunny (jute) bags. Sometimes under high humidity or rainfall condition, the seeds may become slightly mouldy but this does not affect the oil content or viability of seeds (Kulkarni and Ramanamurthy, 1977).

The genetic diversity is a prerequisite for any crop improvement programme and forms the basis for meaningful and effective conservation. The characters prominent in wild forms such as small seededness, seed scattering habit, low germinability and storability might have been lost consequent upon the processes of domestication. While in selection for larger seed size, loss of seed scattering habit associated with better storability seems to be an adaptive character desirable or the long-term storage in Gene Banks. Therefore, the selection of lines with rich potential valuable trails and significant morphological differences would help in quickly identifying the cultivars from diversity rich areas for effective conservation and also for future utilisation. Variation in the caruncle may be one of the most important parameters for distinguishing the castor accessions. This important crop from the Indian region has been least worked out with respect to various morphological parameters in relation to the storability. Thus, a preliminary investigation of this kind would not only help in proper storage of the seed but also in developing cost effective conventional storage techniques in widely distributed species.

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Response of Garden Pea Seeds to Elevated Nitrogen and Carbon Dioxide During Seed Storage

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An experiment was conducted using garden pea (*Pisum sativum* L.) seed germplasm conserved in laminated aluminium foil pouches along with nitrogen, carbon dioxide, and/or in partial vacuum under ambient conditions for 5 years. Seeds of *cv* Green Pearl were viable for 5 years under ambient conditions. High seed quality in terms of viability and vigour was preserved with carbon dioxide storage followed by nitrogen. It is beneficial to pack well-dried seeds along with carbon dioxide in laminated aluminium foil pouches for the maintenance of high viability till next growing or for short-term conservation of seed germplasm. The modified atmosphere storage is effective for preservation of genetic diversity and useful especially in absence of cold storage facility.

Key words: Garden pea, Seed germplasm, Conservation, Gaseous storage, Viability, Vigour, Storability

Garden pea (*Pisum sativum* L.) is an important vegetable crop of temperate and sub-tropical regions. Its fresh green seeds and pods are used for culinary purposes. Seeds are also valued for germplasm conservation. The crop is commonly raised through the seeds. High seed quality plays an important role in crop growth, establishment and production. Further, its maintenance is dependent on suitable storage conditions. The process of seed deterioration is predominantly governed by seed moisture, storage temperature and oxygen contents (Bass, 1980). Further greater level of oxygen in storage container affects the seed viability and storability (Roberts and Abdalla, 1968). Seed storage in elevated oxygen levels increases the deterioration process while in partial vacuum it preserved high seed quality as well as enhanced the storage life (Barton, 1960). Replacement of air with nitrogen or carbon dioxide in storage containers lowers the seed deterioration thereby maintaining higher seed viability and vigour (Bass and Stanwood, 1978; Doijode, 2004). The utility of the gaseous storage differs in different crops and helps in better retention of high quality in terms of viability and vigour which is prerequisite for successful conservation programme. The present experiment was conducted with the view to harness the benefits of gaseous storage during conservation of seed germplasm in garden peas.

Materials and Methods

Garden pea seeds cv Green Pearl (containing 9.2% moisture content) were packed in triple layered laminated aluminium foil pouches along with nitrogen, carbon dioxide and air or in partial vacuum by PAC-vacuum and gas sealing machine. The pouches were impervious in nature, triple sealed all the four sides and there was no escape of gases. To compare seed storability, seeds were packed in paper bags and stored at ambient conditions (16-35°C; 25-90% RH) for 5 years. Seed viability and vigour were determined periodically in stored seeds. One hundred seeds of each replicate were germinated on triple layer moist rolled crepe kraft paper at alternate temperature of 20°C and 30°C for 16 and 8 hours respectively in seed germinator. Seedlings were evaluated for normal and abnormal nature and germination count was taken on normal seedlings. Seedlings with well developed root and shoot systems were considered as normal. Seedling characters such as shoot and root length and seedling dry weight were recorded on 7 days old seedlings and final count was taken after 14 days of sowing. Dry weight was recorded on seedlings dried at 65°C for 48 hours. Seedling vigour was compared by means of vigour indices I and II which were calculated by multiplying percentage germination with seedling length and dry weight respectively. The data was statistically analyzed for variance and means were compared by using protected least significant difference test at 0.05 probability level.

Results and Discussion

Seed quality in terms of viability and vigour was decreased with increase in storage period. Garden pea seeds were viable for 5 years in various treatments. The percentage of germination varied from 11 to 79 during 5th years of storage. The initial viability 92 per cent was maintained for first three years of storage when seeds were packed along with carbon dioxide

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unlike it reduced to almost 50 per cent in control. Similarly seeds stored in nitrogen also exhibited higher viability and vigour during conservation but lower as compared to carbon dioxide storage (Fig. 1).

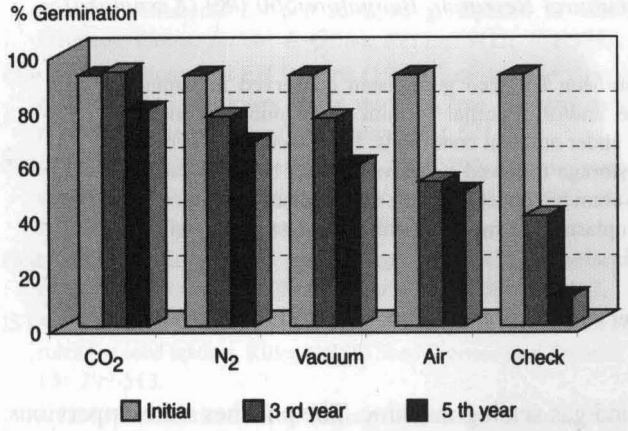

Fig. 1: Seed viability during gaseous storage in garden peas under ambient conditions

There were almost 6 and 7 times increased storage potential in nitrogen and carbon dioxide stored seeds respectively over the control after 5 years of storage. Seed conservation devoid of oxygen was able to maintain an appreciable level of seed quality during storage. Seedling vigour was compared by means of seedling characters as well as vigour indices which was greater for seeds stored in gaseous environment (Table 1). A high level of seed viability and vigour was able to obtain in seeds with carbon dioxide storage.

Garden pea seeds are moderate storer under ambient conditions. A fairly high level of viability was preserved for 5 years under ambient conditions with carbon dioxide storage as compared to only for two years in control. Seeds stored in carbon dioxide environment in laminated aluminum foil pouches exhibited higher seed germination and seedling vigour even after 5 years of ambient storage. Removal of air especially the oxygen is beneficial for maintenance of high seed quality during storage. It promotes the process of seed deterioration especially under ambient conditions (Harrington, 1960). The percentage of germination was decreased with increase in level of oxygen in storage (Roberts and Abdalla, 1968). Seed storage in modified atmosphere is superior over the seeds sealed in air (Harrison and McLeish, 1954). Thus seed storage with nitrogen or carbon dioxide is beneficial in maintaining high quality during seed germplasm conservation. In certain crops such as onion and amaranths seed conservation with nitrogen showed greater viability and vigour on storage (Doijode, 2000 and 2001) and with carbon dioxide in cabbage (Doijode, 2004). There is greater loss of seed viability during initial stages of storage. Several valuable germplasm accessions were lost due to improper handling and non-availability of suitable storage facility. Further, seed longevity is governed by initial level of vigour of an accession. Thus, it is advantageous to pack well dried seeds of an accession in laminated aluminium foil pouches along with carbon dioxide for better retention of high viability and vigour in ambient condition before it is utilized in breeding and /or for long term germplasm conservation.

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Table 1. Seedling characteristics and vigour during gaseous storage of seeds in garden peas

Storage environment/ Year of storage (yrs)	Shoot length (cm)		Root length (cm)		Dry wt. (mg)		Vigour		Vigour index-I		Vigour index-II	
	3	5	3	5	3	5	3	5	3	5	3	5
CO_2	3.7	1.8	7.3	8.3	39.7	25.4	47.8	16.5	1020	798	3084	2005
N_2	4.7	2.4	9.1	8.8	34.8	21.3	50.8	16.9	971	758	2425	1452
Vacuum	4.1	1.8	8.3	8.3	39.2	24.7	55.3	12.2	959	601	2991	1466
Air	3.7	2.1	6.8	6.8	21.9	23.7	35.6	10.6	584	433	793	1162
Check	1.8	–	6.4	–	12.9	–	24.5	2.5	321	–	495	–
CD at 5%	1.1		NS		7.9		9.7		299		300	

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Downy Mildew of Sunflower (*Plasmopara halstedii*), a Disease Introduced and Established in India – Status Report in Relation to Quarantine

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Downy mildew of sunflower (*Helianthus annuus* L.) caused by *Plasmopara halstedii* (Farl.) Berl. and de Toni is potentially a destructive disease. It is distributed almost in all the sunflower growing countries. The disease incidence range from traces to 50%, however, it may exceed up to 95%. In India, downy mildew of sunflower was reported for the first time in 1984 from Latur district of Marathwada region of Maharashtra; it has spread to Karnataka, Andhra Pradesh, Tamil Nadu, Punjab and Madhya Pradesh. The status of the disease world over, physiological races, host range, epidemiology, detection techniques and management is discussed.

Key words: Sunflower, Downy mildew, *Plasmopara halstedii*, Distribution, Races, Management, Quarantine

Sunflower (*Helianthus annuus* L.) is an important oil-yielding crop, which suffers from several diseases. In India, the commercial cultivation of sunflower has become extremely popular in recent years in many states. Simultaneously the common diseases attacking the crop were restricted to rust, *Alternaria* blight, head rot and charcoal rot. Downy mildew of sunflower caused by *Plasmopara halstedii* (Farl.) Berl. and de Toni is potentially a destructive disease. In Europe, after its first appearance in 1941 the disease increased rapidly and by 1977 it was rated a "major disease" in all sunflower-producing countries (Sackston, 1981). In India the occurrence of downy mildew was reported first time in 1984 from Latur district of Marathwada region of Maharashtra (Mayee and Patil, 1986) and subsequently it spread to several states.

The disease is seed and soil-borne and causing considerable economic losses. In western Canada, the incidence of downy mildew increased from 6% in 1988 to > 20% in 1990 and 1991 (Rashid, 1993). In Morocco, Serrhini *et al.* (1994) reported that the incidence of downy mildew ranges from 1 to 40%. In India also, the disease incidence was reported up to 40% in farmer's field in Marathwada region of Maharashtra (Chattopadhyay *et al.*, 1999). A loss of more than 80% of production was also reported due to downy mildew in Spain (Molinero-Ruiz *et al.*, 2003a).

Zimmer and Zimmerman (1972) reported that seeds from plants infected with *Puccinia helianthi* and *Plasmopara halstedii* were significantly smaller, lighter, higher in hull percentage and lower in oil content. Doken (1989) observed that sunflower seeds produced in downy mildewed plants were either under-developed, colourless or, rarely, they look healthy. Such infected seeds were of poor quality, produced abnormal seedlings and low rate of germination.

Geographical Distribution

Plasmopara halstedii has been reported from Albania, Argentina, Austria, Azerbaijan, Bosnia, Brazil, Bulgaria, Canada, Chile, China, Czech Republic, Egypt, Estonia, Ethiopia, France, Germany, Greece, Hungary, India, Iran, Iraq, Israel, Italy, Japan, Kazakhstan, Kenya, Mexico, Moldova, Morocco, Pakistan, Paraguay, Poland, Romania, Russian, Siberia, Slovakia, Spain, Switzerland, Ukraine, Yugoslavia, Georgia, Turkey, South Africa, Uganda, Zimbabwe, Dominican Republic, United States of America, Uruguay, Australia. In New Zealand, it is absent but formerly reported as present (Hall, 1989a; Kucmierz, 1976; CMI, 1988; EPPO, 2003, CABI, 2004).

Introduction and Spread in India

In India, it was reported for the first time in 1984 from Latur district of Marathwada region of Maharashtra (Mayee and Patil, 1986) and by 1989-90 the disease spread to western Maharashtra and Vidharbha in Maharashtra and further southern states (Patil *et al.*, 1993). It has also been reported from Andhra Pradesh (Moses, 1989) Punjab (Thind *et al.*, 1999), Karnataka (Patil *et al.*, 1993), Madhya Pradesh (Agrawal *et al.*, 1991) and Tamil Nadu (Chattopadhyay *et al.*, 1999).

Host Range

Main host: Cultivated sunflower (*Helianthus annuus*)

Other hosts: *Senecio* sp., (Gullino and Garibaldi, 1988)

Asteraceae: *Artemisia vulgaris* (Viranyi, 1984)

Wild species of *Helianthus*: *H. argophyllus*, *H. debilis*

H. divaricatus, H. grosseseratus and *H. petiolaris* (Viranyi, 1984)

Other wild hosts: *Xanthium strumarium* (Viranyi, 1984)

Common ragweed (*Ambrosia artemisifolia*) (Walcz *et al.*, 2000; Vajna, 2002)

Marshelder (*Iva xanthiifolia*) (Gulya, 2002)

Taxonomy and Nomenclature

Plasmopara halstedii belongs to Domain: Eukaryota; Kingdom: Chromista; Phylum: Oomycota; Class: Oomycetes; Order: Peronosporales; Family: Peronosporaceae (CABI, 2004).

The fungus is obligately biotrophic. Mycelium composed of intra-cellular, colourless, aseptate, hyphae 6-20 μm diameter, often irregularly shaped and swollen, bearing small rounded vasicular haustoria 5-10 μm diameter, growing in all plant tissues. Sporangiophores hypophallous or very occasionally epiphyllous, arborescent, 300- 750 μm x 7-14 μm, obconical and pointed at the base, branching in the upper half with the apex of the branching axis, which is frequently swollen; branches in the form of a whorl of 7-8 produced monopodially at right angles to the main sporangiospore axis, each with 2-5 secondary branches 40-86 μm long, bearing 3-5 tips, 8-15 μm long, diverging at right angles. *Plasmopara* is chiefly distinguished from other downy mildew genera by slender sporangiophores, which branch monopodially, usually at right angles and abtuse tips of the branches. Sporangia ovoid to elliptical, 18-30 x 14-20 μm, papillate germinating to give 20 reniform, biflagellate zoospores released by each sporangium. Antheridia club shaped, 12 x 30 μm, formed on distant hyphal branches ('diclinous'). Oogonia spherical, 30-40 μm diameter, colourless. Oospores formed in all the vegetative organs of the host, especially in roots and leaves, just under the epidermis, spherical, 23-30 μm diameter ('aplerotic'), yellow-brown with a slightly wrinkled wall, 3 μm thick, germinating to give sporangia (Hall, 1989a).

Sexual reproduction is by means of oogamy; oogonia, spherical in shape and club-shaped antheridia form on distal hyphal branches separately, those hyphae being of different mating types. Oospores are spherical, hyaline to light brown, thick-walled, temporarily surrounded by oogonial remnants (Hall 1989b).

Originally the fungus causing downy mildew was described as *Peronospora halstedii* by Farlow in 1879 who first collected it from *Eupatorium purpureum* but after a revision of the genus *Peronospora*, the fungus was renamed as *Plasmopara halstedii* (Farl.) Berlese and de Toni. In 1888 it was put correctly as *Plasmopara halstedii* (Farl.) Berl. & de Toni by P.A. Saccardo (*Sylloge fungorum* 7: 242). A number of forms and varieties have been separated from *P. halstedii* and described as a new species by several workers (Leppik, 1966). Novotelnova (1966) described three *forma species* within the fungus on *Helianthus* (1 on annual and 2 on perennial sunflowers) and put the downy mildew fungus to specific rank as *Plasmopara helianthi* Novot., a name widely used in Eastern Europe while in the western world *P. halstedii* is preferred. The taxonomic position is based on morphological characteristics and there is as yet no precise work on developmental biology and physiology to define the pathogen species (Mayee, 1988).

It is important to note that in India, *Plasmopara halstedii* downy mildew has been reported on *Veronia cinera* at Allahabad, Uttar Pradesh (Edward and Naim, 1962). This appears to be a different form than the one occurring on cultivated sunflower and can be raised to the level of species after proper investigation. On *Veronia chinensis* also, a downy mildew caused by *P. veronia-chinensis* Less was reported from Hyderabad and further South (Salam and Rao, 1954; Ramakrishnan and Sundaram, 1954). A perusal of literature indicated that *P. halstedii* is a complex pathogen and is highly specialized, probably several species, forms or varieties exists in it that adapted on to certain host species. The grouping therefore, is yet incomplete and needs to generate more information on the taxonomic position in India (Mayee, 1988).

Race Situation

Zimmer (1974) found evidence for existence of races. Sunflower lines that were found resistant in the USA were also resistant in Europe but vice-versa it was not true. These studies indicated the existence of physiologic races in *P. halstedii*. The existence of pathogenic forms within *P. halstedii* became evident soon after the release of the first mildew-resistant sunflower cultivars. Initially, two pathotypes (races) of the fungus were differentiated: pathotype 1, originally referred to as the European race, and pathotype 2, known as the Red River race (referring to the Red River Valley of North America). By now, over 20 different races/pathotypes of *P. halstedii* have been recorded and several workers suggested new systems for their classification. Gulya *et al.* (1991a) mentioned

the standard method to determine races of sunflower (*Plasmopara halstedii*) and differentiated 8 races in USA. Accordingly, Labrouhe and de Labrouhe (1999) applied a new nomenclature to French type of *P. halstedii* and renamed the prevalent races. Existence of races have been reported from Argentina, Bulgaria, Canada, France, Germany, Hungary, Italy, Morocco, Pakistan, Romania and Spain (Pacureanu *et al.*, 2002; Labrouhe and de Labrouhe, 1999; Gulya *et al.*, 1991b; Rashid, 1993; Zazzerini and Tosi, 1998; Kormany and Viranyi, 1997; Achbani *et al.*, 1996a; Rahim *et al.*, 2002; Molinero Ruiz *et al.*, 2002; Rozynek and Spring, 2000). In India also, consistent resistant reaction of three cultivars *viz.*, RHA-265, RHA-273 and RHA-274 and susceptible reaction of cv. Progress confirmed the identity of Indian isolates as European Race-1 (Patil and Mayee, 1990).

Symptoms on Host Plant

The symptoms produced by *P. halstedii* in sunflower are diverse depending on the age of tissue, level of inoculum, cultivars reaction and environment (moisture and temperature). The variety of symptoms produced by the pathogen is damping off, basal root or stem galls, local foliar lesions, latent infection and systemic symptoms.

A. Damping off

Infected seed when sown in favourable weather conditions particularly under cool and moist conditions showed damping off symptoms in the seedling stage. Seedlings are killed soon after the emergence resulting into reduced plant population. Affected plants become dry and easily blown by winds.

B. Basal Root or Stem Galls

Development of basal gall symptoms occurs independently of the infection that results in systemic symptoms. Root infection may result in formation of root galls at the base of the plants on primary roots. Such roots become discoloured, scurfy and hypertrophied. Plants ultimately show the wilt symptoms. Some time lodging of the plants also occur from the point of infection. Oospores are formed on the affected tissue. Plants with basal galls are more prone to drought stress and lodging than healthy plants.

C. Local Foliar Lesions

Small angular chlorotic spots appear on the leaves as a result of secondary infection through zoospores liberated from wind borne zoosporangia. Spots may coalesce to form a larger patch. These spots or patches show white fungal growth on the undersurface of the leaves usually under high humid conditions. During morning hours it becomes more conspicuous. Chattopadhyay *et al.*, (1999) reported whitish downy growth, chlorosis, stunting, thickening and curling of leaves, erect flower heads, chlorotic local lesions and a reduction of the root system. In Hungary, Vida (1996) reported a local- to systemic infection in some sunflower fields due to favourable weather conditions coupled with unusually high infection pressure.

D. Latent Infection/Symptom

The latent type of infection appears symptomless and affected plants cannot easily be recognized from outside. It may derive either from below ground infections on plants or it may derive from very late infections during flowering stage, when the growth of vegetative parts has finished and therefore no symptoms become visible. The former type is typical and appears in some so-called resistant sunflower genotype (which sometimes allow sporulation on hypocotyls and cotyledons) and the latter mostly leads to seed contamination. In both cases the pathogen stays alive and is able to complete its life cycle through sexual reproduction by the formation of oospores. Plants with latent infections showed enhanced cell division, which restricted the pathogen to the parenchyma (Heller *et al.*, 1997).

E. Systematic Symptoms

In case of systemic symptoms plants become severely stunted. Leaves of systemically infected plants show abnormally thick, downward curled with yellow and green epiphyllous mottling. The chlorosis usually starts from the midribs. Hypophyllous downy growth of the fungus consisting of zoosporgiophores appears and sporangia develop on them. Stem becomes brittle. Systemic infection occurred more readily through hypocotyls than roots and through apical buds than leaves. Sporangial infection caused local lesions on young leaves and some of these infections become systemic (Cohen and Sackston, 1973a). Severely infected plants do not produce any seeds in the heads.

Epidemiology

The nature of the inoculum (oospore or zoospore), weather variables (relative humidity, temperature), infection site (age of tissue), as well as cultivar reaction are the main factors, which determine the infection process, disease incidence, and severity. Zoospores,

originating from either sexual or asexual sporulation, require free water for retaining viability and capability of moving towards infection sites. The symptoms become visible in the seedlings within a week of emergence. Seedlings become stunted and abnormally thick; downward curling of cotyledons and epiphyllous mottling on the true leaves. Severely infected seedlings often succumb to disease or may survive for few weeks. Such type of infection is systemic and results from penetration of the host at an early stage of growth up to the 6-8 true leaf stage. Raghuvanshi *et al.* (1999) reported that rainfall immediately after sowing coupled with high RH and favourable temperature were the main factors affecting downy mildew incidence irrespective of sowing dates. Chattopadhyay and Appaji (2000) observed the maximum growth and sporulation of the fungus at 16±1^{0}C and at 100% RH with no effect of light hours. They also reported that infectivity of the pathogen was negatively correlated with age of seedlings and temperature while a positive correlation was found between humidity and growth/ sporulation of *P. halstedii*. Kormany and Viranyi (1997) found that as little as 20-25 sporangia/ ml suspensions produced sufficient and comparable disease symptoms in sunflower. Secondary infection by wind-borne zoosporangia formed on the leaves.

Brief Life Cycle

In the presence of free water, the zoospores remain in motion for hours and tend to move to infection sites (root, hypocotyl) soon if available. Following encystment and germ tube elongation (the latter usually terminates in an appressorium against a host cell) the fungus develops an infection structure (infection peg) for direct penetration. Gray *et al.* (1985) demonstrated that germ tubes do not usually form appressoria in water but they do so in the presence of host cells. After penetration, the fungus grows intracellularly and then intercellularly, and once being established in a susceptible host (compatible) it starts to colonize the entire plant systemically by growing preferably towards the shoot apex and, to a lesser extent, in the direction of the root. In favourable conditions asexual sporulation takes place on affected leaves and occasionally on below-ground tissues. Fully developed sporangia disseminate by wind and their survival depends on the current weather situation. Oospores are also produced in infected plant parts, primarily in root and lower stem tissues, whereas leaves and upper plant parts, except seeds, are free from these spores (Viranyi, 1988; Onan and Onogur, 1991).

Spring (2000) observed the formation of oospores in the host tissue of all plants infected with single zoospore, which indicated the homothallic nature of sunflower downy mildew. Initiation of sexual reproduction started two to three week after inoculation. The oogonia and antheridia developed in close proximity to each other at the same hypha (Spring, 2000).

Source of Inoculum, its Survival and Transmission

P. halstedii is a seed as well as soil-borne pathogen. Soil-borne oospores serve as primary inoculum to underground tissues of young sunflower seedlings. Oospores develop mainly in root and lower stem tissues of mildewed plants, with or without visible symptoms and, with plant residues of the preceding sunflower crop, they come into the soil. Oospores can remain viable for at least 6-8 years (Sackston, 1981; Virányi, 1988). The spore viability in the soil decreased only after 5-6 years, sometimes after 8-10 years (Vronskikh, 1981).

Infected seeds carry mycelium and/or oospores internally. Sackston (1981) confirmed the seed infection by artificial inoculation. Such infected seeds gave rise to apparently healthy seedlings with no typical symptoms (latent type of infection) but the pathogen sporulates more often during flowering stage on the roots of these symptomless plants. Spring (2001) described the crucial role of such symptomless and non-systemic infections for the distribution of the pathogen.

P. halstedii may also be wind-borne and causes secondary infection of leaves and/or inflorescence. The secondary infection of inflorescence may give rise to latent infection of seeds (Sackston, 1981). Vida (1996) reported that secondary infection by zoosporangia was numerous in some Hungarian fields in 1995 and 1996. The secondary infection is considered as an important factor in the spreading of the disease in certain regions under favourable environmental conditions.

Seed Borne Aspects

Plasmopara halstedii has been found to occur in sunflower seeds from naturally infected plants, either as mycelium or oospores (Novotelnova, 1966). Cohen and Sackston (1974) reported that the pathogen may be present with the seed in three ways i.e. oospores on the surface of the seed; oospores in internal parts of the seed; and mycelium in endosperm and embryo. Cohen and Sackston (1973b) confirmed that sunflower buds inoculated with *P. halstedii* became systemically infected and produced infected seeds at 15-30^{0}C. Oospores were

observed in seeds of inoculated and naturally infected plants in the field. Basavaraju *et al.* (2004) detected the oospores in seed coat and endosperm of systemically infected seeds and confirmed seed transmission of *P. halstedii* in sunflower. However, Doken (1989) reported that the mycelium was found only in the testa and inner layer of the pericarp; it was absent from the embryo. Seed infection regularly occurs in systemically infected plants if they survive up to the flowering stage.

Seed Health Tests

Different techniques for the detection of *Plasmopara halstedii* are as follows:

A. Seed Washing

Basavaraju *et al.* (2004) successfully detected the surface borne oospores of *P. halstedii* in infected seeds by washing test. They took 100 seed from each sample which were immersed in 20 ml of distilled water separately with a drop of Tween 20 and then shook for 10 min. The supernatant solution was discarded and the sediment was suspended in 2 ml of sterile distilled water. On examination of suspension from each samples under light microscope, they successfully detected the surface borne oospores in infected samples.

B. Seed Maceration Technique

Basavaraju *et al.* (2004) detected the fungus in seed and seed components also. They soaked 400 seeds from each sample in a solution of 5% of NaOH (v/v) mixed with Tryptophan blue (0.02% w/v) and incubated for 4 hour at room temperature (the optimum concentration of NaOH and the period for soaking they found). Subsequently, seeds were washed with hot water with agitation to separate different seed parts from each other. The seeds were dehydrated with 70% alcohol and boiled in lectophenol. The material was then transferred to fresh lactophenol. On examination under stereobinocular microscope, they detected the oospores and fungus hyphae of *P. halstedii* in both seed coat and endosperm of systemically infected seeds. They observed the fungus in the cotyledonary surface, plumule, radicle and seed coat also and suggested that the technique is simple and more precise, could be used for detection of *P. halstedii* in sunflower seeds at quarantine stations and even during shipment itself.

C. Blotter Test

Seeds were surface-sterilized, rinsed and placed on 3-4 layers of wet filter paper and were incubated at 25-30^{0}C to germinate them. After a few days of incubation when roots are formed, the fungus if present will sporulate on their surface under humid conditions, which can be observed under stereobinocular microscope. The slides can also be prepared and examined under compound microscope, if necessary. This sporulation may also occur with otherwise symptomless, latent infected plants (Gulya, 1995).

D. Molecular Techniques

P. halstedii can also be detected by immunological tests (Bouterige *et al.*, 2000a) and Polymerase Chain Reaction (PCR) techniques (Roeckel-Drevet *et al.*, 1999). Bouterige *et al.* (2000b) produced two monoclonal antibodies (MAbs) i.e. 12 C 9 and 18 E 2 by immunizing mice with a partially purified extract of *P. halstedii* race 1. Both Mabs detected all races of *P. halstedii* present in France in enzyme-linked immunosorbent assay (ELISA). On inoculation of seed homogenates from infected plants in wells coated with Mab 18E2 resulted in trapping of *P. halstedii* antigens that were identified with biotinylated Mab 12C9. No reaction was observed with seed homogenates from healthy plants. They suggested that these Mabs might be used to develop a sandwich ELISA detection system for detection of fungus in infected seeds of sunflower.

Roeckel-Drevet *et al.* (1999) developed a rapid assay to detect infection of *P. halstedii* in sunflower. Based on the nucleotide sequence information, they designed specific oligonucleotides and used as primers for *in vitro* DNA amplification by PCR. They detected an amplification product on agarose gel stained with ethidium bromide when DNA from various *P. halstedii* races was tested, whereas no amplified DNA was detected when DNA from other origin was tested. The assay successfully reveals the presence of the fungus in infected plants prior to sporulation also.

E. Fatty Acid Analysis

Spring and Haas (2002) reported that fatty acid analysis might become a diagnostic feature for the contamination of sunflower seeds with downy mildew. They also reported that a fatty acid composition of *P. halstedii* revealed a characteristic profile which was different from profile of all other parasitic and pathogenic fungi of sunflower by the dominance of 5Z, 8Z, 11Z, 14Z, 17Z-eicosapentaenoic acid.

Quarantine Risk

Downy mildew of sunflower is seed as well as soil-borne disease. Seeds play an important role in the dissemination of downy mildew from one place to another. The perusal of literature indicated that more than 20 different races/ pathotypes are prevalent in *P. halstedii* world over. Ram Nath *et al.* (1981) intercepted oospores of *P. halstedii* on sunflower seeds imported from Bulgaria while processing for quarantine clearance. Therefore, there is an inherent risk of introduction of the new race or more virulent strain of *P. halstedii* in the country.

Precautions

1. Quarantine regulations should be enforced strictly to restrict the introduction of infected seeds in the country from other countries.
2. Exporting countries should be requested to provide phytosanitary certificates declaring that the seeds are free from downy mildew.
3. Importation of seeds through letter post should be completely prohibited.
4. In case the research workers receive the seed samples directly from abroad they must send the sample to quarantine authority for quarantine clearance.
5. The imported seed should be grown in isolation in the post entry quarantine nursery to reduce the danger of introducing new race/pathotype or more virulent strains.
6. The seeds should be treated with a suitable fungicide to overcome to the risk for spread of the pathogen by latent infection.
7. Domestic quarantine should be enforced strictly in the country to restrict the internal movement of infected seeds among the states.

Disease Management

A. Cultural Control

Muresan and Vranceanu (1972) reported that the incidence of downy mildew decreased with increasing length of rotation (6-7 course rotation) and the incidence was negatively correlated with yield. Jimenez-Diaz (1973) also reported that the incidence of downy mildew in Spain was 15.6% in plots where wheat and sunflower was grown alternatively whereas it was upto 100% in plots without crop rotation. In India also, the disease intensity increased with continuous cultivation of sunflower in the same field (Mayee, 1988). He suggested the cultivation of an alternate crop as per suitable agro-system, roguing of mildewed seedlings during thinning, removal and destruction of diseased plants before flowering by burning and to avoid the seed multiplication in affected areas so as to get the seed from a disease free area for sowing purposes.

Early sowing of crops also suppressed downy mildew incidence and resulted in higher yields than crop sown in the season (Weldekidan, 1986). However, Patil *et al.* (1992a) reported that sowing dates had no effect on sunflower downy mildew in India but frequent rains immediately after sowing play an important role in the disease development and sunflower seedlings become resistant with age to the downy mildew infection. Application of 400 kg ammonium nitrate (AN) or 200 kg AN + 200 kg super phosphate/ha to sunflower also decreased local infection of mildew and increased the seed yield (Grinberg, 1976).

B. Chemical Control

Seed treatment with large number of protectant chemicals such as organo mercurials and thiram did not give encouraging results in France and Soviet Union. Szoko (1973) reported that seed dressing with vitavax 75 [carboxin] @ 500 g/100kg seed reduced infection from 30% to 50%. In Canada, Morocco, Romania, Turkey and former USSR metalaxyl (Ridomil 25 WP or Apron 35 SD) provided complete protection against the disease when the seeds were treated with the chemical @ of 3 to 6 kg/kg seed (Achbani *et al.*, 1996a;). In Spain, seed dressing with metalaxyl (1, 2 or 4 g a.i./kg) prevented *P. halstedii* sporulation on seedling inoculated by dipping root into a zoosporangial suspension (Melero-Vara *et al.*, 1982). In India also seed treatment with metalaxyl (as apron 35 SD) @ 6g/ kg seed gave the best control of downy mildew. Rhodex (fosetyl-aluminium + mancozeb) and fosetyl-aluminium also gave effective control of the disease (Patil and Mayee, 1988; Patil *et al.*, 1991). Chattopadhyay *et al.*, (1999) also reported that three foliar applications of metalaxyl + mancozeb also controlled the disease. However, Molinero-Ruiz *et al.* (2003a) reported the resistance of sunflower downy mildew to metalaxyl while studying the effect of seed treatment with metalaxyl at 0.5, 2.0 and 3.5 g a.i./kg seeds. Tosi *et al.*, (1999) reported that a novel synthetic chemical CGA-245704 [benzo (1.2.3) thiadiazole-7-carbothioic acid S methyl ester (acibenzolar-S-methyl) (BTH)] when applied as a soil drench @ 150 and 200

mg/ kg soil provided 80-82% protection from the disease. Application of CGA-245704 as soil drenching and foliar spray also protected sunflower plants from *P. halstedii*.

C. Host Resistance

The best method for control of downy mildew is the cultivation of resistant varieties. But the disease resistance may break down once the pathogen produces more virulent races. It is relatively easy to produce mildew resistant hybrids by crossing a cytoplasmically male sterile line with a fertility restoring line, if one of the parents is homozygous for resistance. Nine different genes Pl_1, Pl_2, Pl_3, Pl_4, Pl_5, Pl_6, Pl_7, Pl_8, and Pl_9 have been reported as resistant to downy mildew in sunflower by different workers (Sackston *et al.*, 1990). Vear and Leclarcq (1971) reported two independent dominant genes also (H1 and H2) from an American source of resistance to *P. halstedii*, which were different from Pl gene. Presently the Pl gene is being used to give mildew resistance in breeding programme in many parts of the world. A large number of resistant lines/ cultivars have been reported as resistant to downy mildew included from USA, Canada, France, Italy, Romania, Spain, Yugoslavia and Russia (former USSR) (Gulya *et al.*, 1991b; Seiler, 1993; Dedio and Rashid, 1994; Mouzeyar *et al.*, 1994; Molinero-Ruiz *et al.* 2003b;). In India also a number of sunflower cultivars possessing resistance to downy mildew have been reported (Patil and Mayee, 1988, 1990; Patil *et al.* 1992b; Manjula and Seetharam, 2000; Dandnaik and Deshpande, 2003).

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SHORT COMMUNICATION

Introduction of Exotic Barley (*Hordeum bulbosum* L.) for Potential Fodder and Disease Resistance Purposes in Uttarakhand

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Key words: Exotic barley, *Hordeum bulbosum*, Potential fodder, Disease resistance, Uttarakhand

The introduction of exotic germplasm has enriched Indian agriculture since time immemorial. India has a sizeable area under saline and alkaline condition and the crops cannot be grown successfully in such problematic areas. Therefore, the emphasis is given, for the introduction of germplasm having quality traits for value addition and also sources of resistance for various diseases, insects, pests and biotic stresses. One accession of *Hordeum bulbosum* having quality traits such as potential fodder and disease resistance was introduced in Uttarakhand Himalaya.

Hordeum L. belongs to the family Poaceae (Gramineae). *Hordeum* comprises nearly 32 species and 45 taxa. Some of the important species such as *Hordeum vulgare, H. spontaneum, H. bulbosum, H. murinum, H. pusillum, H. intercedens, H. euclaston, H. flexuosum, H. muticum, H. chilense, H. cordobense, H. sterostachys, H. jubatum, H. comosum, H. lechleri, H. procerum, H. arizonicum, H. halophilum, H. seelinum, H. capense, H. bogdanii, H. roshevitzii, H. marinum, H. brevisubulatum* and *H. brachyantherum* are recorded in the literature (Roland *et al.*, 1991).

Among above cited species of barley, *Hordeum vulgare* is widely cultivated throughout mountainous region of Himalaya including Uttarakhand. In 1996, *Hordeum bulbosum* (EC328175) was received from Russia at NBPGR Regional Station, Bhowali, Uttarakhand, along with other exotic barley collections for characterization, seed increase, maintenance and acclimatization.

Plant has luxuriant and vigorous growth (150 cm to 178 cm); culm is erect to some what geniculate; nodes are glabrous, pale sometimes brownish; basal internode bulbous, 1-4 bulbs per culm, ellipsoid, ovoid, sometimes pyriform; lowermost bulbs usually well developed 2-3 cm x 1-1.5 cm; leaves flat; flag leaf-18.5-29.2 cm, leaves-light green in colour, leaf surface with soft hairs especially on the adaxial side; auricles up to 5.7 mm long often completely surrounding the culms.

Spikes generally 12.5-14.2 cm long; awn 2.5-4.7 cm long; anthers yellow to violet in colour; spikes green to greenish-violet; the number of grains 3-7 per spikes.

H. bulbosum is diploid and tetraploid (2n=14 and 28). Due to its diploid and tetraploid nature, the seed setting per spike is very low (3-5 grains per spike). Generally vegetative reproduction through bulbs is considered more successful for large-scale cultivation for fodder purposes, In wild state, *H. bulbosum* is generally found as perennial in Mediterranean region and eastwards to Afghanistan and Southern USSR. The diploid type is found in Greece and Egypt and the tetraploid type is found in Southern Spain. It grows well in wet meadows. Under irrigated condition, the plant growth is luxurious and vigorous and three harvests can be made yearly.

An experiment was conducted for acclimatization and herbage yield for fodder purposes. It yielded 200 q/acre/year green fresh herbage. Domestic animals used to graze it very gracefully. It is a perennial source of green fodder, especially during winter when no grasses are available in the Uttarakhand.

It is highly resistant to yellow rust (*Puccinia striiformis*), powdery mildew (*Erysiphe graminis*) and loose smut (*Ustilago nuda*).

Hordeum bulbosum has been well acclimatized in the sub-temperate climate of Uttarakhand. Its bulbs are available to the farmers for fodder purposes. Breeders can use it in their breeding programme as a disease resistant donor.

Reference

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SHORT COMMUNICATION

IC 259084 – A New Early Maturing Productive Genotype of Cowpea

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Key words: Cowpea, Genotype, Disease resistance

Cowpea is a dual purpose pulse crop of arid and semi-arid regions of India and world. Its grain is consumed by humans, while vegetative part is the principal component of cattle feed. It is thus an indispensable component of farming system. The productivity profile is very low mainly because of lack of disease resistant productive varieties in cowpea.

Cowpea germpalsm (169 genotypes) received from NBPGR, New Delhi were evaluated in RCBD with two replications during rainy seasons of 2004 and 2005 at the Department of Genetics and Plant Breeding, University of Agricultural Sciences (UAS), Dharwad. Each genotype was planted in two rows with check entries GC-3 and C-152. The observations on disease incidence was taken at three different stages of crop duration. Disease scale (0-9) was used to assess the disease and its incidence (Mayee and Datar 1986). Out of 169 lines, the most elite 20 genotypes were selected based on their productive characters and disease resistance (Lesly *et al.*, 2005) for further hybridization programmes. The performance of these genotypes are given in Table 1 and Table 2 in comparison with checks.

From this evaluation, among the 20 genotypes, the most promising genotype IC259084 was identified as an early maturing genotype with productivity of 1855 kg/ha. It took less than 62 days of physiological maturity (Table 3).Its yield level was 10% higher than state check C-152 and National Check GC-3. It grows to a height of 42 cms, flowers within 45 days after sowing. The duration of flowering and maturity is 10 to 18 days lesser than C-152 and GC-3. Its flower colour is mauve-purple. Thus it has the ability to escape terminal drought. The productivity components like number of clusters per plant and number of pods per plant are higher in IC259084 variety than the checks. The key morphological features of IC259084 are provided in Table 4. Diseases are another

Table 1. Means of productive characters of elite cowpea lines with checks

Genotype	Plant height	Days to flowering	Clusters/ plant	Pods/ plant	Pod length	Seeds/ pod	100 seed weight	HI	Yield/ plant
IC97767	39.0	68.0	12.0	20.0	15.5	14.0	12.6	0.27	23.5
IC97829	41.5	77.0	12.0	20.0	12.5	12.0	10.5	0.21	11.5
IC202778	42.5	73.5	5.5	7.5	13.5	11.0	14.9	0.18	12.8
IC202779	44.5	70.0	5.0	6.0	14	11.0	19.8	0.19	13.3
IC202781	40.5	70.5	4.0	4.5	14	11.0	19.8	0.10	8.3
IC202782	41.5	73.0	8.5	6.0	11.5	11.0	9.4	0.23	10.9
IC202786	49.5	74.0	5.5	7.5	11.5	10.5	19.1	0.11	10.2
IC202797	42.5	78.5	11.5	13.0	12	11.0	17.0	0.29	25.3
IC214836	37.5	72.0	6.0	12.0	15.5	13.0	12.1	0.17	12.1
IC219607	37.5	65.0	8.5	10.0	12	10.5	10.7	0.19	11.1
IC243353	37.5	69.5	5.0	10.5	13	11.5	11.1	0.20	12.1
IC259081	38.0	67.0	8.5	16.0	18	11.0	13.6	0.24	20.1
IC259085	53.5	69.5	10.5	15.5	13	11.0	11.1	0.19	19.5
IC202784	40.0	72.0	6.5	8.5	13	11.0	21.0	0.19	14.5
IC68786	41.5	64.5	8.0	18.5	12.5	10.9	10.9	0.25	23.5
IC259084	42.1	44.7	12.6	17.2	13.1	11.4	14.4	0.23	27.4
EC394805	39.5	69.0	5.5	14.0	14.5	8.5	20.0	0.20	12.9
Goa local	46.0	71.0	6.9	15.0	14.5	12.7	12.8	0.24	20.5
Bailahongal local	47.3	74.5	11.6	17.5	13.0	10.6	10.7	0.22	17.8
V118	50.0	56.5	15.0	25.5	14.5	10.0	13.9	0.17	11.8
C152	47.5	52.5	8.5	13.5	12.5	10.5	10.5	0.25	16.4
GC3	47.4	60.7	12.2	15.0	12.5	11.5	14.1	0.23	13.8

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Table 2. Disease resistance and other characters of elite cowpea lines with check

Genotypes	Growth	Physiological	Disease Resistance				Seed characters		Intra Cluster Distance	
	Habit	Maturity	YMV	Rust	BLB	PM	Colour	Size	Season 1	Season2
IC 97767	IS	72.5	R	R	R	MR	Dark Brown	M	23.72	24.74
IC 202797	IB	81	HS	R	MR	MR	Brown	L	28.68	27.39
IC 243353	D	76.5	HS	HS	HS	S	Brown	M	0.00	25.88
IC 259081	IB	75.5	HS	MR	HS	S	Dark Brown	M	20.31	30.53
IC 259085	D	76	HS	S	S	S	Cream	M	27.76	27.75
IC 97829	IB	85	R	HS	S	MR	Brown	M	24.69	0.00
IC 202778	D	79	HS	S	MR	MR	Brown	L	28.36	25.41
IC202782	D	81	S	MR	M	MR	Cream	M	23.33	22.75
IC 214836	IB	81	HS	S	MR	S	Ash	M	22.13	26.80
IC 219607	IB	76.5	S	R	MR	S	Cream	M	24.94	27.47
IC 68786	IS	71.5	HS	R	MR	S	Cream	M	23.55	25.97
IC 202779	D	73	S	S	HS	S	Brown	L	28.68	26.33
IC 202781	IB	79	HS	S	S	MR	Brown	L	22.13	29.77
IC 202786	D	81	HS	MR	S	MR	Brown	L	26.27	24.59
IC 202784	IB	79.5	S	MR	S	MR	Brown	L	28.24	26.99
IC 259084	D	62.0	R	MR	MS	MR	Cream	M	28.24	28.99
EC 394805	IS	81	S	S	MR	S	Brown	L	25.81	25.97
Goa Local	IS	77	S	MR	S	MR	Brown	L	25.47	25.18
Bailahongal local	IB	77	MR	S	S	MR	Brown	M	0.00	25.97
V118	D	65.5	S	MR	MR	S	Cream	M	0.00	28.99
C152	IB	74	HS	HS	MR	S	Brown	M	24.86	28.22
GC3	D	85.5	S	S	S	MR	Cream	M	24.86	28.22

D:Determinate, IB:Inderminate bushy, IS indeterminate spreading, S:Susceptible, HS:Highly susceptible, R:Resistance, MR:Moderately resistance L:Large, M:Medium, S:Small YMV: Yellow mosaic virus, BLB: Bacterial Leaf Blight, PM: Powdery mildew

Table 3. Mean performance of cowpea genotype IC259084 along with check varieties during 2004 and 2005

	Plant height	Days flower Initiation	Days flower termination	Physio logical Maturity	No.of Branches/ plant	No.of Clusters/ plant	No.of Pods/ plant	Pod length	Seeds/ pod	Test weight	Harvest index	Yield Kg/ha	% increase over check
IC259084	42.07	44.75	58.0	62.0	4.1	12.67	17.23	13.14	11.43	14.47	0.23	18.55	10.77
C-152	47.16	52.50	66.0	71.5	4.4	9.35	15.55	13.77	11.65	12.16	0.25	16.44	
GC-3	47.62	60.75	74.5	80.75	4.95	12.27	15.55	12.65	11.60	14.10	0.23	15.33	

Table 4. Key morphological features and disease reaction of cowpea genotype IC259084

Genotype	Seed colour	Seed size	Plant type	Flower colour	Rust	Yellow Mosaic Virus	Bacterial Leaf Blight	Powdery Mildew
IC 259084	Creamish white with black eye	Medium	Determinate	Mauve purple	Moderately resistant	Resistant	Moderately susceptible	Moderately resistant
C-152	Brown	Medium	Semi determinate	Mauve purple	Highly susceptible	Highly susceptible	Moderately resistant	Susceptible
GC-3	Cream	Medium	Indeterminate	Mauve purple	Susceptible	Susceptible bushy	Susceptible	Moderately

challenge to cowpea production. Rust and mosaic virus are most destructive diseases. IC259084 is highly resistant to mosaic virus, moderately resistant to rust and powdery mildew and moderately susceptible to bacterial leaf blight compared to other two checks. The plant type of IC259084 is determinate which is a highly desirable attribute in this crop. The seeds are creamish white in colour with black eye spot and are medium sized with 100 seed weight of 14.47 gms.

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SHORT COMMUNICATION

Development of New Rice Ideotype

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In rice, ideotype breeding is believed to offer great opportunities to enhance the yield potential (Khush, 1984). Since the release of the semi-dwarf high yielding rice variety IR8 by the International Rice Research Institute (IRRI), Philippines, rice yield potential has remained constant (Singh, 1998). The narrow genetic base of the varieties used in breeding progammes seems to be the most important reason for the yield plateau. So broadening the genetic base of future rice varieties is imperative in breeding programmes.

A research programme was carried out in the Department of Plant Breeding and Genetics, College of Horticulture, Kerala Agricultural University with an objective to develop a rice ideotype through distant hybridization. Initially 56 high yielding diverse rice genotypes representing various eco-geographical conditions prevailing in Bangladesh, China, India, Indonesia, Malaysia, Pakistan, Philippines and Srilanka were evaluated for 32 different quantitative and qualitative characters and grouped into nine clusters using Mahalanobis D^2 statistics. The design was RBD with three replications.

Twelve genetically diverse photo insensitive genotypes representing the nine clusters were selected as parents for hybridization programme. They are Mattatriveni, Bhadra, Hraswa, Mahsuri, Vytilla 3, Karthika (Kerala), IR36, IR62030-18-2-2, IR60133-184-3-2-2 (IRRI), Kachsiung SenYu338 (Taiwan); PK335-5-1-4 (Pakistan) and S-9768-PN-25-1 (Indonesia). The selected 12 genotypes were subjected to full diallel crossing (including reciprocals). Twenty two good performing F_1 hybrids were advanced to F_2 generation.

Out of 22 F_2 generations evaluated, the F_2 progenies of the cross combination Karthika x Bhadra showed very little segregation with respect to all phenotypic characters. Most of the progenies of this particular cross combination were similar to F_1 progenies. This was the case in the later generations also. The parents Karthika and Bhadra belong to clusters of the minimum inter cluster distance. Closer relationship between parents together with tight linkage between favourable characters might have resulted in the evolution of an excellent recombinant with early stabilization. Figure 1 shows the panicle vigour of the culture compared to its parents.

The newly developed rice culture (Culture 34) exhibited most of the ideotype features proposed by IRRI. The essential features of the new ideotype in rice proposed by IRRI (Khush, 1984) are low tillering capacity with 3-4 panicles/plant when direct seeded, no unproductive tillers, 200-250 grains/panicle, 90-100 cm height, sturdy stem, vigorous root system, multiple disease and insect resistance, 110-130 days growth duration, harvest index of 0.6 leading to an yield potential of 13-15 ton per hectare. The variety Karthika is a medium duration variety with medium height, straw-coloured lemma and palea and with red kernel. The grain shape is elongate. The variety Bhadra is a long duration variety with short stature, lemma palea colour is brown furrows on straw background, grain shape is bold and with red kernel. The Culture 34 (Karthika x Bhadra) is with medium height, medium duration, straw-coloured lemma palea, long bold grain with red kernel. The yield performance of this line is 7.5 t/hectare which can be increased to the proposed ideotype level of 13-15 ton per hectare by adopting best management levels recommended for yield potential threshold. The average yield performance of most of the popular high yielding varieties in Kerala is 3.3 ton per hectare. Harvest index of the newly developed culture is 0.594 with 224 grains per panicle, 28 tertiary branches per panicle, 10 panicles per plant (for transplanted crop), 1000-grain weight is 26.1 g, duration is 124 days with height 88 cm. One peculiar character of this newly identified rice ideotype is the persistence of dark green colour of leaves even at the time of harvest which shows the extended period of its photosynthetic efficiency and efficient source sink relationship till the time of maturity. This particular nature in turn will help in the increase of grain weight and ultimately the production. Erect stature with non-lodging character is another peculiarity of this culture. Moreover, the art of plant breeding was clearly seen in this culture with beautifully oriented panicles

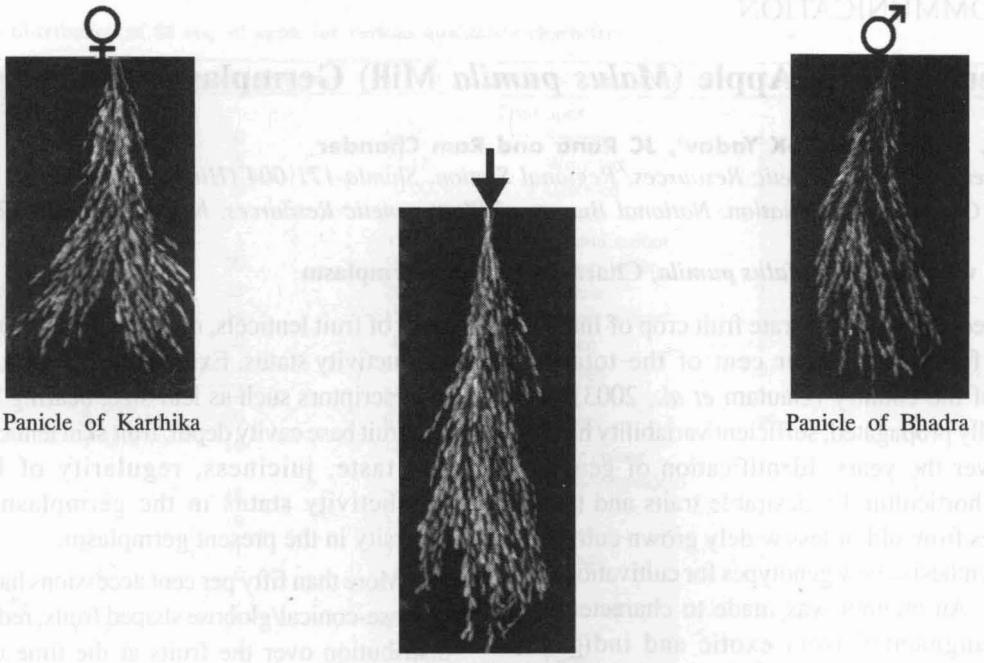

***Fig. 1:** Panicle vigour of the culture 34 compared to its parents*

***Fig. 2:** The newly developed rice culture 34*

and leaves (Fig. 2). The presently developed new rice ideotype have good quality characters like intermediate amylose content (24.2 %), red kernel colour and long bold size which are the quality aspects preferred by the people of Kerala. This culture showed tolerance to stem borer and thrips. This culture is in the pipe line of variety release.

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SHORT COMMUNICATION

Characterization of Apple (*Malus pumila* Mill) Germplasm

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Key words: Apple, *Malus pumila*, Characterization, Germplasm

Apple is a predominant temperate fruit crop of India and it accounts for about 10 per cent of the total fruit production of the country (Gautam *et al.*, 2003). Even though clonally propagated, sufficient variability has been generated over the years. Identification of genotypes which carry horticulturally desirable traits and transfer of these genes from old or less widely grown cultivars is essential to synthesize new genotypes for cultivation (Way *et al.*, 1990). An attempt was made to characterize 88 accessions augmented from exotic and indigenous sources, with easy and quick identification of phenotypes and correlate with practical utilization.

Present study was carried out at field gene bank of National Bureau of Plant Genetic Resources (NBPGR), Regional Station, Phagli, Shimla (31°05' 924" N latitude, 77°09' 580" longitude, 1924 m asl). Eighty eight accessions comprising 76 exotic (from 14 countries) and 12 indigenous were taken up for the present study. All the accessions were 8-12 years old, maintained with the spacing of 3.5x3.5 m. Observations were recorded on 15 qualitative characters (Table 1) and eight quantitative characters (Table 2). Total soluble solids (TSS) in the fruit pulp were measured by using Digital hand-held pocket refractometer 'PAL-1'. Descriptor states for qualitative characters were followed as per the descriptor developed by NBPGR (Mahajan *et al.*, 2002). Fruit data were recorded by randomly selected ten fruits from each accession. Mean values of three years (2002-2004) evaluation data were taken in to consideration to draw the conclusion. Frequency distribution of qualitative characters and variability parameters in quantitative characters were also worked out.

Characterization of germplasm (Table 1) indicated that out of 15 qualitative characters, absolute frequency was high (>70 %) for regular flowering, followed by smooth fruit apex. More than half the entries had upright tree habit, weak tree vigour, medium leaf size, broad-elliptic leaf shape, green-yellow fruit ground colour, low level of fruit lenticels, medium level of juiciness and low productivity status. Existence of all the descriptor states of descriptors such as leaf size, bearing habit, fruit base and fruit base cavity depth, fruit skin lenticels, pulp texture and taste, juiciness, regularity of flowering and productivity status in the germplasm indicate rich diversity in the present germplasm.

More than fifty per cent accessions had either conical/globose-conical/globose shaped fruits, red/dark red colour distribution over the fruits at the time of maturity and medium sweet/sweet fruit taste. More than one third of the accessions had borne fruits in spurs, which can offer immense scope for high density planting along with quality fruits. Eight accessions were found to be acidic and could be used for making sauce or slices. Thirteen accessions showed absence of lenticels on the fruit skin.

Fruit weight ranged from 31.9 to 181g and exhibited a maximum coefficient of variability of 34.3 per cent (Table 2). The traits *viz.* fruit length and width also showed a considerable amount of variation (16.60 per cent). There lies two months difference in fruit maturity of the germplasm studied. The present holding had extra early and early maturing accessions; no late maturing variety after third week of August were available in the present germplasm. This warrants the need for introducing germplasm of late maturing types to prolong the market potential.

Wide range fruit maturity, fruit weight and TSS in apple were also reported by various workers (Chadha and Sharma, 1978; Om *et al.*, 1978). Numbers of promising accessions available for various quantitative characters are given in Table 2.

Variation was noticed in the present germplasm for various characters due to the involvement of material from different source countries and quantum of genetic improvement work put forth for the past 200 years. Characterization and evaluation for specific fruit quality characters and screening for abiotic and biotic stress

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Table 1. Frequency distribution of 88 acq. of apple for various qualitative characters

Descriptor/descriptor state	Code	Absolute frequency	Per cent
Tree habit			
Upright	3	50	56.82
Spreading	5	38	43.18
Drooping	7	0	0.00
Tree vigour			
Extremely weak	1	1	1.14
Weak	3	50	56.82
Intermediate	5	23	26.14
Vigorous	7	14	15.91
Very vigorous	9	0	0.00
Leaf size			
Small	3	13	14.77
Medium	5	59	67.05
Large	7	16	18.18
Leaf shape			
Oval	1	18	20.45
Ovate	2	19	21.59
Broad elliptic	3	51	57.95
Others	99	0	0.00
Regularity of flowering			
Regular	1	82	93.18
Biennial	2	4	4.55
Irregular	3	2	2.27
Bearing habit			
On spur	1	39	44.32
On shoot tips	2	16	18.18
On old shoots	3	5	5.68
Mixed	4	28	31.82
Fruit shape			
Globose	1	18	20.45
Globose-conical	2	25	28.41
Short-globose	3	0	0.00
Flat	4	13	14.77
Flat-globose	5	29	32.95
Conical	6	3	3.41
Long-conical	7	0	0.00
Intermediate conical	8	0	0.00
Ellipsoid	9	0	0.00
Ellipsoid-conical	10	0	0.00
Oblong	11	0	0.00
Oblong-conical	12	0	0.00
Oblong-waisted	13	0	0.00
Others	99	0	0.00
Fruit base			
Narrow	3	25	28.41
Intermediate	5	41	46.59
Broad	7	22	25.00
Fruit base cavity depth			
Shallow	3	37	42.05
Medium	5	34	38.64
Deep	7	17	19.32
Fruit apex			
Smooth	1	63	71.59
Wrinkled	2	4	4.55
Grooved	3	21	23.86
Others	99	0	0.00
Fruit ground colour			
Cream white	1	1	1.14
Yellow	2	11	12.50
Green yellow	3	44	50.00
Green	4	27	30.68
Orange	5	0	0.00
Red	6	5	5.68
Others	99	0	0.00
Fruit over colour			
Yellow (golden)	1	8	9.09
Pink	2	8	9.09
Green	3	5	5.68
Orange	4	3	3.41
Red	5	35	39.77
Dark red	6	18	20.45
Brown	7	6	6.82
Purple	8	3	3.41
Dark brown	9	0	0.00
Others	99	2	2.27
Fruit skin lenticel			
Absent	0	13	14.77
Low	3	44	50.00
Medium	5	24	27.27
High	7	7	7.95
Pulp texture			
Soft	3	24	27.27
Intermediate	5	39	44.32
Firm	7	25	28.41
Pulp taste			
Acidic	1	8	9.09
Sub acidic	2	27	30.68
Medium sweet	3	42	47.73
Sweet	4	11	12.50
Juiciness			
Less	3	17	19.32
Medium	5	48	54.55
High	7	23	26.14
Productivity status			
Low	3	53	60.23
Medium	5	19	21.59
High	7	16	18.18

Table 2. Variability parameters and promising accessions for different quantitative characters in 88 apple accessions

Character	Range	Mean ± SE	CV (%)	No. of promising accessions
Start of flowering	March-April	–	–	–
End of flowering	March-April	–	–	–
Fruit harvest	June-August	–	–	6 (< 3rd June) 17 (1st fortnight of July)
Days to fruit harvest	90-137	115 ± 1.10	8.90	–
Fruit length (mm)	30.60-75.80	48.60 ± 0.90	16.60	2(>65)
Fruit width (mm)	29.90-80.90	55.90 ± 1.00	16.60	13(>65)
Fruit weight (g)	31.90-181.00	81.50 ± 3.00	34.30	7(>125)
TSS (%)	9.50-17.90	12.50 ± 0.20	13.30	10(>14)

tolerance will lead to rapid utilization of the conserved germplasm.

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SHORT COMMUNICATION

Evaluation of Exotic Rapeseed-Mustard Genetic Resources for Quality Characteristics

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Key words: Rapeseed-mustard, Evaluation, Germplasm, Quality characteristics

Because of known adverse effects of high erucic acid in oil (Ackman *et al.*, 1977) and glucosinolate content in seed-meal (Bille *et al.*, 1983) in rapeseed-mustard, reducing erucic acid up to 2 per cent (low) and glucosinolate content up to 30 μ moles/defatted seed-meal (low) and combining both the traits to develop double low varieties has been the focus of Indian breeding programme in recent years. The Indian cultivars are rich in erucic acid (30.9-56.7 per cent), low in oleic acid (6.7-22.6 per cent) and high in glucosinolates (41.0-108.9 μ moles), thus variability for desirable level of these traits is lacking in indigenous rapeseed-mustard genetic resources. Nevertheless, a few lines with low erucic acid and or low glucosinolate content have been registered with National Gene Bank at National Bureau of Plant Genetic Resources, New Delhi (Anonymous, 2004). In Australia, Europe and America, the double low varieties are largely grown though predominantly of rapeseed. Recently, a double low mustard variety has been released in Canada and many promising lines are available in Australia. Such exotic germplasm lines would serve as an important reservoir of useful gene(s) besides quality parameter. It is also expected that utilization of this gene pool would lead to broadening of the genetic base of Indian cultivars because of divergent nature due to diverse selection pressure in varied ecological conditions. Hence, there is need for evaluating the available exotic genetic resources to search for new sources for low and double low characteristics, agronomic characters for utilization in breeding programme to diversify the genetic base of indigenous available, lines/varieties.

The materials for the present investigation comprised one hundred thirty two exotic accessions of rapeseed-mustard grown in 3-row plots of 5-meter length during 2003-04 crop season in augmented design. The plant spacing was 30 x 10-15 cm. A fertilizer dose of 40:20 kg/ha of N and P_2O_5 was applied just before sowing and another dose of 40 kg/ha of N was top dressed after first irrigation. The plant protection measures were taken as and when required. Plant height was measured on 5 plants while days to maturity were computed on line basis. The open- and self-pollinated seeds of each accession were harvested. A composite sample of open-pollinated seeds was used to estimate oil and protein content by NIR (Kumar *et al.*, 2003). The self-seeds were used for fatty acid analysis by gas liquid chromatograph (Nucon Model 5765) using SP 2300 + 2310 SS columns. The detailed method for fatty acid analysis has been described elsewhere (Chauhan *et al.* 2002). ELISA Reader at 405 nm analyzed the glucosinolate content of the open-pollinated seeds from single plant following tetrachloropalladate method (Kumar *et al.* 2004). To assess variation, the range, mean and coefficients of variability (CV) for each character were computed using standard statistical methods.

The variability for various agronomic, oil and seed meal quality characteristics is presented in Table 1. The variability was maximum for glucosinolate content and minimum for oil content. The variability was low for days to maturity and protein content. Among the fatty acids, eicosenoic acid followed by erucic acid showed substantial variation (Table1).

Plant height and days to maturity showed moderate variation (Table1). The plant height ranged from 105 cm (EC511436) to 247 cm (EC511399). The genotypes showing short plant height were EC511436 (105 cm), EC511713 (116.0 cm), EC511663 (125 cm), EC511599 (130cm) and EC511589 (130.8 cm). The days to maturing varied from 131 days (EC511724) to 163 days (EC511794). The early maturity genotypes were EC511724 (131 days), EC511434 (133 days), EC511435 (134 days), EC511433 (135 days) and EC511-615 (135 days).

Palmitic and Stearic Acid

These are the saturated fatty acids and being hypercholesteremic (Mathur and Sharma, 1993), thus their excessive intake increases cholesterol level in blood

Table 1. Mean, range and coefficient of variability (CV) for various quality parameters and agronomic characters in exotic rapeseed-mustard germplasm

Character	Range	Mean ± SEm	CV (%)
Plant height (cm)	105.0–247.0	184.6 ±2.2	13.8
Maturity (days)	131–163	147.0 ±1.2	8.9
1000–seed weight (g)	1.2–4.6	2.0 ± 0.05	27.6
Oil content (%)	35.2–42.6	40.1 ±0.12	3.3
Protein content (%)	19.1–26.7	22.9 ±0.18	9.4
Palmitic + stearic acid (%)	1.3–5.0	3.5 ±0.05	16.2
Oleic acid (%)	11.0–40.8	32.3 ±0.72	25.6
Linoleic acid (%)	19.3–46.9	39.1 ±0.59	17.5
Linolenic acid (%)	7.0–36.3	18.6 ±0.33	20.7
Eicosenoic acid (%)	5.2–16.1	10.8 ±0.29	31.4
Erucic acid (%)	0–46.4	33.3 ±0.82	28.5
Glucosinolate content*	17.1–99.6	30.7 ±1.75	64.8

*μ moles / g defatted seed meal

consequently risk of coronary heart diseases. Preferred edible oil should have only upto 7 per cent saturated fatty acids. In this context, rapeseed-mustard oil is quite desirable since it contains low amount of saturated fatty acids. In the present collection, palmitic and stearic acid ranged from 1.3 (EC 511713)-5.0 per cent (EC 511678).

Oleic acid is a mono-saturated fatty acid (C 18:1) and contributes to increased shelf life of the oil by reducing photo-oxidation. It also plays an important role in reducing the cholesterol level in the blood (Grundy, 1986), a major component associated with coronary heart diseases. The desirable level of oleic acid is about 60 per cent in double low cultivars. However, oleic acid in the present collection was low and ranged from 11.0-40.8 per cent, the highest being recorded in the accession EC511429. Ten accessions showed moderate oleic acid (> 38.1 per cent) and their characteristics are presented in Table 2. In earlier studies, oleic acid has been reported to vary between 6.7-22.7 per cent in indigenous germplasm (Anonymous, 2003).

Linoleic and Linolenic Acid

These are the two polyunsaturated fatty acids and not naturally synthesized in the body. Linoleic acid (C18:2) plays an important role in the synthesis of prostaglandins, which regulate various body functions (Mathur and Sharma, 1993). Linolenic acid (C 18:3), although only present in rapeseed-mustard oil and pretty desirable but it also imparts instability to the oil and thus reduces shelf life. Linoleic acid in the present exotic germplasm accessions ranged from 19.3 per cent (EC511434) to 46.9 per cent (EC511517) with a mean of 39.1± 0.59 and CV of 17.5 per cent whereas linolenic acid varied from 7.0 per cent (EC511724) to 36.3 per cent (EC511411).

Table 2. Characteristics of germplasm lines having relatively high oleic acid content (> 38.1%)

Character	EC511408	EC511538	EC511534	EC511665	EC511563	EC511566	EC511460	EC511429	EC511704	EC511419
Plant height (cm)	196.0	195.0	186.0	174.0	180.6	144.3	179.3	192.0	200.0	199.8
Maturity (days)	146	152	145	147	155	157	143	137	156	151
1000-seed - weight (g)	2.0	2.0	2.2	1.8	2.1	1.8	1.8	2.0	2.0	1.9
Oil content (%)	38.7	40.4	40.0	40.4	40.6	41.1	40.1	41.0	40.9	40.4
Protein content (%)	23.1	23.1	22.4	24.4	22.6	23.1	22.4	21.5	24.2	23.6
Palmitic + stearic acid (%)	3.7	3.9	4.2	4.0	4.2	4.1	3.9	3.7	3.7	3.8
Oleic acid (%)	40.0	38.7	38.1	39.3	39.5	40.0	40.5	40.8	40.4	40.0
Linoleic acid (%)	39.6	39.2	44.4	38.8	38.9	38.4	39.0	37.0	40.4	36.8
Linolenic acid (%)	11.4	18.1	13.2	17.8	17.2	17.4	16.6	18.4	15.3	19.3
Eicosenoic acid (%)	5.2	NIL	NIL	NIL	NIL	NIL	NIL	Nill	Nill	Nill
Erucic acid (%)	< 2.0	< 2.0	< 2.0	< 2.0	< 2.0	< 2.0	< 2.0	< 2.0	< 2.0	< 2.0
Glucosinolate content*	17.1	17.5	19.8	18.1	19.7	19.1	19.6	77.6	22.1	29.8

* μ moles/g defatted seed meal

Eicosenoic and Erucic Acid

These are long chain unsaturated fatty acids and considered anti-nutritional because of their adverse effects. Eicosenoic acid (C20: 1) showed wide variation in the present collection (Table 1) and EC 511408 had the lowest amount (5.2 per cent). Nevertheless, it varied from 5.2-16.1 per cent. In previous studies a range of 4.4-15.0 per cent was reported for this fatty acid (Anonymous, 2003). Erucic acid (C 22:1) ranged from 0.0-46.4 per cent and varied substantially in the present collection. 111 accessions had desirable level of erucic acid (< 2 per cent) only 5 accessions showed erucic acid in the range of 41.0-46.4 per cent. In earlier studies a wide variation of 30.9-56.7 per cent was reported in indigenous rapeseed-mustard varieties (Anonymous, 2003).

The present collection of exotic rapeseed-mustard accessions showed wide variation for glucosinolate content, CV 64.8 per cent. The overall mean was 30.7± 1.75 with a range of 17.1-99.6 μ moles/ g defatted seed meal. 51 accessions had very low glucosinolate (< 20 μ moles / g defatted seed meal) and further, 46 accessions also showed desirable level of < 30μ moles / g defatted seed meal. Of these, 51 accessions also had < 2 per cent erucic acid.

Oil and Protein Content

The varieties with high oil content get premium in the market. Development of high oil yielding genotypes is the major breeding objective in rapeseed-mustard. The present collection showed very low variability for oil content (CV 3.3 per cent). Nevertheless, 11 accessions had relatively high oil content (> 41.5 per cent). Further, eight of these accessions were also of double low types (Table 3). Rapeseed-mustard seed meal is a protein rich feed. The seed protein content in the present collection varied from 19.1-26.7 per cent but the variability is low for this character. The high protein content lines were EC511448 (26.7 per cent), EC511714 (25.9), EC511632 (25.4 per cent), EC511633 (25.1 per cent) and EC511493 (24.7 per cent).

The present collections prove to be a reservoir of important double low traits of oil and seed meal quality. Of the 132 accessions, 51 possess desirable level of both glucosinolate content and erucic acid which could be utilized in the quality breeding programme to diversify the base of Indian available low/ double low advanced breeding lines.

Table 3. Characteristics of germplasm lines having relatively high oil content (>41.5%)

Accession	Oleic acid (%)	Erucic acid (%)	Glucosino-late content*	Protein content (%)	Oil content (%)	1000-seed weight (g)	Plant height (cm)	Maturity (days)
EC511413	15.4	29.3	74.7	19.1	42.5	3.6	212.0	141
EC511419	40.0	< 2.0	29.8	21.5	41.9	2.0	204.0	150
EC511507	33.6	< 2.0	18.7	23.6	41.9	2.0	176.3	147
EC511415	37.4	< 2.0	26.1	22.7	42.0	2.0	203.0	143
EC511568	36.7	< 2.0	18.3	22.7	41.6	2.3	206.0	159
EC511411	21.4	8.5	39.2	21.1	42.3	2.0	215.0	140
EC511478	33.4	< 2.0	29.6	21.1	41.6	1.8	200.0	143
EC511690	34.8	< 2.0	19.1	22.3	41.5	2.0	125.0	148
EC511407	26.9	< 2.0	28.6	21.9	41.9	2.2	205.6	142
EC511490	31.5	< 2.0	19.0	23.1	41.5	2.0	198.5	147
EC511433	21.8	39.9	22.0	19.9	42.6	3.8	155.0	135

* μ moles / g defatted seed meal

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SHORT COMMUNICATION

Genotypic Variability for Root Length in Soybean Germplasm

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Key words: Soybean, Genotypic variability, Root length

Soybean is the second most important oilseed crop of India. Yellow seeded soybean was introduced in India in 1963-64. Over a period of four decades there has been an exponential increase in area and production of the crop, but the productivity is stagnant at around one ton per hectare (Lal & Rana, 2000). The lack of soybean varieties to deal with terminal drought is the greatest handicap in the fight against the drought.

Soybean season in India spreads over four months. Usually, it starts with the onset of monsoon in the second fortnight of June and ends in the month of September. However, it might extend into the month of October, if there is delay in sowing. The analysis of rainfall and evapotranspiration data of Indore center shows that there is recurrent drought during the month of September, which affects grain formation resulting in low yield (Anonymous 2006). There is ample rainfall during the months of July and August; therefore, the crop has to survive on residual moisture during the month of September. Under the terminal drought, the water extracted by the root system and the efficiency of water use determines the amount of dry matter produced. Root length and density are important traits in inducing tolerance to drought. Indirect selection for drought can be made through these traits. Under similar conditions deep-rooted soybean has been found to be tolerant to drought in USA. A drought tolerant plant introduction (PI 416937) was identified in the USDA soybean germplasm collection and is characterized by tolerance to wilting during severe drought stress (Sloane *et al.*, 1990).

The studies on drought tolerance in soybean with respect to role of root system can be classified into three different areas, those related with screening of germplasm to study the variability for root length, those related with root growth models and predictions; and those related with efficient methods for studying the root system. Hida *et al.* (1995) studied differences in dry matter production and root system development between soybean cultivars under deficient soil moisture conditions. It is suggested that root system development may be responsible for the differences in ecophysiological characters. Mehetre *et al.*, (1997) studied correlation and path analysis studies of partitioning in root growth and yield characters in soybean (*Glycine max* (L.) Merrill).

Seventy-four genotypes comprising of eight early maturing (<85 days), thirty nine medium duration (86-105 days) and twenty-seven late maturing duration (>106 days); were analyzed at three different stages for studying the variation in root length and density in two different studies. Forty genotypes comprising of eight early maturing (<85 days), eighteen medium duration (86-105 days) and fourteen late maturing lines (>109 days) were grown in polythene bags (75 X 45 cm), with five replication during the first year. A set of 34 lines with 21 genotypes from medium maturity group and 13 genotypes from late maturity group were screened during the second year. Observations were collected at three different stages at 15, 30 and 45 days after sowing, for studying the variation in root length.

The results from first year of screening were subjected to statistical analysis. The analysis of variation among different accessions for root length revealed statistically significant variation in root length at all the three stages (Table 1). In the early maturity group mean root length was 38.71 cm with the maximum root length of 56 cm (Table 2). In the medium maturity group mean root length observed was 45.54 cm and the maximum root length was 58 cm. In the late maturity group the mean root length observed was 40.14 cm and the

Table 1. ANOVA for root length 45 days after sowing

Sources	Degrees of Freedom	Sum of squares	Mean squares	F value	Probability
Replication	1	92.99	92.988	6.888	0.012
Genotypes	3	9267.87	237.638	17.60	0.000
Error	39	526.54	13.500		

Coefficient of Variation: 10.05%

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Table 2. Variation in Root length (in cm)

Duration	Mean	SD	CV	Range	
				Minimum	Maxmum
Early maturity	38.7188	14.89213	38.46	23.0	56
Medium maturity	45.5417	12.07704	26.51	19.0	58
Late maturity	40.1428	17.23138	42.92	17.5	87

	15 days after sowing		30 days after sowing		45 days after sowing	
	Min	Max	Min	Max	Min	Max
Genotype	EC471522	EC458370	EC471510 EC471522	EC458370	EC471372	TGX1864-19F
Length	2.9cm	15.75cm	6.0cm	20.5 cm	15.75	87.0 cm

Table 3. ANOVA for root length (in cm) in 34 germplasm lines of soybean

Sources	Degrees of Freedom	Sum of squares	Mean squares	F value
Genotypes	33	20599.315	624.222	21.4215
Error	33	961.621	29.140	
Total	67	961.621		

Coefficient of Variation: 9.23%
CD: 5.39 cm

Table 4. Variation in root length (in cm) in 34 germplasm lines of soybean

Duration	Mean	SD	CV	Range	
				Minimum	Maxmum
Medium maturity	55.32	15.84	28.63	26.00	90.00
Late maturity	63.46	21.03	33.13	36.25	92.75

maximum root length observed was 87 cm. No significant correlation was observed between days to maturity and root length. The data for second year of screening was analyzed. Similar results were obtained in the second year also. There were significant differences between the root lengths of the genotypes screened. However, correlation between the root length and days to maturity was non-significant (Table 3 & Table 4). Similar results were reported by Turman *et al.*, (1995). They studied cultivar and planting date effects on soybean root growth.

From this study four promising early maturing lines with longer roots length (EC 471373, EC471514, EC471568 and EC 471585) were selected for use in the breeding programme for inducing resistance against terminal drought.

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SHORT COMMUNICATION

Karjat 6: A Medium Duration Quality Rice Variety for Maharashtra State

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Key words: Karjat 6, Resistance, Quality, Medium, Rice variety, Maharashtra

Rice is the second important food grain crop after Jowar in Maharashtra State. Total area, annual production and productivity of rice crop are 15 lakh hectares, 25 lakh tonnes and 1.7 ton per hactare respectively in the state. The rice crop is grown under varied agro-ecological situations with varied grain quality preferences of the farmers. There is a greater preference for fine grain varieties among the rice farmers in the state due to higher market prices and more demand of consumers (Anonymous, 2005). Keeping the requirements of farmers and trade efforts were made to develop a superfine and medium duration rice variety suitable for mid-lands in the state.

A cross was made between Heera and Karjat 184 using Heera as female parent at Regional Agril. Research Station, Karjat. The selections were made for super fine and high yielding progenies from the segregating generations. Among the several selections in segregating populations, a promising pure line KJT-12-6-25-9-13-50-13 was further tested in various trials on station, state and national programme, co-ordinated trials at various locations in the state and country. The culture was screened for resistance to various insect pests and diseases at endemic sites and quality parameters. The yield data of various trials were statistically analysed according to Panse and Sukhatme (1967). Based on yield data of various trials, superior grain quality disease and insect pest reactions and stable yield performance at various test locations, Karjat 6 (KJT-12-6-25-9-13-50-13) rice variety was recommended to release in the state of Maharashtra for commercial cultivation during the year 2005.

The yield performance of Karjat 6 (IET-19032) rice variety in various trials conducted during 2000 to 2004, is presented in Table 1. Karjat 6 (KJT-12-6-25-9-13-50-13) rice variety recorded 8.57 and 5.26 per cent increase in grain yield over check Mahsuri in Initial and Advance variety trials (station) during *kharif*-2000 and 2001, respectively at Regional Agril. Research Station, Karjat (Anonymous, 2001). The variety showed 10.34 and 33.33 per cent increase in yield over check during *kharif* 2002 and 2003, respectively in state co-ordinated trials conducted at nine locations in the Maharashtra state (Anonymous, 2003).

The above rice variety was evaluated in All India Coordinated Initial Variety Slender Grain Trial at 22

Table 1. Yield performance of Karjat 6 (IET-19032) in different trials and demonstrations*

Particulars	Year (t/ha)	Average grain yield		Per cent increase over check
		Karjat 6	Check	
Initial Station trial (1 location)	2000	3.8*	3.5	8.57
Advance Station trial (1 location)	2001	4.0*	3.8	5.26
Initial State Co-ordinated trial (9 locations)	2002	3.2*	2.9	10.34
Advance State Co-ordinated trial (9 locations)	2003	3.6**	2.7	33.33
AICRIP trial SG (22 locations)	2004	3.7*	3.5	5.71
Adaptive trial (19 locations)	2004	4.9**	3.8	28.95
Agronomical trial (1 locations)	2004	4.0**	3.2	25.00
Average		3.88	3.34	16.16

(Anonymous, 2005);

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

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Table 2. Salient features of the rice varietj Karjat 6 (KJT-12-6-25-9-13-50-13)

Character	Particulars
Duration (days)	130-135 days (*kharif*) 135-140 (*rabi*-hot weather season)
Plant height (cm)	95-100
Lodging	Non-lodging
Panicle length (cm)	20
Spikelets/ panicle (nos)	190-200
Test weight (1000 kernel weight)	13.30 g
Plant type	Compact
Awns	Absent
Panicle threshability	Easy
Shattering	Non-shattering
Scent	Absent
Average grain yield (t/ha)	3.5-4.0
Potential yields (t/ha)	7.0-8.0
Milling (%)	68.1
Head Rice Recovery (%)	65.0
Kernel Length (mm)	5.51
Kernel Breath (mm)	1.80
Length and Breath ratio	3.06
Kernel chalkiness	Absent (translucent)
Grain type	Short slender
Kernel elongation length after cooking (mm)	8.1
Alkali spreading value	4.5
Amylose content (%)	25.43
Gel consistency (mm)	43
Reaction to disease and Insect pests	
Bacterial leaf blight	Resistant
Leaf blast	Resistant
Neck blast	Moderately resistant
Sheath rot	Moderately resistant
Brown plant hopper	Resistant
Stem borer	Resistant
Gall midge (Biotype-5)	Resistant

locations during *kharif* 2004 in the country. It showed an average increase of 5.71 per cent in grain yields over the check in these trials indicating it's wider adaptability in varied agro-ecological situations in the country (Anonymous, 2004). The variety recorded 28.95 per cent more grain yield over check in 19 Adaptive trials conducted on farmer's fields during *kharif* 2004. The field experiment on levels of nitrogen and spacing was conducted at Agril. Research Station, Palghar during *kharif* 2004. Rice variety Karjat 6 showed significant and highest yield at 150 kg N/ha (4.29 t/ha) and 20 x 15 spacings (4.19 t/ha) indicating responsive to cultural packages. The saline features of Karjat 6 recorded at the research station are presented in Table 2.

Karjat 6 is midlate in duration (130-135 days duration in *kharif* and 140-145 days duration in *rabi*/ hot weather seasons), Semi dwarf (95-100 cm plant height), short slender kernel type (S.S.), average 1000 kernel weight of 13.30 g with an average grain yield of 3.2 to 4.9 t/ha. The variety' is non-lodging and non-shattering type. The milling and cooking qualities of Karjat 6 rice variety was estimated at the Directorate of Rice Research, Hyderabad during the year-2004. It showed excellent kernel quality features like a popular quality rice variety check Samba Mahsuri (BPT-5204). The variety Karjat 6 showed higher milling (68.1 %) and head rice recovery (65.0 %). The kernel length (5.51 mm), kernel breadth (1.80 mm), length:breadth ratio (3.06) and translucent kernel observed to be an inherited traits in this rice variety which contribute to higher milling and head rice recovery in Karjat 6 (Bhattacharya, 1980). Karjat 6 recorded an intermediate amylose content (25.43 %) indicating better cooking qualities of kernels (Anonymous, 2004b) (Shobha Rani, 2003). The variety showed medium gel consistency (43 mm) and Alkali spreading value (4.5) like BPT-5204. The above observations indicate that the new variety. Karjat 6 meets the requirements of millers and consumers for higher monitory returns to farmers.

The rice variety Karjat 6 was screened for reaction to various diseases and insect pests at endemic locations in the state and country. The variety showed resistant to bacterial leaf blight, leaf blast and brown plant hoppers (Anonymous, 2004c,d). While, it recorded moderate resistance to neck blast, sheath rot, stem borer and gall midge (Biotype-5) under endemic test locations (Anonymous, 2001b).

In view of higher yields, superior grain quality and field tolerance to major insect pests and diseases, the rice variety Karjat 6 (IET-19032) recommended to release for commercial cultivation in the state of Maharashtra during the year 2005. It will meet the requirement of farmers and consumers in the state.

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SHORT COMMUNICATION

A Note on New Rice Varieties and Hybrids from Karjat, Maharashtra State

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Key words: Rice, *Oryza sativa*, Hybrids, Maharashtra

Maharashtra state contributes to 3.7 per cent area and 2.8 percent production of rice at national level. The total area under rice crop, total rice production and average productivity in Maharashtra state during the last decade has remained stable around 15 lakh ha, 23 to 24 lakh tones and 1.7 t/ha respectively. The productivity of rice crop in state during 60's was around 0.8 t/ha. It rose up to 1.7 t/ha by introduction, development and adoption of 51 new high yielding. rice varieties and coupled with improved packages of crop production (Agriculture epitome, 1997-98). The state has four agro-climatic regions, out of which 71 per cent area comes under the traditional rice growing area, characterised by assured and high rainfall conditions where rice transplanting is practiced where as in remaining 29 per cent area, rice crop is cultivated by non-traditional method i.e. by drilling under upland rained conditions. This was essential to develop different duration. high yielding and quality grain rice varieties and rice hybrids suitable for different ecosystems in the state so as to increase the production and productivity of the state. Following are the six new high yielding rice varieties and four rice hybrids developed at RARS, Karjat.

Karjat 1 (IC412923)

Karjat 1 is early duration rice variety maturing in 110-115 days. It is selection from a cross between Holmaldiga X IR 36, bred at RARS, Karjat by Prof. VH patil and his co-workers. It is dwarf variety (65 to 70 cm) with dark green foliage having short bold non scented kernel. 1000-grain weight: 24.0 g, high protein content (8.97 %) and high rice bran oil content (8.89 %). It is recommended for bacterial blight endemic pockets. It is resistant to BHP and bacterial blight at flowering stage and immune at vegetative stage. It is moderately resistant to blast and leaf scald. Non-lodging and non-shattering variety, seeding to 50% flowering period is 80 to 85 days. Average yield ranged between 3.5 to 4.5 t/ha. It was released by State Variety Release Committee in 1987.

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Karjat 2 (IC412924)

Karjat 2 is late duration rice variety maturing in 140 days and is developed by hybridization between RPW 6-17 (Phalguna) x RP 4-14 (Prakash) followed by pedigree method, bred at RARS, Karjat by Prof. VH Patil. It was tested under IET No. 12331. It is dwarf (100-105 cm), erect with dark green leaves, flag leaf disposition is vertical with medium size. leaf blade is narrow, less hairy and dark-green and panicles, are compact, dense with less sterility. The glume colour of the variety is yellowish, coleoptiles: white, awns: absent. The rice variety having long slender grains with translucent kernel with grain size is length (6.46 mm), breadth (2.05 mm). L/B ratio 3.23, I000-grain wt. 22.9 g. It can be successfully grown in soils where mid-late to late varieties are grown with either assured rainfall or with protective irrigation as followed in eastern part of Vidarbha region. The seed rate is 40 kg/ha. The average grain yield ranged between 4 to 4.5 t/ha. It is non-lodging and non-shattering variety, seeding to 50% (lowering period is 05 days. It is moderate y resistant Io stern borer and resistance to gall midge, blast and neck blast. It showed moderate resistance to brown spot and moderate susceptibility to BLB. It is released by State Variety Release Committee in 1994.

Karjat 3 (IC412925)

Karjat 3 is an early duration rice variety maturing in 110-115 days and is evolved by hybridization between IR 36 x KJT 35-3 followed by pedigree method of selection, bred at RARS by Prof. VH Patil and his co-workers. It was tested under IET No. 1248I. It is mid tall variety (95-100 cm height) with dark-green leaf blade and leaf sheath, having excellent phenotypic appearance, medium tillering abilitv and fully exerted compact panicle. The four characters are glume colour: straw, awns: absent, grain size (LxB): 5.78 mm x 2.54 mm, L/B ratio; 2.27. 1000-grain wt.: 24.00 g. It is having grain type: short bold, white belly: present translucent intermediate, milling recovery: 75 %, alkali value: 4.4, amylose per cent: 23.94 per cent. The varietv is suitable for rainfed uplands as

well as irrigated areas, cultivated during *kharif* and *rabi* season in Konkan region and eastern part of Vidarbha and is responsive to nitrogenous fertilizers. Seed rate for transplanting varies between 55-40 kg/ha and 60-70 kg/ha for drilling, average grain yield ranged between - 1.5 to 5 t/ha. The variety has erect plant type having non-lodging and non-shattering ability, duration from seeding to 50 per cent flowering is 85 days. It is resistant to blast, moderately resistant to bacterial leaf blight and brown spot. Karjat 3 rice variety is stress tolerant having wide adaptability and is released by the State Variety Release Committee in 1994.

Karjat 4 (IC412926)

Karjat 4 is an early duration rice variety maturing in 110-115 days having superfine grain type which is evolved hybridisation (IR 22 x Zinia 63) followed by pedigree method, bred at RARS. Karjat by Prof. VN Deshpande and his co-workers. It is tested under IET No. 14227. It is dwarf 75-80 cm), erect with dark green leaves: flag leaf disposition is vertical with medium size, medium tillering ability with excellent phenotypic appearance with, fully exerted compact panicle. It has glume colour straw, awns absent, grain size (LxB) 4.87 mm x 1.6 mm, L/B ratio 3.04, 1000 grain wt 10.5 g. This rice variety having short slender grain type with translucent and non-scented kernel. The hulling per cent is 79.10%, milling; 73.96%, head rice recovery: 70%, alkali value: 6.0 amylose per cent 20.45%. It is recommended for four districts of Konkan region under suitable environmental conditions where early duration rice varieties are grown during both the seasons *kharif* and *rabi* hot weather. The seed rate is 30-35 kg/ha. average grain yield ranged between 3 to 3.5 t/ha. It is non-lodging and non-shattering variety and the duration from seeding to 50 per cent flowering is 80-85 days. Karjat-4 rice variety is moderately resistant to leaf folder. Tolerant to moisture stress. It was released by State Variety Release Committee in 1998.

Karjat 5 (IC545081)

Karjat 5 (IC545081) is a medium duration (125-130 days) rice variety having long bold grain type and appeared to be a prominent, alternative to jaya evolved through selection form BR-827-35-3-1-1-1 by BV Ongale, BD Waghmode and others at RARS, Karjat which is tested under IET No. 18905 in AICRIP traits. It is mid tall in stature (110-120 cm), high milling percentage (77.5%) and 61.11 per cent head rice recover with 27.0 g 1000 grain weight. It has given average yield ranged between 5.0 to 5.5 t/ha and 6.5 to 7.0 t/ha straw yield. It showed multiple resistance to diseases and pests (HR Neck Blast, MR – Leaf blast, RTV, Brown spot and sheath rot and MR Stem borer. The leaf folder, HR whorl maggot, MT-WBPH and PPH). It was released for transplanted conditions during *kharif* season for commercial cultivation in rice growing areas of Maharashtra state during 2005.

Karjat 6 (IC545080)

It is mid late in duration (128-130 days) having short slender (superfine) with translucent kernels evolved through hybridization (Heera x Karjat 184) followed by pedigree method, bred by BV Ingale, BD Waghmode and others at RARS. Karjat was tested under IET No. 19032 in AICRP traits. It has 13.30 g 1000 grain weight, with 3.06 L/B ratio, grain without chalkiness, high milling (75.8%) and high head rice revovery (70.2%) per cent, intermediate amylose content (25.43 %) in grain, average yield ranged between 3.5 to 4.5 t/ha. It has multiple resistance to major diseases and pests. (HR-leaf folder, R-SBPH, MR-BPH, GMBS, leaf blast, neck blast, brown spot and sheath rot). It was released for transplanted conditions in *kharif* season for commercial cultivation in rice growing areas of Maharashtra during 2005.

Sahyadri (IC412927)

Sahyadri is midlate duration (125-130 days) rice hybrid developed by using CMS line (IR 58025A) and restorer line (BR 827 35-3-1-1-1-R), bred at RARS. Karjat by Prof. VN Deshpande and his co-workers. It is medium tall plant (115-120 cm) with intermediate habit, high tillering ability and well exerted panicle. Husk colour: straw, awns: absent, grain size (LxB): 7.18 x 2.39 mm, L/B ratio: 3.0 and 1000 grain weight is 28.0 g. Sahyadri has long slender translucent grain without white belly, slightly scented, hulling: 78%, milling: 67.3% and head rice revovery: 51.5%. It is recommended for rice growing districts of Maharashtra state including Kharland (coastal saline soils) in Konkan region. It is widely adopted in various agro ecological situations. It has given average yields rnaged between 6 to 6.5 t/ha. It is non-lodging and non-shattering plant: days required to 50 per cent flowering are 95-100 days. The rice hybrid is resistant to leaf blast and leaf scaled and moderately resistant to BLB. It was released by State Variety Release Committee in 1998 for commercial cultivation in Maharashtra state.

Sahyadri 2 (IC545072)

Sahyadri 2 is an early duration (115-120 days) rice hybrid developed by using CMS line (IR58025A) and restorer line (KJTR-2), bred at RARS, Karjat by Dr BV Ingale, BD Waghmode and others which is tested under IET No. 17661 in AICRP trials. It has better grain quality (LS) 1000 grain weight: 23.5 g, good milling (71.5%) and Head rice recovery (56%), intermediate amylose content (22.7%), yield potential 6.0 to 6.5 t/ha with multiple diseases and pest resistant (HR–false smut, MR–neck blast, sheath rot, BLB, RTV and stem borer). It is suitable for uplands and double cropped areas in the state. It was released for transplanted conditions in *kharif* season for commercial cultivation in rice growing areas of MS during 2004.

Sahyadri 3 (IC545076)

Sahyadri 3 is mid late duration (125-130 days) rice hybrid developed by using CMS line (IR 58025A) and restorer line (KJTR-3), bred at RARS, Karjat by Dr BV Ingale, BD Waghmode and others which is tested under IET No. 18829 in AICRP trials. It has better grain quality (LS) 1000 grain weight: 28.0 and good milling (74.5%) and head rice recovery (60.2%). Intermediate amylose content, grain chakiness: absent, optimum aroma, average grain yield ranged between 6.5 to 7.5 t/ha. It has multiple resistance to diseases and pests (R–blast, L–neck blast, MR–brown spot, sheath blight, sheath rot, and MR-stem borer, R–leaf folder, MR–WBPH and BPH). It is suitable for irrigated ecosystem in the state. It is released for transplanted conditions in *kharif* season for commercial cultivation in rice growing areas of MS during 2005.

Sahyadri 4 (IC545078)

Sahyadri 4 (KJTRH 2) is an early duration (115-120 days) rice hybrid developed by using CMS line (1K-5S025A) and restorer line (KJTR-I), bred at RARS,. Karjat by Dr. BV Ingle, BD Waghmode and others which is tested under IET No. 18610 in AICRIP- trials. The plant height of the rice hybrid is 100 cm with high panicles/m^2: 369. The rice hybrid Sahyadri 4 recorded average grain yield 5.5-6.6 t/ha in different trials conducted at national and state levels. The rice hybrid Sahyadri 4 having long slender grain type with 6.74 mm. Kernel length. 1.76 mm: Kernel breadth and 3.82 : L/B ratio. It has 69.4 % milling with High ASV (7.0) desirale AC (21.38 %), and soft GC (69 mm) and very occasionally grain chalkiness. Sahyadri -4 rice hybrid is moderately resistant to leaf blast, neck blast, brown spot and rice tungro virus. It has wider adaptability in different agro ecosystems in transplanted and direct sowing conditions at national level. Sahyadri 4 rice hybrid has been ideniificd for release for commercial cultivation in five states of the country *viz.*, Punjab, Haryana (North western region); Uttar Pradesh, West Bengal (Eastern and north eastern region) and Maharashtra (Western region), by the Central Varietal Identification Committee, during 41st All India Rice group meeting held at Hyderabad on April, 16th 2006.

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SHORT COMMUNICATION

Medicago scutellata – A Possible Source of Weevil Resistance for Lucerne Improvement

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Key words: ***Medicago scutellata*, Lucerne, Weevil resistance**

Alfalfa or lucerne *(Medicago sativa* L.) is a herbaceous, perennial legume that has often been called the "Queen of forages." It is the third most important forage crop in India and occupies more than one million hectare area and provides 60 to 130 tones green forage per hectare (Hazra, 1995). Lucerne is well-adapted to a wide range of climatic and soil conditions. It is relatively drought tolerant but also responds very well to irrigation. It tolerates some alkalinity, but does not perform well on highly-alkaline or salty soils. It is a perennial, out-crossing, autotetraploid crop domesticated presumably in the Near East (Iran, plain of Mesopotamia) and/ or in central Asia around 5000 BC.

The lucerne weevil (*Hypera postica*) is one of the primary insect defoliators of lucerne. This is the most damaging pest of lucerne, occurring in all the lucerne growing areas of the country and is particularly severe in north-western part, western Himalaya, Gangetic and central plains. Besides lucerne, it also damages sweet clover, peas, species of *Medicago* and *Mains* spp. The damage is mostly caused by the larvae that feed within the plant tips, on the young leaves and under heavy infestation the lower foliage is also consumed. The adults also feed on the foliage. Though difficult to estimate, the insects is estimated to reduce yields by 10 to 15% annually (Fig. 1a) where forage quality not taken into account (Pandey and Faruqui, 1990). A number of insecticides are available for control of this weevil, but due to inherent property of these chemicals to have residual toxicity, to non-target species and causing ecological disruptions, their use is restrictive. Integrated Pest Management (IPM) is a commonsense approach to crop protection. This concept relies on combinations of insect suppression and crop production techniques to optimize yield and quality. Developing resistant variety is an important aspect of IPM. However, earlier research conducted at IGFRI, Jhansi, has not yielded any lines of *M. sativa* showing reasonable level of weevil resistance. In order to search resistant material, germplasm of exotic species were procured and evaluated under hot-spot condition at Indian Grassland and Fodder Research Institute, Jhansi to identify and characterize the suitable genetic materials. Six accessions of *M. scutellata* (L.) Mill. along with 43 different species belonging to *Medicago* genus (data not given) were evaluated during 2004-05 and 2005-06. Genomic DNA from six accessions of *M. scutellata* was isolated from young, fresh leaves and PCR amplification was carried out as described earlier. The SSR amplification was performed by following the procedure of Diwan *et al.* (1997). Similarity matrices of both RAPD and SSR data sets were calculated using NTSYS computer software. SAHN clustering was used to construct the dendrogram employing UPGMA module.

Germination of all six accessions of *M. scutellata* was more than 90 % with intense flowering and seed setting. The level of infestation caused by weevil insect among the lines varied from 5-75 %. Accessions EC541686 and EC541685 showed 5 to 10 % infestations (Fig. 1b). The results indicate the presence of reasonable level of weevil resistance in these lines (Table 1). The identified weevil resistant lines of *M. scutellata* can be exploited in breeding with cultivated *M. sativa* for transferring the gene responsible for weevil resistance. It is generally agreed that the basic chromosome numbers for the genus *Medicago* are x = 7 and x = 8. Most species are 2n = 2x = 16, 2n = 4x = 32 or 2n = 6x = 48. The cultivated and perennial *M. sativa* is 2n = 4x = 32. Before

Table 1. Level of infestation and other details of different accessions of *M. scutellata* lines

Accession number	Per cent infestation
EC541685	75
EC541686	5
EC547738	35
EC543739	30
EC547740	10
EC547741	30

Fig. 1: *Highly weevil infested M. sativa plant (a) and No infestation observed on M. scutellata (b)*

1984, *M. scutellata*, was considered as annual and tetraploid with 2n = 32 (Simon and Simon, 1965; Lesins and Lesins, 1979). Thus, hybridization between this annual species and *M. sativa* may be possible because of their common ploidy level. The only successful hybridization between *M. scutellata* and *M. sativa* was reported by Sangdeun *et al.* (1982), who recovered one plant from the cross. However, this plant was chimeric and sterile. Contrary to the earlier report, Bauchan and Elgin Jr (1984) cytologically observed counts of 2n = 30 in *M. scutellata* at both mitotic and meiotic stages. Diploid accessions were not found and meiosis was normal with 15 bivalents forming at metaphase I suggested *M. scutellata* is an allo-tetraploid species. Further authors have suggested the presence of two pairs of SAT-chromosome in *M. scutellata* and probably this led to the erroneous counts of 2n - 32, recorded previously. Two hypothesis has been proposed for the development of a somatic number of 2n = 30, one is the hybridization of a 2n = 14 and a 2n = 16 species followed by the polyploidization of the hybrid. Another possibility would be the loss of a pair of chromosomes from a 2n = 32 polyploid. The gain of a pair of chromosomes is unlikely because a 2n - 28 species has not been found in the genus *Medicago.*

The next logical step in improving the *M. sativa* was to identify the two progenitors of *M. scutellata* and study the relationship among the genotypes of two progenitors of *M. scutellata* to pinpoint the most closely associated accessions of progenitors. Based on phenolic-taxometric studies *M. rigidula* (L.) All., *M. murex* Willd., *M. doliata* Carmian., *M. muricoleptis* Willd. and *M. rotata* Boiss. species showed a close relationship to *M. scutellata* (Classen *et al.,* 1982). Two of the species are 2n = 14 *(M. murex* and *M. rigidula)* and the others are 2n = 16. The presence of these species and close relationships *M. scutellala* suggest that 2n = 30 species may have arisen through hybridization followed by polyploidization (Bauchan and Elgin Jr., 1984).

Molecular analysis of six species of *M. scutellala* indicated variability among the lines. Four hundred ninety-nine RAPDs and 150 SSR markers when employed for analysis through unweighted pair group method with arithmetic mean (UPGMA) algorithm and dendrogram formed by Sequential Agglomerative Hierachical and Nested (SAHN) clustering showed two clusters by both marker systems (Figs. 2a, 2b). The

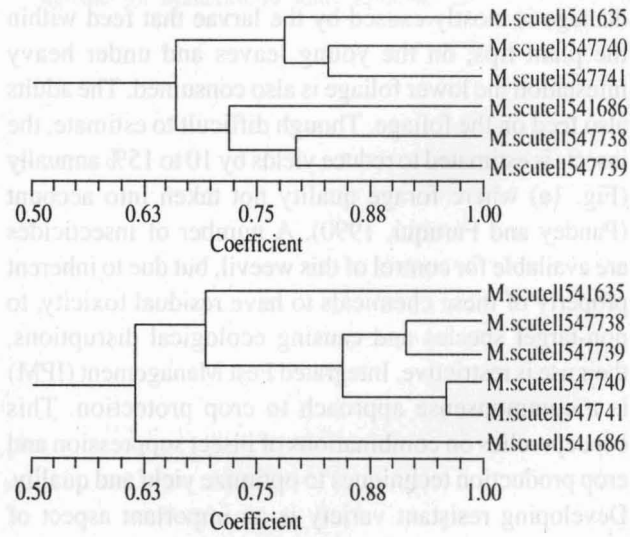

Fig. 2: *Dendrogram showing genetic ^elatedness among six accessions of M. scutellata based on RAPD (top) and SSR (bottom) markers*

genetic distance ranged from 0.58 to 0.96 with RAPD and 0.59 to 0.83 with SSR markers indicated large variability among the lines could be exploited in breeding programme.

Since the crosses between species with unequal ploidy levels have been successful due to the production of unreduced gametes (Bingham and Saunders, 1974) and the identification of weevil resistant *M. scutellata* having different ploidy to that of *M. sativa* can be used in attempting the crosses for introgression of weevil resistant genes. The results also indicated a reasonable level of genetic variability among the *M. sculellata* lines, better for crossing. If success rate of getting fertile plant is less, the biotechnological tools like embryo rescue can be attempted. Another possibility of getting resistant *M. sativa* (2n = 4x = 32) would be to cross the diploid *M. sativa* lines with the progenitors of *M. scutellata* especially those possessing 2n = 16 chromosome.

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BOOK REVIEW

Handbook of Industrial Crops

VLChopra and KVPeter (Editors) 2005

Food Products Press® and The Haworth Reference Press™, imprints of The Haworth Press, Inc., 10 Alice Street, Binghamton, NY 13904-1580. www.HaworthPress.com; ISBN 1-56022-283-2 (soft: alk.paper)

Ever since man took to agriculture from the *Neolithic Revolution* to the *Green Revolution,* the pressure has been building on increasing agricultural production and natural resources. As a result, this has triggered and unprecedented worldwide awareness of the importance of our natural reserves of plant genetic resources in different crops which includes industrial crops as well. The information on different industrial crops are scattered and not easily accessible without investment of considerable time and effort. Perhaps it is in this context the publication *Handbook of Industrial Crops* is timely and has greater relevance.

The *Handbook of Industrial Crops* presents the available information and research findings on twelve potential industrial crops. It is an attempt to bring together the available relevant information at one place. It examines all aspects of cultivation and trade in addition to the available information on the evolution and adaptation of twelve important industrial crops viz., areca nut (*Areca catechu*), cardamom (*Eletteria cardamomum*), cashew (*Anacardium occidentale*), cinchona (*Cinchona* sp.), cocoa (*Theobroma cacao*), coconut (*Cocos nucifera*), coffee (*Coffea arabica*), oil palm (*Elaeis guineensis*), palmyra (*Borassus flabellifer*), rubber (*Hevea brasiliensis*), tea (*Camellia sinensis*) and wattle (*Acacia mearnsii* and other species), each under a separate chapter written by eminent scientists and crop specialists. From food and drug industry products to palm oil and timber, this extensive resource provides detailed, up-to-date information on each species. Each chapter presented an overview on origin and evolution, botany, germplasm collection, genetic improvement, pests and diseases and future outlook. The well researched chapters contributes to better understanding of the challenges involved in maintaining and utilizing 'crop diversity' in these species within rapidly changing agriculture.

I am sure, the publication will serve as valuable reference for genetic resource scientists, crop growers, policy makers, teachers and students. Dr. VL Chopra and Dr. KV Peter, distinguished scientists and editors of this book deserves all our appreciation and congratulations for bringing out much needed volume on industrial crops.

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Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of **ICAR in its XVth meeting held on 29th July 2006** at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 47 germplasm lines out of the 135 proposals considered.

DWR51 (IC546940; INGR 06001), a barley (*Hordeum vulgare*) germplasm, with excellent malt quality

RPS Verma, B Sarkar and Sewa Ram
Directorate of Wheat Research, PB No. 158, Karnal-132 001 (Haryana)

A new two-row barley genetic stock DWR51, with better malting quality was developed recently through pedigree breeding method at Directorate of Wheat Research (DWR), Karnal. The genotype is a product of a cross between a two-row barley variety, BCU73 (exotic) with a popular six-row variety PL172 of Punjab. The evaluation of this genotype for three years under All India Coordinated Wheat and Barley Improvement Programme (AICW&BIP) during 2002-03 to 2004-05 crop seasons, showed that it possesses excellent overall malting quality as indicated by the weighted score with specific advantage for important individual grain and malt quality traits like test weight, germinative energy, husk content, grain beta glucan content, hot water extract, malt friability and wort filtration rate, when compared with check DWR28 (Table 1). DWR51 is a high tillering (186/meter) genotype with erect growth habit, medium height (88 cm) and medium maturity duration. The ear is parallel in shape with intermediate density. The ear and awn colour at maturity are light yellow. The leaf sheath and ear are waxy in nature. The grains are medium hard, bold and oval in shape. The average number of grains per spike is 26 with 47g per thousand grain weight. DWR51 is moderately resistant to yellow and brown rusts.

Table 1. Quality traits of DWR51 in comparison to check DWR28 in NWPZ

Traits	DWR51				DWR28 (C)				Desirable limits
	02-03 (8)	03-04 (8)	04-05 (7)	Mean	02-03 (8)	03-04 (8)	04-05 (7)	Mean	
Test weight (Kg/hl)	66.0	65.3	65.0	65.4	62.0	62	61.0	61.6	> 65
Bold (%)	71.0	88.4	87.0	82.1	87.0	91.3	92.0	90.1	> 90
G.E. (%)	98.0	96	97	97	71	90	97	86	> 96
Husk (%)	9.9	9.5	11.2	10.2	10.6	12.2	12.2	11.7	< 10.5
Protein (%)	12.8	12.3	12.2	12.4	12.1	12.3	12.2	12.2	< 11.0
Beta glucan (%)	4.2	4.8	-	4.5	4.9	5.5	-	5.2	< 5.0
H.W.E. (%)	78.2	77.8	79.4	78.5	75.9	74.5	77.4	75.9	> 80.0
Friability (%)	71	65	60	65.3	60	46	40	48.6	> 70
Filtration (ml/hr)	280	244	289	271	221	176	199	198	> 250
Viscosity (mpas)	1.596	1.519	1.533	1.549	1.761	1.721	1.744	1.742	< 1.500
Kolbach Index	0.35	0.40	0.44	0.40	0.34	0.38	0.45	0.39	0.40-0.44
Overall weighted score*	19	19	17	18.3	14	10	10	11.3	-

( ) = number of locations in each year; * = out of maximum possible score of 27

* *Communicated by Dr. Anurudh Kumar Singh, Member Secretary, Plant Germplasm Registration Committee, National Bureau of Plant Genetic Resources, New Delhi-110012*

VSR 8 (IC546941; INGR 06002), a Paddy (*Oryza sativa*) Germplasm, Resistant to Blast

JC Bhatt, CS Reddy, SN Sushil, VP Singh, HS Gupta and RK Sharma
Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora-263 601 (Uttarakhand)

A paddy germplasm VSR-8 was developed through pedigree method of breeding at IARI, New Delhi, from the cross IR 64/P1121-92-8-2-13. The seed initially was received by Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora, as AF2-2-3 in 1998 from IARI, New Delhi where further selections were made based on resistance from F2 onward. The selected resistant plant was multiplied at VPKAS, Almora and DRR, Hyderabad during *kharif* and *rabi* season. The resistant progeny obtained, was tested by the designation SRSN-8 at Almora in 2000 and afterwards by the name VSR-8. VSR-8 possesses good quality characters with intermediate plant height of around 110 cm, medium tillering ability of about 10 effective tillers per plant with well-exerted panicles. In hills it takes on an average 149 days to maturity. The average grain length and width (mm) is 10.46 and 2.48 respectively, with a grain weight of 25.3 g per 1000 grain. Grain yield per plant is 18.47 grams. The leaf length and width is 40 and 1.14 cm respectively (Bhat *et al.* 2003).

It has been evaluated at more than 14 different hot spot locations for leaf blast under Donor Screening Nursery (DSN) of All India Coordinated Improvement Programme of Directorate of Rice Research, Hyderabad (2001, 2002 and 2003). The average severity index of leaf blast for VSR-8 during the three years was 2.5 as compared to 6.45 in the susceptible check HR 12. It also showed tolerance to brown spot disease and scored 3 as against 5 and 7 in TN-1 at Gudlur and Hazaribagh in 2001. In addition, the genotype consistently exhibited neck blast resistance with multiple tolerances to stem borer and leaf folder in the tests at VPKAS, a hot spot location for blast. VSR-8 is therefore, a potential source of blast resistance with multiple tolerance in the medium aromatic background.

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NAP HAL (IC354308; INGR 06003), a Wheat (*Triticum aestivum*) Landrace/Traditional Variety, with Glu-D1 Double Null Trait Associated with Weak Gluten and Puroidoline

Sewa Ram, Jag Shoran, B Mishra and S Kundu
Directorate of Wheat Research, PB No. 158, Karnal-132 001 (Haryana)

NAP HAL, an Indian landrace of wheat, contains unique characteristic of double null trait at Glu-D1 locus i.e.; both the X and Y genes for high molecular weight glutenin subunits coded by the locus are absent (Sewa Ram *et al.*, 2003). The material was received from NBPGR, New Delhi with alternate identities PI 176217 and DWR ID No. 3674 in 1993 and subsequently grown and analyzed for genetic, molecular and quality traits at DWR, Karnal. In addition to double null at Glu-D1, NAP HAL exhibited null alleles at Glu-A1 while subunits 7+8 (Glu-B1b) were encoded at Glu-B1 locus. Double null trait at Glu-D1 in NAP HAL is unique in nature and is not available in bread wheat studied so far (Sewa Ram, 2003). It exhibits very low gluten strength as reflected in low sedimentation volume (16.0 cc, 6 g test), lower Farinograph peak time (2.0 minutes) and lower Farinograph tolerance (higher break down 140 BU) to mixing. PCR analysis of puroindoline genes showed the presence of both *pinA* and glycine type *pinB* associated with soft grain texture of wheat (Giroux and Morris, 1997; Sewa Ram *et al.*, 2002)). Wheat with soft grain characteristic and weak gluten are suitable for biscuit making quality (Sewa Ram and Singh, 2004).

On the basis of growth habit, NAP HAL can be grouped as facultative type wheat not exactly as spring wheat, with height around 95 cm. It is very late maturing with profuse tillering, weak stem, light green foliage, light red small size grains, awnletted long ear heads and

VSR 8 (IC546941; INGR 06002), a Paddy (*Oryza sativa*) Germplasm, Resistant to Blast

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On the basis of growth habit, NAP HAL can be grouped as facultative type wheat not exactly as spring wheat, with height around 95 cm. It is very late maturing with profuse tillering, weak stem, light green foliage, light red small size grains, awnletted long ear heads and

is susceptible to lodging. At Karnal, it produced shrivelled grains but the harvest from VPKAS, Hawalbagh located at an altitude of 1250 m produced fully plumped grains which were analyzed at DWR, Karnal for chemical, rheological and baking properties as per AACC methods. Therefore, it is adapted to hilly regions with low temperature conditions.

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TANK (IC398287; INGR 06006), Wheat (*Triticum aestivum*) Germplasm with Long Awns

Arun Gupta, Lakshmi Kant, Vinay Mahajan, HS Gupta and Hari Govind
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WH730 (IC546937; INGR 06007), a Wheat (*Triticum aestivum*) Germplasm, Tolerant to Heat

Iqbal Singh, RK Rana, SS Dhanda and Renu Munjal
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It has 110 cm height, dark green foliage; intermediate leaf width, takes 90 days in heading and 135 days in maturity. It does not show any waxiness throughout the growing season. The ears are white in colour, tapering and medium dense with average 1000-grain weight of 40 g. Also, WH 730 was found to have higher C TD (5.6) and keeps its canopy cool even under high ambient temperature. Therefore, it is expected to perform better under late sown environment and had shown higher grain yield in comparison to other genotypes under late sown conditions in All India Coordinated Multi-location Thermo-tolerant Trials (2004-05). Stomatal conductance and hence transpiration cooling has been found higher in WH 730 maintaining better water status. Leaf AGPase were also found to be higher

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The semi-dwarf wheat developed using 'Reduced height' (Rht) genes of Norin-10 have revolutionized production of wheat. Chaudhary Charan Singh, Haryana Agricultural University has made efforts to transfer Rht_1/Rht_2 genes from Norin-10-Nor-59, Olesen and S948A and Rht_3 from Tordo's into C 306, C 591, K 68, NP 846 and Kharchia 65 and develop dwarf near-isogenic lines. DI-717, a semi-dwarf plant ideotype of C 306 having Rht-3 gene. Hybridization between Indian quality wheat variety C 306 and Mexican germplasm lead to hybrid lethality due to complementary action of necrotic genes, Ne 1 and Ne 2, present in C 306 and Tordo's', respectively. Hence, C 306M10 (a mutant of C 306, which is non-carrier of Ne_1 and Ne_2 (ne_1 ne_2), but has grain quality like C 306 was chosen to incorporate reduced plant height gene (Rht_3) from Tordo's'. Restricted backcrossing (4) to recurrent parent C 306M10 was adopted. In following generation dwarf near isogenic lines were isolated. The cryptic genetic variability for spike traits was observed in stabilizing process. The grain quality of C 306M10 was maintained during restricted backcrossing and subsequent selection. Distinguishing features of DI-717 is reduced plant height (96 cm) of making it resistant to lodging, responsive to high, inputs and tolerant to post-harvest sprouting. It is early in maturity. Other distinctive features are peduncle length (37.7cm), days to 75% spike

emergence 85.0, days to maturity 130.0, number of grains per pike 61.0 and dwarfing gene Rht_3. It has recorded significantly higher grain yield than C 306 and was at par with other dwarf genotypes.

References

Kumar S, VS Kadian, S Madan and SK Sharma (2005) Effect of organic and inorganic nutrition on wheat genotypes. *Res. on Crops* 6(2): 194-196.

Singh KP, RK Behl, SK Sharma and Sameena (2006) Plant genes influencing heat tolerance in wheat. Proc. International Conference on Sustainable Crop Production in Stress Environment – Management and Genetic Options, JNKVV, Jabalpur, February 9-12. Agri-Bios Publishers, Jodhpur.

HDM 04-1 (IC537352; INGR 06009) an Early Pigeonpea (*Cajanus cajan*) Germplasm

Ram Kumar Yadav and RS Waldia

Chaudhary Charan Singh, Haryana Agricultural University, Hisar-125 005 (Haryana)

Genotype HDM 04-1 has been categorized as having shortest maturity duration. It was developed through induced mutation using 10 kR of gamma rays on ICPL 88039 at Chaudhary Charan Singh, Haryana Agricultural University, Hisar. The genotype has 100 cm height, dark green small leaflets, indeterminate growth habit, takes 45-50 days to flower initiation and 100 days to maturity. The flower is yellow in colour. The seed is round, bold and brown in colour. Average 100 seed weight is 8.8 gm (Ram Dhari and Waldia, 2005). It is dwarf, therefore will be useful for insect management and also for drought conditions. This genotype fits well for pigeonpea-wheat rotation and therefore will help in increasing the area under pulses. The per day productivity of this genotype is higher than the popular varieties of the state.

Reference

Dhari R and RS Waldia (2005) Dwarf and extra early mutant of pigeonpea [*Cajanus cajan* (L.) Millsp.] *Natnl. J. Pl. Improv.* **7 (1):** 61.

RG2819 (IC346591; INGR 06010) a Castor (*Ricinus communis*) Germplasm, Resistant to *Macrophomina* Root Rot and *Fusarium* Wilt

K Anjani

Directorate of Oilseeds Research, Hyderabad-500 030 (Andhra Pradesh)

The accession RG 2819 (IC346591) is a unique multiple disease resistant selection from a castor (*Ricinus communis* L.) landrace collected from Tamil Nadu. It showed consistently high resistance reaction against *Macrophomina* root-rot as well as against *Fusarium* wilt over years and locations, in screening trials using wilt sick and root-rot sick plots.

RG 2819 has green colour stem with bloom on it. The primary spike is predominantly female with medium size spiny green non-dehiscent capsules. Seeds are small and mottling on seed is conspicuous. Caruncle is present. As multiple resistance to the above diseases is not available in castor cultivars, this accession would be highly useful to breed castor varieties/parental lines resistant to both the diseases. It would a useful base material to tag genes responsible for resistance to these diseases and study linkage between them, if any.

emergence 85.0, days to maturity 130.0, number of grains per pike 61.0 and dwarfing gene Rht_3. It has recorded significantly higher grain yield than C 306 and was at par with other dwarf genotypes.

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Wilt and Reniform Nematode Resistant Parent Germplasm in Castor (*Ricinus communis*)

HC Pathak, KP Chaudhari, MS Patel, SR Chaudhari, DB Patel and PS Patel
Sardarkrushinagar-Dantiwada Agriculture University, Sardarkurshinagar, Banskantha-385 506 (Gujarat)

Castor (*Ricinus communis* L.) is an important non-edible oilseed crop of arid and semi-arid region of the world, having wide range of industrial uses. India has the maximum area and production under this crop. India is principal producer and exporter of castor seed, castor oil and some of its derivatives. The major growing states in India are Gujarat, Andhra Pradesh, Rajasthan, Tamil Nadu, Karnataka and Orissa, Gujarat is the leading castor growing state of the country where the crop is grown in 3.05 lakh hectares of area with 4.65 lakh tones of total production and average productivity of about 2000 kg/ha. For production of hybrids with resistance to some of the major diseases parents described below have been identified.

SKP 84 (IC537353; INGR 06011) a Pistillate Castor (*Ricinus communis*) Germplasm with Resistance to Wilt and Reniform Nematode

SKP 84 is a pistillate line identified with resistance to wilt and reniform nematode at Sardarkrushinagar-Dantiwada Agriculture University, Sardarkurshinagar, Banskantha, Gujarat. It was used as the female parent in development of GCH-7.

SKP 215 (IC537354; INGR 06012) a Castor (*Ricinus communis*) Germplasm, with Resistance to Wilt and Reniform Nematode

SKP 215 is a line identified with resistance to wilt and reniform nematode at Sardarkrushinagar-Dantiwada Agriculture University, Sardarkurshinagar, Banskantha, Gujarat. It was used as the male parent in development of GCH-7.

Identification of Useful Germplasm in Rapeseed and Mustard

JN Sachan, Basudeo Singh, SP Singh, DP Pant, Dhirendra Singh and AK Singh
Department of Genetics and Plant Breeding, GB Pant University of Agriculture and Technology, Pantnagar-263145, US Nagar (Uttarakhand)

PRQ-2005-1 (IC546946; INGR 06013)

Brassica oil crops normally contain high levels of erucic acid (40-50%) in oil. Cultivars with little or no erucic acid were first identified in *Brassica napus* L. and in *B. rapa*, and more recently in *B. juncea*. The first low erucic acid rapeseed (LEAR) cultivars developed were Orlo in *B. napus*, Sapn in *B. rapa* and Zem-1 in *B. juncea*. Although, low erucic acid genes are also available in *B. juncea* but only few commercial cultivars of *B. juncea* have low erucic acid content. The research efforts at GB Pant University of Agriculture and Technology, Pantnagar resulted in the development of a low erucic *B. juncea* strain, PRQ-2005-1. It is a transgressive segregant from a cross between *B. juncea* genotypes, RC-781 (high erucic acid, black seeded) and Zem-1 (Australian low erucic acid and yellow seeded cultivar).

PRQ-2005-1 maintained its low erucic characteristics (<1.08%) and its superiority in seed and oil yield, compared to the national checks, Kranti and Varuna in multilocation testing under AICRP trials during 2002-03 and 2003-04 (Anonymous 2003 and Anonymous, 2004). Observations on seed colour and physio-morphological characters recorded at Pantnagar revealed that PRQ-2005-1 contain yellow seed coat colour and is similar to national checks in almost all the physio-morphological characteristics.

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References

Anonymous (2003) Annual progress report on All India Coordinated Research Project on Rapeseed-Mustard. ICAR National Centre on Rapeseed-Mustard, Sewar, Bharatpur, India.

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PAB 9511 (IC 546948; INGR 06014)

A mustard strain developed by pedigree selection from a double cross [(RC 78 x Krishna) x (PHR-1 x Poorbiraya)] at GB Pant University of Agriculture and Technology, Pantnagar, showed moderately resistant reaction to *Alternaria* blight (score 2.39) at leaf stage and resistant (score 1.16) at pod stage in the scale of 0-5 (0=diseases free, 1=highly resistance, 2=resistant, 3=moderately resistance, 4=susceptible and 5=highly susceptible) under multilocation testing in National Screening Nursery of All India Coordinated Research Project (AICRP) between 1996-97 to 1998-99 (Bhartaria PI Patho AICRP R&M 1996). This strain combines *Alternaria* blight (AB) tolerant genes from RC 781 and PHR-1 with enhanced expression for AB resistance and agronomical features from Krishna and Poorbiraya. It was reported as a promising source for *Alternaria* blight resistance. Patini *et al.* (2005) suggest that moderately resistant reaction is due to more incubation and latent periods, less size of spot, less sporulation index and less leaf and cotyledon damage area. It has been recommended for rapeseed-mustard varietal improvement programme to enhance the level of resistance to stabilized/ sustain higher yield (AICRP R&M, Annual Report 2004). The strain PAB 9511 yielded consistently higher than Varuna under protected and unprotected conditions for last four years under AICRP Trials (AICRP R&M Annual Report, 2004).

References

Anonymous (1996-2004) *Annual progress report on All India Coordinated Research Project on Rapeseed-Mustard.* ICAR National Centre on Rapeseed-Mustard, Sewar, Bharatpur, India.

Patini CS, SJ Kolte and RP Awasthi (2005) Screening of Indian mustard (*Brassica juncea* (Berk) sacc. isolates based on infection reducing resistance. *J. Interacad.* **9(4):** 498-507.

VLS 59 (IC 546949;INGR 06015) a Soybean (*Glycine max*) Germplasm, with Low Linolenic Acid

Vinay Mahajan, SK Shukla, HS Gupta, MS Khati, Vineet Kumar, Anita R Kumar, SM Hussain and GS Chauhan

Vivekanand Parvatiya Krishi Anusandhan Sansthan, Almora-263 601 (Uttarakhand)

The shelf life of soybean oil depends upon the oxidative stability of soybean oil as determined by its fatty acid composition. Partial hydrogenation, the process to increase oxidative stability, is not only cost-ineffective, but also leads to formation of trans fatty acids that implicates serious health concern (Lichtenstein *et al.* 2003). Monounsaturated (M): poly-unsaturated fatty acids (P) ratio is considered as an indicator of oxidative stability of a vegetable oil. Generally, soybean oil possesses M:P ratio of 0.5 as compared to 7.0, 2.3, 1.0, 0.5, 0.2 values of olive, canola, peanut, corn and sunflower oil, respectively. In order to develop high yielding lines with better shelf life efforts were made to develop genotype with higher M:P ratio. VLS 59 was developed out of the cross "VS 96 x EC 361336" with a selection history as [(VS 96 x EC 361336)-3-1-1-2]. VLS 59 exhibits the lowest linolenic acid i.e. 3.96 (C18:3), which indicates improved oxidative stability of soybean oil. The other quality characteristics for VLS 59 are C16:0 (12.16), C18:1 (3.26), C18:2 (33.06), M:P (0.645), N-6:N-3 (11.9) and 100 seed wt. (13.3g). VLS 59 plants are 73.75 cm tall with average 100-seed weight of 14.28g. In multi-location trials it flowered in 58-69 days (average: 63.5 days) and matured in 119-129 days (124 days). It is tolerant to bacterial blight and *Cercospora* leaf spot (Table 1). VLS 59 can be employed in breeding for high yielding varieties with improved oxidative stability of soybean oil.

Reference

Table 1. Summary of ancillary characters VLS 59 compared to other advance lines

Entries	VLS 59	Bragg	VLS 2	Shivalik	JS 335	VLS 47
Plant height (cm)	73.75	89.66	70.67	73.33	87.75	110.00
Days to flower	63.50	56.34	50.00	57.00	64.34	76.50
Days to maturity	124.00	123.80	121.00	118.33	125.34	131.00
100 seed weight (g)	14.28	16.32	12.93	13.07	12.29	15.05

(Initial Varietal Trial, *kharif* 2003 and Advance Varietal Trial I, *kharif* 2004)

Lichtenstein AH, AT Erkkila, B Lamarche, US Schwab, SM Jalbert and M Ausman (2003) Influence of hydrogenated fat and butter on CVD risk factors remnant like particles, glucose and insulin, blood pressure and C reactive protein. *Atherosclerosis* **171**: 97-103.

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Reference

Table 1. Summary of ancillary characters VLS 59 compared to other advance lines

Entries	VLS 59	Bragg	VLS 2	Shivalik	JS 335	VLS 47
Plant height (cm)	73.75	89.66	70.67	73.33	87.75	110.00
Days to flower	63.50	56.34	50.00	57.00	64.34	76.50
Days to maturity	124.00	123.80	121.00	118.33	125.34	131.00
100 seed weight (g)	14.28	16.32	12.93	13.07	12.29	15.05

(Initial Varietal Trial, *kharif* 2003 and Advance Varietal Trial I, *kharif* 2004)

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CSD 123 (IC546953; INGR 06016) a daincha (*Sesbania aculeate*) germplasm, with early maturity

RK Singh, RK Gautam and B Mishra[1]
Central Soil Salinity Research Institute, Karnal-132 001 (Haryana)
[1] *Project Director, Directorate of Wheat Research, Karnal-132 001 (Haryana)*

Sesbania (*dhaincha*) is a very useful source of green manuring for soil enrichment. This also serves as a biological amendment in the salt affected soils. Early maturity in this crop facilitates early vacation of field for the timely sowing of next crop. In the Uttar Pradesh Council of Agricultural Research (UPCAR) funded project on "Screening of Suitable Sodicity Tolerant, Early Maturing and High Foliage Yielding Sesbania Varieties", amongst 140 lines of *Sesbania aculeata* and *S. rostrata*, one line CSD123 was found to possess characteristically distinct and consistent early maturity across locations and years. CSD123 is a local collection from Block Khandauli in District Agra, Uttar Pradesh. Three years of evaluation of this line revealed uniform expression of earliness at Karnal (Haryana), Lucknow and Pratapgarh Uttar Pradesh. This results in early seed harvest by about 25 days than other lines. The earliness trait has been characterized in the CSD123 on molecular basis through RAPD polymorphic bands.

It gives about 16, 91, 154, 160 and 176 g of fresh foliage yield/plant respectively at 40, 45, 50, 55 and 60 days after sowing. With regards to other agro-morphological features, CSD 123 in sodic soils attains about 2.60 m plant height, produce 15 primary branches, 37 secondary branches, 115 pods/plant and 15.0 g test seed weight and takes about 90 days for pod bearing.

A New Apomictic Cytotype with 2n=56 of *Pennisetum squamulatum* (IC546955; INGR 06017)

AK Roy, P Kaushal, SN Zadoo and RN Choubey
Indian Grassland & Fodder Research Institute, Jhansi-284 003 (Uttar Pradesh)

Pennisetum squamulatum Fresen is a very important species, as it contains genes for perenniality, apomixis and tolerance to many abiotic and biotic stresses (Hanna *et al.*, 1989). Considerable success has been reported in transfer of apomixis to pearl millet utilizing *P. squamulatum* as donor species (Ozias-Akins *et al.*, 1998, Roche *et al.*, 2002). Previous reports on cytological as well as in hybridization studies have designated *P. squamulatum* as a hexaploid species with 2n = 6x = 54 chromosomes (Raman *et al.*, 1959, Patil *et al.*, 1961, Dujardin and Hanna, 1989).

Studies at Indian Grassland and Fodder Research Institute, Jhansi have identified a new cytotype of *P. squamulatum* with 2n=56 (Roy *et al.*, 2003). Chromosome number, meiotic behaviour and crossability of the cytotype with *P. glaucum* justifies its octoploid nature based on x =7 and inclusion in the secondary gene pool of *P. glaucum*. The plant exhibits perennial habit. There is good pollen viability (as indicated by pollen staining), but has low seed set. Detailed cytological analysis revealed that bivalent formation is most prevalent and average configuration at diakinesis is 0.06 VI + 3.46 IV + 20.06 II + 1.6 I. Mostly normal disjunction of chromosomes at metaphase and anaphase was seen with occasional laggards and univalents.

The plants are around 2 m tall, average leaf length 37 cm with 1.3 cm leaf width. Leaf sheath is glabrous and average spike length is 18 cm. The mature stigma colour is purple and number of spikelets /spike is up to 270. It often has occurrence of trifid stigma (frequency 16%). It can be propagated by rooted slips or by seeds and harvested 2-3 times per year to provide good biomass for cattle.

References

Dujardin M and WW Hanna (1989) Crossability in pearl millet with wild *Pennisetum* species. *Crop Sci.* **29:** 77-80.

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Patil BD, MW Hardas and AB Joshi (1961) Auto-alloploid nature of *Pennisetum squamulatum* Fresen. *Nature* **189:** 419-420.

CSD 123 (IC546953; INGR 06016) a daincha (*Sesbania aculeate*) germplasm, with early maturity

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Sesbania (*dhaincha*) is a very useful source of green manuring for soil enrichment. This also serves as a biological amendment in the salt affected soils. Early maturity in this crop facilitates early vacation of field for the timely sowing of next crop. In the Uttar Pradesh Council of Agricultural Research (UPCAR) funded project on "Screening of Suitable Sodicity Tolerant, Early Maturing and High Foliage Yielding Sesbania Varieties", amongst 140 lines of *Sesbania aculeata* and *S. rostrata*, one line CSD123 was found to possess characteristically distinct and consistent early maturity across locations and years. CSD123 is a local collection from Block Khandauli in District Agra, Uttar Pradesh. Three years of evaluation of this line revealed uniform expression of earliness at Karnal (Haryana), Lucknow and Pratapgarh Uttar Pradesh. This results in early seed harvest by about 25 days than other lines. The earliness trait has been characterized in the CSD123 on molecular basis through RAPD polymorphic bands.

It gives about 16, 91, 154, 160 and 176 g of fresh foliage yield/plant respectively at 40, 45, 50, 55 and 60 days after sowing. With regards to other agro-morphological features, CSD 123 in sodic soils attains about 2.60 m plant height, produce 15 primary branches, 37 secondary branches, 115 pods/plant and 15.0 g test seed weight and takes about 90 days for pod bearing.

A New Apomictic Cytotype with 2n=56 of *Pennisetum squamulatum* (IC546955; INGR 06017)

AK Roy, P Kaushal, SN Zadoo and RN Choubey
Indian Grassland & Fodder Research Institute, Jhansi-284 003 (Uttar Pradesh)

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Agros-4 (IC 546954; INGR 06018) a New Cytotype of *Pennisetum pedicellatum*

SN Zadoo, AK Roy, RN Choubey and P Kaushal
Indian Grassland & Fodder Research Institute, Jhansi-284 003 (Uttar Pradesh)

Pennisetum pedicellatum Trin. popularly known as Dinanath Grass is an annual fodder plant widely cultivated on poor and marginal soil. It produces good and nutritious biomass for cattle consumption. The species having basic chromosome constitution of x = 9 has two known euploid races i.e. tetraploid (2n = 4x =36) and hexaploid (2n = 6x = 54) (Zadoo, 1986) and some aneuploid derivatives (Joshi *et al.*, 1959, Singh *et al.*, 1989, Zadoo, 1986).

The present material is an octoploid cytotype (2n = 8x = 72), which is a new report for the species (Zadoo et al., 1997). The material was obtained from Birsa Agricultural University, Ranchi as Type 'Agros-4'. At IGFRI, Jhansi the cytology was carried out from the germplasm and it was found to be an octoploid cytotype hitherto unreported. Average number of chromosome associations per cell was observed to be 2.2VIII + 1.7VI + 0.05V + 3.15IV + 0.95III + 13.65II + 1.21I.

The plants are perennial as compared to other genotypes of this species which are annual in nature. The material forms tussocks with multi tillering (up to 100 tillers) nature. The plant has good regeneration capacity and can be harvested three to four times in year. It has good seed set with, approximately 60% germination. It can be grown by seeds or by rooted slips. Seeds can be sown in good well drained soil 2-3 cm below surface. It can also be planted by rooted slips usually at 50 x 50 cm distance. It requires less water and can be grown as rainfed crop in *kharif* season. It can be harvested 3-4 times in a year. Nitrogen fertilizer in form of Urea after each cut increases biomass production.

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Zadoo SN (1986) Cytological analysis of *Pennisetum pedicellatum* Trin accessions. *Cytologia* **51:** 473-478.

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COVC 2003 165 (IC538549; INGR 06019) a sugarcane (*Saccharum officinarum*) germplasm, with woolly aphid resistance

SN Swamy Gowda and D Rajanna
University of Agricultural Sciences, Dharwad (Karnataka)

COVC 2003 165 is a sugarcane germplasm (*Saccharum officinarum*) with resistance to woolly aphids developed at Agricultural Research Station, University of Agricultural Sciences (UAS), Bangalore and Agricultural Research Station Visweswaraiah Canal Farm, Mandya, Karnataka. It has good agronomic features, such as high tillering capacity, high sucrose contents and high yielding ability.

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The plants are perennial as compared to other genotypes of this species which are annual in nature. The material forms tussocks with multi tillering (up to 100 tillers) nature. The plant has good regeneration capacity and can be harvested three to four times in year. It has good seed set with, approximately 60% germination. It can be grown by seeds or by rooted slips. Seeds can be sown in good well drained soil 2-3 cm below surface. It can also be planted by rooted slips usually at 50 x 50 cm distance. It requires less water and can be grown as rainfed crop in *kharif* season. It can be harvested 3-4 times in a year. Nitrogen fertilizer in form of Urea after each cut increases biomass production.

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KP/AK/77 (IC 415397; INGR 06020), a Spineless Meetha Karela (*Cyclanthera pedata*)

JC Rana, K Pradheep and VD Verma
NBPGR Regional Station, Phagli, Shimla-171 004 (Himachal Pradesh)

Meetha Karela (*Cyclanthera pedata*) is a minor kitchen garden vegetable in mid to high hill areas. In the hills almost every household grows Meetha Karela in their backyards for vegetable purpose. Majority of the cultigens have spines on fruits and are not preferred for cooking as vegetable. The proposed accession named '415397' was collected from Shimla district has almost no spines on the fruits, however, occasionally few (4-5 rudimentary) spines were found in some fruits. A single plant was selected from this accession and multiplied for obtaining the seed. Apart from spineless character the accession was also found to be high yielding and fruits were more straight, pulpy, less seeded and long, compared to commonly available germplasm. Splitting of fruits at maturity was also less and was quite late compared to common types. Splitting at early stage makes the collection of seeds difficult. The morphological features of this accession are summarized in Table 1.

Table 1. Characteristic feature of the germplasm accessions 'IC 415397'

Characters	Mean value	Characters	Mean value
Days to 50% flowering	70.00	Fruit yield/plant (g)	482.00
Leaf length (cm)	9.82	Early plant vigour	Very good
Leaf width (cm)	2.19	Plant growth habit	Spreading
Fruit length (cm)	7.26	Flower colour	Creamish
Fruit diameter (cm)	2.56	Stem branching	Very good
Fruit weight (g)	6.95	Fruit surface	Smooth
No. of fruit/plant	62.00	Fruit shape	Straight
Days to maturity	132.00	Fruit splitting	Less
1000 seed wt. (g)	5.45	At maturity	

JX123 (IC547013; INGR 06021) a Potato (*Solanum tuberosum*) Germplasm, Resistant to Early Blight

Raj Kumar, GS Kang and SK Pandey[1]
Crop Improvement Section, Central Potato Research Station, Jalandhar-144 003 (Punjab)
[1] *Crop Improvement Division, Central Potato Research Institute, Shimla-171 001 (Himachal Pradesh)*

Early blight (*Alternaria solani*) is a disease of potato occurring across the geographic range of crop (Pavek and Cornisi, 1994). It is one of the most common diseases of potato in warm-growing-season/areas of potato production, and is of economic importance in plains of India (Lakra, 1997).

JX 123 is high yielding under early harvest (75 days) and has good general combining ability for yield at very early (60 days) and early (75 days) harvests (Raj Kumar, 2004). It is a selection from the progeny of the cross, JE 812 × CP 2144. The cross was made during 1985 at the Central Potato Research Station, Kufri, Himachal Pradesh. The clone was selected from the progeny of this cross at Central Potato Research Station, Jalandhar, Punjab. The breeding methodology used was clonal selection from the cross between selected parents.

The tubers of JX 123 are oval shape, yellow skined, large sized with shallow eyes and light yellow flesh colour. It flowers moderately at Kufri. The plant is medium tall, leaflets are oval with entire margin and rough surface and flower is white. Under early harvest (75 days), this germplasm yielded at par with best early maturing variety Kufri Ashoka in Indian plains and plateau in multi-location trials under All India Coordinated Potato Improvement Project from 1993-1994 to 1996-1997. This accession is moderately resistant to late blight. This line performs well under early harvest (75 days) in Indian plains and plateau region.

References

Lakra BS (1997) Prevalence of diseases of potato crop in Haryana. *Crop Research* **14**: 357-360.

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IC547016; INGR 06022, a Wild Cashew-nut (*Semicarpus kurzii*) Germplasm

DR Singh
Central Agricultural Research Institute, PB No. 181, Port Blair-744 101 (Andaman and Nicobar Islands)

Wild cashew nut, *Semicarpus kurzii* is an endemic species widely distributed in the tropical rain forests of Chidratepu, South Andaman Islands. The tribal and the aborigines are using the exudates of this cashew-nut tree for curing skin allergies. The leaves of this plants are also used for treating malaria and as an anti-helminthetic. The plants of the species are medium sized trees with a height of 4.65 – 6m and light grey glabrous bark. The fruits are orange in colour, drupe sealed in a fleshly receptacle. The nuts are dried and used for extraction of oil. The pulp is rich in Vitamin C. This species can be used as a root stock for cultivated cashew-nut, because of its resistance against soil pathogens.

Identification of Potential Germplasm in Medicinal and Aromatic Plants

KA Geetha, Satyabrata Maiti and Narendra Gajbhiye
National Research Centre for Medicinal & Aromatic Plants, Boriavi, Anand-387 310 (Gujarat)

The genus *Aloe* (family Liliaceae) containing about 300 species (Reynolds, 1966) is native to Africa, Canary Islands, Spain and Mediterranean countries from where it was introduced to India, China, East and West Indies, southern USA, Central America and other countries. Among the different species reported, *Aloe barbadensis* Mill (*A.vera* L.) is well known for its therapeutic values. It is a perennial herb of about 2 feet high having short stem, rosette leaves shallow root system and found in semi-wild state in many parts of the country. Leaves are smooth and irregularly white blotched. Bright orange to saffron coloured small flowers are borne on a simple or a branched raceme. The flowers usually appear during September to March. Aloes are the major sources of anthraquinone glycosides, a bitter yellow juice, which exudes from the leaf. The principal active component of aloe is aloin- a mixture of glucosides, among which barbaloin is the chief constituent. Chemically, it is aloe-emodin anthrone C-10 glucoside and is water-soluble.

The significance of *A. barbadensis* achieved great momentum in medicinal plant cultivation due to the use of aloe gel. Aloe gel-a polysaccharide- is formed in inner parenchyma cells of the leaf, is slightly viscous and clear. The gel is used in topical therapeutic applications and also in many cosmetic products. The gel possesses good moisturizing properties. Germplasm screening at NRCMAP, resulted in the identification of two promising genotypes *i.e.* IC 283932 and NMRM 2, which were high yielding in terms of gel and aloin, respectively.

IC283932; INGR 06023, an aloe (*Aloe barbadensis*) Germplasm with Superior Gel Content

IC 283932 is a gel rich clone which yields about 2191.18 g of gel per plant. The main morphological and agronomic features of this germplasm are summarized in Table 1. The germplasm stocks are maintained in Active Gene Bank of NRCMAP and are under *in vitro* mass multiplication for distribution.

Table 1. Salient morpho-agronomic description of IC 283932 (INGR No. 06023)

Characters	IC 283932
Height of plant (cm)	50.20
Number of leaves/ plant	14
Leaf length (cm)	48.60
Characters	IC 283932
Leaf breadth (cm)	8.75
Leaf thickness (cm)	1.85
Leaf rind thickness (cm)	1.29
Number of spines per leaf margin	44.8
Number of inflorescence per plant	2
Peduncle	Branched or un-branched
Number of flowers per inflorescence	109.41
Inflorescence length (cm)	159
Number of capsules per inflorescence	4
Total leaf yield per plant (g)	2937.53
Weight of gel per plant (g)	2191.18
Dry matter % of gel	3.26
Leaf exudates-dry weight basis (g/ plant)	10.39
Aloin A %	19.13

IC547016; INGR 06022, a Wild Cashew-nut (*Semicarpus kurzii*) Germplasm

DR Singh
Central Agricultural Research Institute, PB No. 181, Port Blair-744 101 (Andaman and Nicobar Islands)

Wild cashew nut, *Semicarpus kurzii* is an endemic species widely distributed in the tropical rain forests of Chidratepu, South Andaman Islands. The tribal and the aborigines are using the exudates of this cashew-nut tree for curing skin allergies. The leaves of this plants are also used for treating malaria and as an anti-helminthetic. The plants of the species are medium sized trees with a height of 4.65 – 6m and light grey glabrous bark. The fruits are orange in colour, drupe sealed in a fleshly receptacle. The nuts are dried and used for extraction of oil. The pulp is rich in Vitamin C. This species can be used as a root stock for cultivated cashew-nut, because of its resistance against soil pathogens.

Identification of Potential Germplasm in Medicinal and Aromatic Plants

KA Geetha, Satyabrata Maiti and Narendra Gajbhiye
National Research Centre for Medicinal & Aromatic Plants, Boriavi, Anand-387 310 (Gujarat)

The genus *Aloe* (family Liliaceae) containing about 300 species (Reynolds, 1966) is native to Africa, Canary Islands, Spain and Mediterranean countries from where it was introduced to India, China, East and West Indies, southern USA, Central America and other countries. Among the different species reported, *Aloe barbadensis* Mill (*A.vera* L.) is well known for its therapeutic values. It is a perennial herb of about 2 feet high having short stem, rosette leaves shallow root system and found in semi-wild state in many parts of the country. Leaves are smooth and irregularly white blotched. Bright orange to saffron coloured small flowers are borne on a simple or a branched raceme. The flowers usually appear during September to March. Aloes are the major sources of anthraquinone glycosides, a bitter yellow juice, which exudes from the leaf. The principal active component of aloe is aloin- a mixture of glucosides, among which barbaloin is the chief constituent. Chemically, it is aloe-emodin anthrone C-10 glucoside and is water-soluble.

The significance of *A. barbadensis* achieved great momentum in medicinal plant cultivation due to the use of aloe gel. Aloe gel-a polysaccharide- is formed in inner parenchyma cells of the leaf, is slightly viscous and clear. The gel is used in topical therapeutic applications and also in many cosmetic products. The gel possesses good moisturizing properties. Germplasm screening at NRCMAP, resulted in the identification of two promising genotypes *i.e.* IC 283932 and NMRM 2, which were high yielding in terms of gel and aloin, respectively.

IC283932; INGR 06023, an aloe (*Aloe barbadensis*) Germplasm with Superior Gel Content

IC 283932 is a gel rich clone which yields about 2191.18 g of gel per plant. The main morphological and agronomic features of this germplasm are summarized in Table 1. The germplasm stocks are maintained in Active Gene Bank of NRCMAP and are under *in vitro* mass multiplication for distribution.

Table 1. Salient morpho-agronomic description of IC 283932 (INGR No. 06023)

Characters	IC 283932
Height of plant (cm)	50.20
Number of leaves/ plant	14
Leaf length (cm)	48.60
Characters	IC 283932
Leaf breadth (cm)	8.75
Leaf thickness (cm)	1.85
Leaf rind thickness (cm)	1.29
Number of spines per leaf margin	44.8
Number of inflorescence per plant	2
Peduncle	Branched or un-branched
Number of flowers per inflorescence	109.41
Inflorescence length (cm)	159
Number of capsules per inflorescence	4
Total leaf yield per plant (g)	2937.53
Weight of gel per plant (g)	2191.18
Dry matter % of gel	3.26
Leaf exudates-dry weight basis (g/ plant)	10.39
Aloin A %	19.13

NMRM2 (IC283932; INGR 06024) an Aloe Germplasm (*Aloe barbadensis*) with Superior Aloin-A content

NMRM 2 is another aloe germplasm (*Aloe barbadensis*) with rich aloin content. It contains about 26.13% aloin-A. Important morphological characters of this clone are presented in Table 1. The germplasm stocks are maintained in Active Gene Bank of NRCMAP and are being under mass multiplied for distribution using *in vitro* techniques.

Table 1. Salient morpho-agronomic description of NMRM 2 (INGR No. 06024)

Characters	NMRM- 2
Height of the plant (cm)	55.13
Number of leaves/ plant	13.63
Leaf length (cm)	51.20
Leaf breadth (cm)	9.09
Leaf thickness (cm)	2.31
Leaf rind thickness (cm)	1.14
Number of spines per leaf margin	49.51
Number of inflorescence per plant	1
Peduncle	Branched or un-branched
Number of flowers per inflorescence	112.25
Inflorescence length (cm)	173.00
Number of capsules per inflorescence	2.5
Total leaf yield per plant (g)	1922.50
Weight of gel per plant (g)	1460.38
Dry matter % of gel	2.25
Leaf exudates-dry weight basis (g/ plant)	8.39
Aloin A %	26.13

Reference

Reynalds GW (1966) The *Aloe* of tropical Africa and Madagascar. *The Aloes Book Fund*, Swaziland.

A Giloe (*Tinospora cordifolia*) Germplasm (IC283959; INGR 06025)

Tinospora cordifolia (Willd.) Hook f. & Thomas is an important medicinal plant recognised as a wonderful immunomodulator in modern medicine (Kapil and Sharma, 1997). The plant belongs to family, Menispermaceae and is widely distributed in India, Bangladesh and Sri Lanka. The plant is also reported from South East Asian countries. Mature stem is reported to be acrid, bitter, hot, restorative, aphrodisiac and alleviative of all the three *doshas* or morbidities and also used as digestive tonic. It cures fever, jaundice, thirst, burning sensation, diabetes, piles, skin ailments, respiratory disorders, neurological diseases and improves intellect. Starch (Giloe-ka-sat or Guduchi satva) from the aqueous extract of the dry stems is used as tonic against several diseases causing debility and is having high demand in Ayurveda industry.

About 45 accessions (21 female plants and 31 male plants) of *T. cordifolia* germplasm collected from different parts of Gujarat are maintained in the field gene bank of National Research Centre for Medicinal & Aromatic Plants. Phyto-chemical screening of the accessions revealed wide variability in starch content. A starch rich-clone (IC 283959) was identified containing about 13.32% starch (dry weight basis). Important morphological characters of the clone were presented in Table 1.

Table1 1. Salient morpho-agronomic features of IC 283959 (INGR No. 06025)

Characters	IC 283959
Gender of the plant	Male
Leaf length/ breadth ratio	0.93
Stem diameter at base (mm)	4.91
Stem diameter at base (range in mm)	3.84 to 6.81
Stem diameter at 30 cm above base (mm)	4.49
Stem diameter at 30 cm above base (range in mm)	3.30 to 5.70

Reference

Kapil A and S Sharma (1997) Immunopotentiating compound from *Tinospora cordifolia*. *J. Ethnopharmaco.* **8**: 89-95.

CLTP123 (IC 547018; INGR 06026) a high caryophyllene black pepper germplasm (*Piper nigrum*)

Sashi Kumar, T John Zacharia, KV Saji, K Johnson George and PN Ravindran
Indian Institute of Spices Research, Chelavoor P.O., Kozhikode-673 012 (Kerala)

Black pepper accessions rich in caryophyllene are useful in breeding black pepper for better quality, as caryophyllene is implicated in aroma and flavour of the commodity. The present note deals with a black pepper accession with 41.8 per cent caryophyllene, collected and conserved at the genebank of Indian Institute of Spices Research, P.O. Marikunnu, Kozhikode, Kerala. It was collected from a farmer's homestead plot in Kottayam district, Kerala. This is being maintained and is being used as donor parent in breeding for high quality black pepper lines. The important quality features of the *line* are given in Table1.

Table 1. Salient quality attributes of the high per cent caryophyllene and other essential oil contents

Accession	Essential oil	Caryo-phyllene	Pinene	Sabinene	Myrene	Limonene
1019 (CLTP-123)	3.2	41.8	7.3	27	2.6	10.3

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Number of spines per leaf margin	49.51
Number of inflorescence per plant	1
Peduncle	Branched or un-branched
Number of flowers per inflorescence	112.25
Inflorescence length (cm)	173.00
Number of capsules per inflorescence	2.5
Total leaf yield per plant (g)	1922.50
Weight of gel per plant (g)	1460.38
Dry matter % of gel	2.25
Leaf exudates-dry weight basis (g/ plant)	8.39
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Stem diameter at base (range in mm)	3.84 to 6.81
Stem diameter at 30 cm above base (mm)	4.49
Stem diameter at 30 cm above base (range in mm)	3.30 to 5.70

Reference

Kapil A and S Sharma (1997) Immunopotentiating compound from *Tinospora cordifolia*. *J. Ethnopharmaco.* **8**: 89-95.

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Identification of Cardamom Germplasm (*Elettaria cardamomum*) with Different Panicle Types

D Prasath and MN Venugopal
Indian Institute of Spices Research, Cardamom Research Centre, Appangala, Madikeri-571 201 (Karnataka)

Cardamom, "Queen of Spices", is the dried fruits of perennial rhizomatous herb, *Elettaria cardamomum* Maton and belongs to the family Zingiberaceae. This crop is indigenous to South India (Western Ghats) and Sri Lanka (Purseglove *et al.*, 1981) occurring at an altitudes between 600 m and 1500 m. The normal inflorescence in cardamom is a long panicle with few flowered racemes, arising from the base of the matured tillers. However, being a cross-pollinated crop, a lot of phenotypic variants exists in nature (Madhusoodanan *et al.*, 1994) having various types of panicles-branched panicles (compound panicle), branched raceme, female sterility and cleistogamy (Sudarshan *et al.*, 1988; Prasath and Venugopal, 2004). Some useful variant identified are described below

APG248 (IC349541; INGR 06027)

One of the notable variant for panicle characters includes branching in the panicle (basal, terminal and branching through the panicle) instead of normal type. The number of branches per panicle varies from 0 to 25. The compound panicle types directly contribute to yield per plant, and therefore to crop improvement programme. Accession APG 248 (IC 349541) was a clonal selection made at the Indian Institute of Spices Research, Cardamom Research Centre, Appangala, Karnataka from open pollinated progenies in the local plantation with medium bold capsules and highest number of branches per panicle (24.5 branches per panicle). It has branches throughout the panicle with maximum number of branches per panicle and high yield.

The plants are Malabar type with a height of 2.95 m, number of tillers per clump 27, green aerial shoot and leaf length and width of 70.8 x 13.5 cm. Number of panicles per plant 41, number of branches per panicle 24.5, number of racemes per panicle 62.5, number of capsules per raceme 2.5, number of flowers per panicle 525, per cent fruit set 17.55, panicle length 107.5 cm, internode's length 4.25cm, and number of capsules per panicle 93. Fresh capsule colour green, dry capsule colour yellowish green, capsule size 1.95 x 1.25 cm and number of seeds per capsule 22. Seed weight is 67.3 per cent with essential oil of 5.0 per cent. Fresh yield per plant is 2053.5 g, per cent dry recovery 23.5 and yield per hectare 1206 Kg/ha.

APG251 (IC249544; INGR 06028)

This notable variant for panicle characters includes branching in the panicle (basal, terminal and branching through the panicle) instead of normal type. The compound panicle types directly contribute to yield per plant, hence the natural segregants needs attention in crop genetic resources and crop improvement programmes. Accession APG 251 (IC 249544) was a clonal selection made at the Indian Institute of Spices Research, Cardamom Research Centre, Appangala, Karnataka from open pollinated progenies and identified as an elite accession with branching only at the base of the panicle with bold capsules. It has compound panicle with basal branching and bold capsules.

The plants are Malabar type with a height of 2.95 m, number of tillers per clump 39, green aerial shoot and leaf length and width of 71.6 and 14.1 cm. Number of panicles per plant 58.5, number of branches per panicle 3.5, number of racemes per panicle 43.5, number of capsules per raceme 3.25, number of flowers per panicle 207.5, per cent fruit set 44.12, panicle length 77.5 cm, internodes length 4.25cm, and number of capsules per panicle 91.5. Fresh capsule colour green, dry capsule colour green, capsule length and width 2.25 and 1.25 cm and number of seeds per capsule 22. Seed weight is 72.90 per cent with essential oil of 5.0 per cent. Fresh yield per plant is 3541 g, per cent dry recovery 20 and yield per hectare 1771 Kg/ha.

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Identification of Cardamom Germplasm (*Elettaria cardamomum*) with Resistance to Diseases

MN Venugopal and D Prasath
Indian Institute of Spices Research, Cardamom Research Centre, Appangala, Madikeri-571 201 (Karnataka)

Cardamom,"Queen of Spices", is the dried fruits of perennial rhizomatous herb, *Elettaria cardamomum* Maton and belongs to the family Zingiberaceae. This crop is indigenous to South India (Western Ghat) and Sri Lanka (Purseglove *et al.*, 1981) occurring naturally at altitudes between 600 m and 1500 m. It suffers from several diseases. Resistance sources have been identified from naturally occurring populations.

APG306 (IC349599; INGR 06029)

The major virus disease of cardamom is mosaic or 'katte' disease caused by *cardamom mosaic virus*. It is a maclura virus, under poty viridae, transmitted by aphid *Pentalonia nigronervosa* f *caladii*. Cardamom being perennial crop the reduction in yield is up to 69% within 2-3 years after infection and the total decline of plants would takes 3-5 years. Resistant sources were identified by collecting 134 disease escapes from hotspots of virus infection in South India and screening them in green house, sick plot and hot spots. Testing of promising collections in four hot spots and also against natural infection confirmed the resistant nature of the 17 collections (Venugopal, 1999). Accession APG 306 (IC 349599) is a clonal selection from open pollinated progenies, collected from mosaic-infected areas by the Indian Institute of Spices Research, Cardamom Research Centre, Appangala. The accession is resistant to mosaic or 'katte' disease and has an average yield of 643 kg/ha. The potential yield is 979 kg/ha. It has 77 per cent capsules with good appearance. It is adapted to Karnataka and Wayanad region of Kerala and recommended for moderate rainfall and moderate to high shaded mosaic infested areas.

The plants are Malabar type with a height of 1.72 m, number of tillers per clump 36, green aerial shoot and leaf length and width of 61 and 11 cm. Number of panicles per plant 34, number of racemes per panicle 23, number of capsules per raceme 2.6, number of flowers per panicle 99, per cent fruit set 41.6, panicle length 43 cm, internodal length 2.82 cm, and number of capsules per panicle 55. Fresh capsule colour green, dry capsule colour yellowish green, capsule length and width 1.62 and 1.22 cm and number of seeds per capsule 17.9. Seed weight is 65.65 per cent with essential oil of 7.9 per cent. Fresh yield per plant is 981 g, per cent dry recovery 22 and yield per hectare 643 Kg/ha.

APG343 (IC349634; INGR 06030)

Rhizome rot also called clump rot is an important disease of cardamom (*Elettaria cardamomum* Maton.) throughout South India (Siddaramaiah *et al.*, 1988). The disease is responsible for partial or total decay of plants of all stages and is caused by *Pythium vexans* de Barry and *Rhizoctonia solani* Kuhn. (Thomas *et al.*, 1988). The leaf blotch is caused by *Colletotrichum gloeosporioides* and is a major problem in low shade open areas. Accession APG 343 (IC 349634) is a clonal selection from open pollinated progenies in the rhizome rot prone areas. The accession was evaluated for its resistance to rhizome rot both under field and artificial inoculation at the Indian Institute of Spices Research, Cardamom Research Centre, Appangala. The accession is resistant to rhizome rot disease and also has resistance to leaf blotch. It has a capacity for higher biomass with dark green leaves.

The plants are Malabar type with a height of 2.29 m, number of tillers per clump 34, green aerial shoot and leaf length and width of 74 and 14.2 cm. Number of panicles per plant 33.1, number of racemes per panicle 19, number of capsules per raceme 2, number of flowers per panicle 88, per cent fruit set 32.6, panicle length 44 cm, internodal length 3.11 cm, and number of capsules per panicle 35.4. Fresh capsule colour green, dry capsule colour yellowish green, capsule length and width 1.61 and 1.12 cm and number of seeds per capsule 18.9. Seed weight is 60.34 per cent with essential oil of 6.1 per cent. Fresh yield per plant is 438 g, per cent dry recovery 20.6 and yield per hectare 345 Kg/ha.

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D-3 (IC 370425; INGR 06031) a Chinese Cassia (*Cinnamomum cassia*) Germplasm with High Oil and High Cinnamaldehyde Content

B Krishnamoorthy, J Rema and PA Mathew
Indian Institute of Spices Research, PB No. 1701, Marikunnu P.O., Kozhikode-673 012 (Kerala)

Cinnamomum cassia Blume (Syn. *C. aromaticum* Nees) (Family: Lauraceae) known as cassia cinnamon or Chinese cassia is a medium sized and straight trunked evergreen tree reaching a height of about 20 m. It has originated in China, which is the main producer and exporter of cassia cinnamon. Chinese cassia is commercially grown for its aromatic bark, used as a spice. Besides bark, cassia oleoresin and cassia oil are the other important products, which can be marketed. It has tremendous potential in the spice industry for flavouring food, beverages and in the manufacture of value added products. Also, it has immense medicinal properties and is used by the pharmaceutical industry. To a limited extent, it is used in the perfume industry.

Indian Institute of Spices Research, Calicut conserves 25 accessions of *Cassia* in the field repository. They were evaluated for various quality parameters. The bark oil content in these accessions, ranged from 1.20 % to 4.90 %. Accession D-3 (IC- 370425) was identified as an elite accession with high bark oil (4.9%) and high cinnamaldehyde content in bark oil (90.5%). This accession could be commercially exploited for production of cassia bark oil because of its high bark oil and high cinnamaldehyde content in the oil.

Morphologically, an eight years old plant is 6 m tall with three main shoots and 44 secondary shoots. The girth of main shoots is 17 cm at one m above ground level. Leaves are lanceolate, light green with velvety texture, may be dark green above and light green below, triplinerved, opposite and alternate. The leaf length is 21 cm, breadth 6.5 cm and ratio 3.23, while the petiole is 1.5 cm long, brown and is very pungent. Bark is spicy, sweet and pungent, bark oleoresin is 8.65 per cent, essential oil 4.90 per cent, leaf essential oil 1.15 per cent, cinnamaldehyde content in bark oil 90.5 and in leaf oil is 75 per cent respectively.

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Development of Sources of Rust Genes with Good Agronomic Background in Wheat (*Triticum aestivum*)

MK Menon, KA Nayeem, M Sivasamy, AJ Prabakaran, SMS Tomar, M Prashar, A Saikia, Bojan and RK Gupta
IARI Regional Station, Wellington-643 231 (Tamil Nadu)

HW2001 (IC 524288; INGR 06032)

A popular Indian Wheat 'Sonalika' was bred from 1154.383/AN/3/Y154/N 10 B/ LR 64, Mexican cross, simultaneously at IARI, New Delhi and G. B. Pant University of Agriculture and Technology, Pantnagar in early green revolution era (1964-65). It has bold and amber coloured grains and matures in 100-110 days, and found suitable under late sown conditions across the wheat zones of the country. However, the variety has exhibited 90 S to brown rust, 60 S to stem and 60 S to yellow rusts.

A Near Isogenic Line (NIL) of Sonalika with *Lr* 24 and *Sr* 24 has been derived with F (Free) to brown and TMS-S for stem rust, by using the gene source as "TR 380" by Menon and Tomar (2001). The variety has high degree of resistance to brown rust for seedling and adult plant reaction in Wellington conditions. Although 'Sonalika' has shown 40S for Ug 99, but this back cross line due to presence of *Sr* 24, is resistant to this race.

HW2004 (IC 524292; INGR 06033)

HW2004 has been derived through seven back crosses of C 306, after effecting hybrid with R 380 – 14* 7/3 Ag 14, so as to transfer two linked genes for brown and stem rust resistance, namely, *Lr* 24 and *Sr* 24 (Menon and Tomar, 2001). The incorporation of genes has been confirmed at DWR, Shimla with expression of resistance against the most virulent races *viz.*, IRS (12-2), 421-1

D-3 (IC 370425; INGR 06031) a Chinese Cassia (*Cinnamomum cassia*) Germplasm with High Oil and High Cinnamaldehyde Content

B Krishnamoorthy, J Rema and PA Mathew
Indian Institute of Spices Research, PB No. 1701, Marikunnu P.O., Kozhikode-673 012 (Kerala)

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A Near Isogenic Line (NIL) of Sonalika with *Lr* 24 and *Sr* 24 has been derived with F (Free) to brown and TMS-S for stem rust, by using the gene source as "TR 380" by Menon and Tomar (2001). The variety has high degree of resistance to brown rust for seedling and adult plant reaction in Wellington conditions. Although 'Sonalika' has shown 40S for Ug 99, but this back cross line due to presence of *Sr* 24, is resistant to this race.

HW2004 (IC 524292; INGR 06033)

HW2004 has been derived through seven back crosses of C 306, after effecting hybrid with R 380 – 14* 7/3 Ag 14, so as to transfer two linked genes for brown and stem rust resistance, namely, *Lr* 24 and *Sr* 24 (Menon and Tomar, 2001). The incorporation of genes has been confirmed at DWR, Shimla with expression of resistance against the most virulent races *viz.*, IRS (12-2), 421-1

R – 63-1 (77-5), 21 R 31-1 (104-1) and 21 R 55 (104 – 2) for brown rust. It has shown high degree of resistance to the four most virulent races viz., 62 G 29, 62 G 29-1, 37 G 79 and 7 G 11. HW 2004 has shown resistance with 'R' type reaction to four most virulent pathotypes of brown rust (leaf rust). Recently, at Najoro, Kenya (2005-06), scientists found *Sr* 23 gene very effective against Uf 99 race.

HW 2004 has been released for the Central Zone mainly for Gujarat, Madhya Pradesh, Chattisgarh and parts of Rajasthan for rain fed timely sown conditions. The optimum sowing time for this variety is between last week of October to first week of November and it responds well up to 60 Kg nitrogen per hectare. The plant height of this variety is 90 cm, and matures in 125 days under Central Zone conditions. The variety possesses white and pubescent glumes with slight clubbing at top of the spike and has good grain appearance, thousand grain weight (39 g) with 12 per cent desirable protein. It has yielding ability of about 25-30 q/ha, under rain-fed conditions.

HW2006 (IC 524294; INGR 06034)

Lok-1, a popular wheat for Central and Peninsular Zones is highly susceptible to all the rusts. In these zones leaf rust is very important and there are losses to wheat crop and production due to incidence of brown rusts. The variety Lok-1 is high yielding, with bold grain showed suitability for both normal sown and late sown conditions of Maharashtra, Gujarat, Rajasthan and Karnataka.

Lok-1 was crossed with TR 380-14 and back crossed with Lok-1 for seven generation to transfer leaf rust resistant gene *Lr* 24 by Menon and Tomar (2001). The gene has been successfully incorporated and its gene postulation has been done in relation to reaction to most virulent rust races of all three rusts at DWR, Shimla. The recombinant line HW 2006, has shown resistance to IR5, 421R63–1, 21R– 31–1 and 21 R 55 races of brown rust. Similarly, the gene *Sr* 24 has exhibited effectiveness against the recently identified pathotype "Ug99" (Uganda-99) at Kenya (Najoro).

Reference

Menon MK and Tomar SMS (2001) Transfer of *Agropyron elongatum* derived rust resistance genes *Sr* 24 and *Lr* 24 in to some Indian bread wheat cultivars. *Wheat Information Service* **92**: 20-24.

HW2015 (IC 524302; INGR 06035)

North Eastern Plain Zone has large area under very late sown wheat and the variety recommended is HUW 234. The variety although high yielding with better adaptation, is highly susceptible to brown rust. Leaf and yellow rust are the main diseases of this area. It is essential to check the spread of leaf rust in this area. The variety is a derivative from IB and IR genomes from rye and completely resistant to stripe rust.

Tomar and Menon (1998) used TR 380–14, as source of brown rust resistance for transfer of effective gene Lr 24, which is linked with stem rust resistant gene Sr 24. After seven back crosses a near isogenic line HW 2006 with all the characters of HUW 234 has been derived. The HW 2006 was subjected to the most virulent brown rust races viz., 12-5, 77-5, 77-7, 77-8 and 104-2 and found resistance to these pathotypes. Similarly, this was also subjected to 62 G 29, 62 G 29-1, 37 G 79 and 7 G 11, the most virulent black rust pathotypes and has exhibited total to moderate resistance reaction to black rust. At Kenya, (Najoro 05-06) wherever *Sr* 24 gene is incorporated it has shown resistant even to the 'Ug99' race of black stem rust.

References

Tomar SMS and MK Menon (1998) Introgression of alien genes for leaf rust (*Puccinia recondita*) resistance in to bread wheat (*Tricum restivum*) cultivars. *Indian J. Agric. Sci.* **68(10)**: 675-81.

F-6050 (IC528034; INGR 06036) a Jointless Tomato (*Lycopersicon esculentum*) Germplasm

M Rai, HC Prasanna and Rajesh Kumar
Indian Institute of Vegetable Research, Varanasi (Uttar Pradesh)

F-6050-1 is a jointless tomato germplasm (*Lycopersicon esculentum*), yielding on an average 4.81 kg. of fruits per plant. On an average it bears around 70 fruits, each weighing 70-80 g with an average of two locules. It has a thick pericarp of around 6.2 mm. The ripening of fruit starts after 100 days of transplanting.

R – 63-1 (77-5), 21 R 31-1 (104-1) and 21 R 55 (104 – 2) for brown rust. It has shown high degree of resistance to the four most virulent races viz., 62 G 29, 62 G 29-1, 37 G 79 and 7 G 11. HW 2004 has shown resistance with 'R' type reaction to four most virulent pathotypes of brown rust (leaf rust). Recently, at Najoro, Kenya (2005-06), scientists found *Sr* 23 gene very effective against Uf 99 race.

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BF-CMS-5-1eB (IC524011; INGR 06047), a Maintainer Line for WA Type CMS Lines with Elongated Uppermost Internode in Rice (*Oryza sativa* L)

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The BF-CMS-5-1eB (IC524011), the country's first elongated uppermost internode maintainer line for WA type CMS lines has been developed by the Barwale Foundation through transferring *'eui-1'* gene into the maintainer line, IR58025B from a donor, IR91-1591-3 using marker-assisted backcross breeding. Newly developed maintainer line, BF-CMS-5-1eB exhibit elongated uppermost internode/higher panicle exertion at flowering time and is comparable to recipient maintainer line, IR58025B for most of the agronomic and grain quality characters.

The maintainer line, BF-CMS-5-1eB can be used as valuable genetic stock by hybrid rice breeders to improve the panicle exertion of existing WA type CMS lines and/or develop new CMS lines with complete panicle exertion which in turn may not require GA_3 application in hybrid rice seed production.

References

Gangashetti MG, S Singh, P Khera and P Kadirvel (2006) Development of STS marker linked to elongated uppermost internode (*eui-1*) gene in rice (*Oryza sativa* L.). *Indian J. Crop Sci.* **1(1-2):** 113-116.

Gangashetti MG, KK Jena, VV Shenoy and WH Freeman (2004) Inheritance of elongated uppermost internode and identification of RAPD marker linked to *eui* gene in rice, *Cur. Sci.* **87(4):** 469-475.

Identification of Post Flowering Stalk Rot Resistant Inbred Lines

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Post Flowering Stalk Rot is one of the most severe causes of reducing maize production in India. The disease is caused by a complex comprising three fungi namely, *Cephalosporium acremonium, Macrophomina phaseolina, Fusarium_moniliforme* and one bacterium *Erwinia carotovora var. zeae.* The diseases symptoms chiefly include premature plant drying after flowering, starting from the basal inter nodes. In severe cases ear formation is hampered. A resistant pool was synthesized at Agricultural Research Station, Amberpet, ANGRAU, Hyderabad, India in 1990, from which 21 lines resistant to PFSR were derived. Full-sib recurrent selection was adopted for improving this pool prior to derivation of the inbred lines by the standard ear-to-row method. Inbreeding was carried out with tooth-pick screening in PFSR disease sick plots that is selfing accompanied by tooth-pick inoculation with causal organisms. The PFSR pool included resistant hybrids composite varieties and synthetics evaluated in All India Co-ordinated Maize Trials. The inbred lines BPTTI 35, BPTTI 37, BPTTI 38 and BPTTI 44 showed higher levels of resistance on 1 to 9 scale, where 1 is healthy and 9 is highly susceptible.

The lines can be adopted across the country. The cultivable seasons are *kharif* and Rabi. The ideal sowing time is 1st week of June to first fortnight of July in *kharif* and October 15th to November 15th in Rabi. The recommended fertilizer dose; $N:P_2O_5:K_2O$ is 120:60:40 Kg./ha. Nitrogen is to be applied half as basal and remaining half in the splits at 30 and 50 days after planting.

BPPTI 35 (IC396388; INGR 06043)

BPPTI 35 (35-1-2-1-1-1-2-0 bulk) is a maize (*Zea mays)* in-bred line with a score of 2.4 on 9 point scale for PFSR resistance. The plant height is 124 cm taking 69 days to silk. Ear length is 47 cm, length 9 cm, girth 10 cm having 12 kernel rows and 16 kernel per row, and 19.5 g 100 kernel weight on an average. It yields 3.5 tons grains per hectare. It has orange flint and belongs to full season maturity.

BPPTI 37 (IC396390; INGR 06044)

BPPTI 37 (37-1-2-1-1-1-2-0 bulk) is a maize (*Zea mays)* in-bred line with a score of 2.8 on 9 point scale for PFSR resistance. The plant height is 116 cm taking 70 days to silk. Ear length is 45 cm, length 10 cm, girth 10 cm having 12 kernel rows and 16 kernels per row, and 28.0 g 100 kernel weight on an average. It yields 4.4 tons grains per hectare. It has orange flint and belongs to full season maturity.

BPPTI 38 (IC396391; INGR 06045)

BPPTI 38 (38-1-2-1-1-2-2-0 bulk) is a maize (*Zea mays)* in-bred line with a score of 2.8 on 9 point scale for PFSR resistance. The plant height is 125 cm taking 74 days to silk. Ear length is 54 cm, length 11 cm, girth 9 cm having 14 kernel rows and 16 kernel per row, and 22.5 g 100 kernel weight on an average. It yields 4.5 tons grains per hectare. It has orange flint and belongs to full season maturity.

BPPTI 44 (IC 396393; INGR 06046)

BPPTI 44 (4-1-1-1-1-2-1-0 bulk) is a maize germplasm (*Zea mays)* in-bred line with a score of 2.8 on 9 point scale for PFSR resistance. The plant height is 112 cm taking 69 days to silk. Ear h is 41 cm, length 10 cm, girth 11 cm having 12 kernel rows and 18 kernel per row, and 24.0 g 100 kernel weight on an average. It yields 3.9 tones grains per hectare. It has yellow flint and belongs to full season maturity.

Reference

Payak MM (1983) "Premature Drying in maize". Bulletin on *Techniques of scoring for resistance to important diseases of maize*. All India Co-ordinated Maize Improvement Project, New Delhi-12, pp. 96-100.

F-7028-1 (IC526807; INGR 06037) a Tomato (*Lycopersicon esculentum*) Germplasm, with High Lycopene and Carotenoids Content

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VR Tamatar-7028-1 (F-7028-1) is a tomato *Lycopersicon esculentum* germplasm, with high lycopene (7.86 mg per 100g) and carotenoids (12.10 mg. per 100g.) contents. The number of fruits per plant vary from 40-50, each fruit weighs around 80-100 gm. The fruits mature after 90 days of transplanting.

Identification of Tea Clones (*Camellia sinensis*) for Desirable Traits

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UPG-2 (ATK-1) (IC522955; INGR 06038)

In India tea is grown in areas of low rainfall (< 1500 mm) as well as high rainfall (> 4000 mm). Majority of the South Indian tea gardens face drought during February to April with low crop production. The clone ATK – 1 was derived through selection by Boris during 1956–58 from the field of Attikunna division (Gudalur Taluk of Nilgiri District) of present M/S Parry Agro Industries Limited mainly for its good performance even during summer months and is widely grown in South Indian gardens particularly where drought is a problem. The nursery and field performance of this clone is quite acceptable, the rooting of vegetative cutting is faster and high, the establishment of plant in the nursery and field is good. The leaves are medium sized and chinary type (Balasaravanan *et al.*, 2003), light green with semi erect posture. Despite its tolerance to drought, it is fairly tolerant to certain pests and diseases particularly collar canker (Sasidhar and Sanjay, 2000). The average yield potential of this clone is around 4500–5000 kg made tea/ha/year and has moderate cup quality (Babu, 2004). Being a drought tolerant clone it has been used as a better root stock in grafting programmes with high yielding and quality clone scions which are susceptible to drought and to provide better field establishment (Spurgeon Cox and Subair, 1999). Considering all the characters this clone may be adjudged as a desirable parent for future breeding programme for development of drought tolerant seed stocks.

References

Babu S (2004) Tea Descriptor–Series 1. *Planters' Chron.* **100**: 23-26.

Balasaravanan T, PK Pius, R Rajkumar, N Muraleedharan and AK Shasany (2003) Genetic diversity among South Indian tea germplasm (*Camellia sinensis, Camellia assamica* and *Camellia assamica ssp. lasiocalyx*) using AFLP markers. *Plant Sci.* **165**: 365-372.

Sasidhar R and R Sanjay (2000) Incidence of color canker in High range and Anamallais. *Newsl. UPASI TRF* **10**: 4.

Spurgeon Cox and MA Subair (1999) Performance of cultivar ATK-1 in Nilgiri – Wynaad. *Newsl. UPASI TRF* **9**: 3-4.

UPG-4 (C-17) (IC522957; INGR 06039)

UPG-4, clone C- 17 is a variety released by M/S Bombay Burma Trading Corporation during early sixties. It was derived through selection. Being old clone and not very much in use currently, it needs to be maintained in the germplasm bank. The nursery performance of this clone showed that it is a good rooter and establishes well with more than 80 per cent success rate, the growth of the plant in the nursery is quite acceptable. Establishment in the transplanted field is initially slow but picks up well subsequently. It is a chinary type of plant (Balasaravanan *et al.*, 2003) with medium sized leaves. The leaves are smooth, flat and prominently pubescent. The biochemical estimation revealed that the contents of polyphenols, catechins, reducing sugars and amino acids were above normal; black tea has good liquor and flavour characteristics (Babu, 2004). Normally chinary type of plants is compact and tolerant to drought and this also has good quality.

References

Babu S (2004) Tea Descriptors Series – 1. *Planters' Chron.* **100** (12):23-26.

Balasaravanan T, PK Pius, R Rajkumar, N Muraleedharan and AK Shasany (2003) Genetic diversity among South Indian tea germplasm (*Camellia sinensis, Camellia assamica* and *Camellia assamica ssp. lasiocalyx*) using AFLP markers. *Plant Sci.* **165**: 365-372.

UPG-7 (TTL-1) (IC 522960; INGR 06040)

The polyphenol and catechins are very much responsible for the colour and strength of the tea, whereas the reducing sugars and amino acids are responsible for flavour. The clone TTL-1 was selected from the seedling population by M/S Tata Tea Limited and approved as a new planting material with moderate yield and acceptable quality by the Tea Board of India during 2001. The performance of this clone is good considering that the vegetative cuttings root well in the nursery with a success rate of more than 90 per cent. The initial establishment in the transplanted field is also good. The plant possess medium sized (cambod type) leaf, medium dark green in colour (Balasaravanan *et al.*, 2003). The leaf surface is rugose, smooth and flat with prominent pubescence. The shoots are semi-erect with good pluckable shoots. The average yield of the clone is estimated to be around 3000 to 3500 kg made tea/ha/year at a bush population of 10000/ha. The biochemical estimation of this clone revealed that it possesses good liquor colour with medium flavour and the infusion is bright (Babu, 2005).

References

Babu S (2005) Tea Descriptor Series – 2. *Planters' Chron.* **101(1):** 12-15.

Balasaravanan T, PK Pius, R Rajkumar, N Muraleedharan and AK Shasany (2003) Genetic diversity among South Indian tea germplasm (*Camellia sinensis, Camellia assamica* and *Camellia assamica ssp. lasiocalyx*) using AFLP markers. *Plant Sci.*, **165**: 365-372.

UPG-10 (IC522963; INGR 06041)

UPG-10, clone K–18 was released by M/S Tata Tea Limited through selection programme during sixties from clones of Chinese affinity. The nursery performance of this clone by vegetative propagation is good with high success rate of more than 85 per cent. It also roots well in the soil medium with the pH and EC of 4.9 and 0.05 dsm^{-1}, respectively. The initial establishment in the nursery and transplanted area is good and shows moderate tolerance to moisture stress during summer. It has orthotropic branching pattern, medium sized leaf with low pubescence. The leaves are slightly up fold with medium sized flush shoots. The biochemical estimation revealed that the precursor for flavour like reducing sugar and amino acids are slightly higher and it is adjudged as a clone with acceptable flavour and liquor characteristics (Babu, 2005). It has moderate yield, acceptable quality and moderately tolerant to drought.

Reference

Babu S (2005) Tea Descriptor Series – 2. *Planters' Chron.* **101(1):** 12-15.

UPG-16 (IC522969; INGR 06042)

In areas with high relative humidity, low temperature and low sunshine hours, tea suffers from high incidence of the fungal disease, blister blight, which can cause 25–30 per cent yield losses (Radhakrishnan and Baby, 2004). The clone SMP-1 is a selection from the Parvathi division of Sevenmalai estates of M/S Tata Tea Limited, Munnar (presently KDPH Co. Pvt. Ltd.) and known for its high tolerance to blister blight disease (Haridas and Aiyamma, 1988). The nursery and field performance of this clone is fairly good. The initial establishment in the nursery and rooting through vegetative propagation is over 70 per cent. It is initially slow but establishes well in the later stages when transplanted to the field. This clone has medium sized cambod type leaves, rugose, lathery with medium pubescence and moderate quality (Babu, 2005). Despite intolerance to drought and moderate yield and quality this clone is highly suitable for planting in areas prone to blister blight incidence.

References

Babu S (2005) Tea Descriptor Series – 3. *Planters' Chron.* **101(4):** 27-30.

Haridas P and BC Aiyamma (1988) The clone SMP – 1. *Bull. UPASI Tea Sci. Dept.* **42(1):** 8.

Radhakrishnan B and UI Baby (2004) Economic threshold level for blister blight of tea. *Indian Phytopath.* **57(2):** 195-196.