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PLANT DIVERSITY OF ANDAMAN AND NICOBAR GROUP OF ISLANDS AND THEIR ROLE IN ECO-DEVELOPMENT OF THE REGION

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Prosperity of a nation is chiefly determined by its capacity to utilize and conserve its resources. Suitable strategies based on an understanding of the nature and extent of physical and biological resources of a region, thus need to be formulated for bringing out rapid development and economic progress. In this paper, the role of agro-biodiversity of Andaman and Nicobar Group of Islands, their geographic distribution, regional diversity and present state of exploitation and utilization are critically examined to explore some avenues and action plan for their conservation and use.

Key words: Agro-biodiversity, A&N Group of islands, status, conservation

The Andaman and Nicobar Group of Islands consist of about 300 islands covering an area of 8293 sq. km., spread over a length of 700 km and breath of 250 km. The Islands are situated between 6 - 14° N and 92 - 94° E, in the Bay of Bengal. The general terrain, land formation and topography of Andaman group of islands are hilly and undulating, enclosing narrow valleys. The highest peak is the Saddle peak (732 m) whereas the Nicobar group of islands are invariably encircled by coral reefs and shallow sea. Some of the islands are naturally endowed with long narrow stretches of sandy coasts. Principal islands of the Andaman group, viz., North Andaman and Rutland islands are separated by narrow straits. Little Andaman is an important island. Northern-most point is approximately 901 km from mouth of Hooghly river basin and 190 km from Myanmar coast. The Great Nicobar island is the southernmost island of Andaman and Nicobar Group of Islands situated between 8 45° - 7 15° N latitudes and 93 37° - 93 56° E longitudes with an estimated area of nearly 1,045 sq. kms. It has aproximately a width of about 30 kms in north and very narrows (about 3 m) at southern tip, known as Indira Point (Pygmalion Point) which is only 144 kms away from Indonesian island Sumatra. In these isrands, Car Nicobar and Katchal are almost flat while other islands have a hilly terrain. The land surface of Little Nicobar and Great Nicobar is very irregular, undulating and often cut up by steep hills and valleys. The hot humid tropical climate prevalent in the close proximity of equator has enriched the landmass with evergreen forests. The region is characterized by an average rainfall of about 3000 mm, distributed over the greater part of the year. The relative humidity is as high as 80 - 90 per cent and temperature ranges from 23.2 - 30.7° C during the year. The islands are subjected to both south-west and north-east monsoons, the former from May to October and the latter from November to December. The aboriginals of the Andaman islands may be described as a race by themselves. One of them, the Negrito stock, includes Andamanese, Jarawas, Onges and Sentinels tribes generally found in Andaman group of islands. The second group,

Mongoloid in origin, includes the inhabitants of Nicobar group of islands, i.e., Nicobarese and the Shompens. Some of these aboriginals are in fact seriously threatened with extinction. Agriculture is not generally practiced by these Stone Age people. They are natural hunters and gatherers of food and move in groups for game, fishing, collecting wild yams, banana and *Pandanus* fruits. 'Onge' tribe too collects wild roots tubers and fruits which they use as food.

I. How the agro-biodiversity developed ?

Wide climatic and physiographic diversity has offered immense opportunities for the cultivation of large array of food, fodder, fruits, other horticultural/plantation crops and medicinal plants in fertile valleys, on the hilly terraces and in the exposed flat hill tops under irrigated and rainfed conditions of Andaman and Nicobar group of islands and thereby enormous variability developed in these crops. Primitive agricultural system followed by aboriginals of raising crops under stress conditions have generated much variability. Further, in the isolated islands which are different from each other, the tribal people belonging to various ethnic groups and settlers grow their own preferred cultivars of different crops. In the course of time, the process was accelerated and genetic diversity has been augmented enormously through conscious and unconscious selections by the people. Diverse plant types brought into the region from mainland India and through trade routes through sea from Myanmar (maize, *Coix*, sword bean and other beans, oil palm) and through Indonesian islands (rice, medicinal plants etc.)

II. Present status of agro-biodiversity wealth

The greater portion of the islands are under dense forest vegetation. Only in the areas of settlements, rice and plantation crops are cultivated. Area reserved for aboriginals (4671 sq. km), under forest (7,144 sq. km) and crops/plantations are given below :

Rice	:	11,963 ha
Coconut	:	4,898 ha
Areea nut	:	2,000 ha (approx.)
Rubber	:	6,000 ha
Oil palm	:	6,305 ha (approx.)
Cashewnut	:	600 ha
Other crops	:	-

Rice is the staple food and is grown on about 12000 ha yielding 21,000 t; planted in June/July/August and harvested between October/November, depending upon region, varieties and farming systems. Most of rice cultivars are not the landraces of this region but are old varieties brought by settlers from mainland India or improved varieties introduced by various agencies. Tapioca grows well on hilly slopes. In due course of time, wide variability has been generated in different agri-horticultural crops introduced by Britishers, and Indian settlers from Tamil Nadu, Kerala, Bihar, Tamilian refugees from Sri Lanka, and Bangala Desh refugees. The crops/species, which have now become naturalized and well established are listed in Table 1.

IIa. Forest flora of Andaman and Nicobar Group of Islands

(i) Andaman group of islands resemble each other in land formation, topography and other climatic factors. Little variation exists due to elevation and edaphic factors. Giant evergreen forests occur along larger streams endowed with dèep alluvial soil. Prominent tree species included *Dipterocarpus alatus, Artocarpus chaplasha, Sterculia campunulata.* Under tropical evergreen forest, vegetation was not luxuriant. *Dipterocarpus grandiflorus* has been a conspicuous species occurring on moist clayey hill slopes. Valley forests include *Musa* spp. and tree ferns. Cane brakes are distributed throughout evergreen and semi-evergreen climaxes. Creeping bamboo (*Dinochloa*) and wet bamboo brakes occur along streams. *Bambusa schizostachyoides* and

Oxytenanthera spp. are very common. Some of the important species which constitute deciduous forests include *Pterocarpus dalbergioides, Canarium euphyllum, Chukrassia tabularis, Dillenia pentagyna, Lannea coromandelica* and *Sagaraea elliptica Artocarpus lakoocha, Lagerstromoea hypoleuca.* Important plant species forming littoral forest vegetation include : *Manilkara littoralis, Calophyllum inophyllum, Thespesia populnea, Crinum asiaticum* and *Pongamia pinnata.*

(ii) Mangrove forests are adapted to survive tidal mud permanently wet with salt water. *Rhizophora mucronata, Bruguiera conjugata,* and *Avicennia officinalis* are major species of significance.

(iii) Major forest types identified in Nicobar group of islands have some Malaysian and Indonesian species component. These include *Dendrolobium umbalatum, Casuarina equisetifolia, Pandanus tectorius, Mangifera comptosperma, Rhizophora epicula, Sonneratia caseolaris, Areca catachu* and *Elaeocarpus serratus.* Plants cultivated by the aboriginals and those introduced by the settlers include coconut (*Cocos nucifera*), *Pandanus* and banana. Tree species such as *Pterocarpus dalbergioides, Tectona grandis* and several others are also grown.

(iv) The flora of Andaman and Nicobar group of islands is unique in the sense that it exhibit multidimensional affinities to north - eastern region of India and Myanmar in north, Thailand and Malaysia in the east and Sumatra and Java towards South. The vegetation and environmental factors have not allowed large scale introduction of either plant or animal species. About 1,425 species of angiosperms comprising 1078 dicotyledons and 347 monocotyledons occur in this region. Of these, only 14 per cent species are endemic to these islands; 54 per cent occur in mainland India and remaining 32 per cent extend their distribution to adjacent areas of SE Asia, Malaysia and Indonesia. There is phytogeographic distinctness between Andaman and Nicobar group of islands. Only 28 per cent of species have common distribution.

Table 1. Crops/species grown in Andaman and Nicobar Group of Islands

Crop group and Crop species
I. AGRICULTURAL CROPS
Brassica campestris, B napus, Raphanus sativus, Abelmoschus esculentus, Gossypium barbadense, Hibiscus mutabilis, Cajanus cajan, Canavalia ensiformis, Cyamopsis tetragonoloba, Lablab purpureus, Vigna trilobala, V. unguiculata, Benincasa hispida, Citrullus lanatus, Cucumis melo, C. sativus, Cucurbita maxima, C. moschata, Coccinea grandis, Lagenaria siceraria, Momordica charantia, Luffa cylindrica, Trachyspermum involucratum, Trichosanthes anguina, T. cucumerina, Coriandrum sativum, Ipomoea batatas, Lycopersicon esculentum, Solanum melongena, Sesamum indicum, Manihot esculanta, M. glaziovii, Discorea alata, D. esculenta (yams), *Colocasia esculenta, Capsicum frutescens, Echinichloa colona, Eleusine coracana, Saccharum officinarum, Zea mays, Portulaca oleracea, Pachyrrhizus erosus, Phaseolus lunatus, P. vulgaris, Pisum sativum* and *Sesbania grandiflora.*
II. HORTICULTURAL CROPS
Anona reticulaae, A. muricata, A. squamosa, Garcinia mangostana (mangosteen), *Durio zibithinus* (durian), *Aegle marmalos* (bel), *Citrus grandis, Ananas comora* (pine apple), *Belamcanda chinensis, Anacardium occidentale, Mangifera indica, Moringa oleifera, Carica papaya, Achras sapata* (sapota), *Diospyros discolor* (raspberry), *Musa paradisiaca* (banana), *M. textilis and Punica granatum* (pomegranate).
III. MEDICINAL PLANTS
Centella asiatica, Catharanthus roseus, Ocimum tenuifolia, Plantago major, Cannabis sativa, Zephyranthus carinata and *Z. rosea.*
IV. WILD GRASSES AND LEGUMES
Bothriochloa pseudo-ischaemum, Brachiaria distachya, B. mutica, B. paspaloides, Cymbopogon nardus, Dactyloctonium aegyptium, Heteropogon contortus, Imperata cylindrica, Paspalum scrobiculatum, Panium miliaceum, Rothboellia exaltata, Alysicarpus vaginalis, Clitoria ternatea, Crotalaria retusa, Atylosia scarabaeoides and *Mucuna* species.
V. PLANTATION CROPS
Elaesis guineansis (oil palm), *Cocos nucifera* (coconut), *Myristica fragrans* (jaiphal), *Piper betle* (betel), *Theobroma cacao* and *Areca catachu* (Arecanut).
VI. MISCELLANEOUS PLANTS
Bombax ceiba, Bixa orellana, Ceiba pentendra var. *indica, Glyciridia sepium, Cassia fistula, Lagerstromoea indica* and *Eucalypus botryoides.*

(v) Rare endemic plant species (187) included *Bauhinia nicobarica, Cyrtandiomoea nicobarica, Mangifera comptosperma,* which were previously known to occur in Vietnam, Thailand and Myanmar, and now occur in Car Nicobar. *Phalaenopsis speciosa* is a rare endemic orchid occuring in these islands, besides *Amomum acullatum, Mangifera andamanica, Amorphophallus camosus, Tinospora andamanica* and *Syzygium andamanicum.*

(vi) Some of the indigenous medicinal plants used by the aboriginal tribes as cure of sickness and injuries, are *Aristolochia tagala, Calophyllum filiformis, Ficus rumphii, Vitex negundo, Myristica elliptica, Merremia peltata* and *Corymborkis veratrifolea.*

(vii) The main food, of the aboriginals are *Artocarpus chaplasha, Mangifera andamanica, Pandanus lerum* (it is a large orange coloured fruit and constitute staple food of the Nicobarese and Shompen tribe). Banana and coconut provide food for survival of these tribals (Bhargava, 1981).

IIb. Faunal diversity of Andaman and Nicobar Group of Islands

In comparison to plant wealth, Andaman and Nicobar group of islands are poor in faunal wealth. Wild pigs (*Susanda mononsis*) and civet cat (*Paguma larvata tytleri*), spotted dear (*Axis axis*), barking deer (*Mutinus muntjak*) are found. The islands are rich in avifauna. Out of 145 species reported to be occuring in this region, the important species are : Lesser whilstling Teak (*Dendroegyna javanica*), grey partridge (*Francolinus pondicerianus*), Moor Hen (*Gallinula chloropus orientalis*), Andaman Wood Pigeon (*Columba palumboides*), Nicobar pigeon (*Calaenas nicobarica*), Crow pheasant (*Centropus andamensis*), Hill Myna (*Gracula religiosa andamensis*) etc.

III. Ecological status of the islands

In order to meet the growing demands and high population pressure, man has to exploit natural resources for his existence. The Andaman and Nicobar group of islands constitute a generalized ecosystem and is characterized by high species diversity index. In such terrestrial ecosystems, therefore, net primary productivity tends to be high and many ecological riches are available to naturally occurring plant species at each tropical level. The ecosystem possesses greater stability, homeostasis, better every flow and high diversity index. The agricultural utilization of a natural ecosystem may be accomplished by manipulation rather than by transformation through drastic changes. It would be advantageous that an artificial ecosystem perhaps could be created to replace the natural one on a limited scale. Cultivation/plantation may possibly proceed in this ecosystem by substituting certain preferred domesticated species such as coconut, oil palm, cashew, areca nut, pepper and rubber for wild species that occupy equivalent riches. Thus, an assemblage of cultivated trees and shrubs, climbers, herbs and perhaps root crops may take over spatial and functional roles essentially similar to those fulfilled by wild species of natural ecosystem. In fact, probably cultivation began by the manipulation of generalized ecosystem where the high diversity wild species would encourage the use of wide variety of plants and animals for subsistence. Among various tree species of economic importance to man, the red oil palm is one which gives high return with least disturbance to the ecosystem. A large area (6300 ha) now is under oil palm (*Elaeis guineansis*) cultivation across these islands.

IV. NBPGR's role in conservation of genetic resources

The agro-biodiversity noticed in the Andaman and Nicobar group of islands is enormous. The resources vary widely and will remain so if the plant cover is carefully managed and exploited. There is an urgent need to tap these resources. Andaman and Nicobar groups of islands have

shown a vast scope for agriculture, horticulture, animal breading, poultry farming, fishery, forestry and allied avenues of economic upliftment of the society. Extension workers are fast approaching distant tracts. It is of utmost importance that the native diversity occurring across the whole islands should be speedily collected and conserved in the National Gene Bank for present and future use. The NBPGR has developed state-of-the-art in the field of plant germplasm collection, evaluation and maintenance.

The NBPGR, under National Agricultural Technology Project on Plant Biodiversity (NATP PB), is in the process of formulating a programme of germplasm collection and characterization/ evaluation for direct utilization and as useful donors for adaptive traits such as resistance to drought, cold and for quality characteristics in collaboration with Central Agricultural Research Institute (CARI) and Botanical Survey of India, located at Port Blair and other Government/ Non-Government Organizations. The available landraces will be collected from the region, evaluated and conserved in the National Gene Bank for posterity. Public sector and nongovernment and private organizations may come together to establish a consortium to share genetic resources on committed contribution basis. *Ex-situ* conservation, on-farm conservation of landrace diversity and *in-situ* conservation will be judiciously integrated. *In-vitro* and cryopreservation techniques will be refined and these will find increasing use in germplasm conservation of vegetatively propagated and difficult recalcitrant group of species. Work on unique identity of genetic diversity available in germplasm collections determined through critical screening for biotic and abiotic stresses, quality attributes and characterization of germplasm holdings is expected to progress rapidly on prioritized species and group of crops. Isozyme profiles and DNA Fingerprinting will be used for establishing unique identity of genotypes and this information alongwith video images of plant samples will be available in the computer database. Core subsets of primary germplasm collections having diverse genes for resistance/adaptation/preferred specific traits will become available in priority selected crops. Quarantine services will be more efficient because of increasing use of ELISA and DNA probes for early detection of viruses and viroids in high risk seed material/plant propaguies. A new activity during the coming decade is likely to be the rejuvenation and evaluation of seed samples kept under long term storage. Thus plant genetic resources activities are going to enhance manifold. The access to PGR needs to be regulated keeping in view the Sovereign Rights of states and with the enforcement of new legislations relating to Plant Variety Protection (PVP) and TRIPS. Role has also to be played to regulate/oversee/monitor the influx of new patented material and extend help in resolving disputes. Thus the component of Indian National Plant Genetic Resources System will go a long way in the conservation of immensely valuable genetic diversity required for sustained production and food security and thus alleviation of hunger and poverty. The NBPGR's Gene Bank can conserve over 10.5 lakh accessions. The Gene Bank facilities include 12 long-term module (-20C), and medium term storage (+10C) at Headquarters and medium term storage facilities at its regional stations and National Active Germplasm Sites (NAGS). In addition, cryo-bank has the facility to conserve 2 - 5 lakh samples in liquid nitrogen.

V. Future strategies for Eco-development of the region

Because of the geographical location and difficult access, much of the biodiversity in these islands, from micro to the macro has been preserved. Across the whole group of these islands, large areas are under-developed and financial

resources of the farmers are extremely poor. Therefore, special programmes are to be tackled by an integrated programme of development. Fortunately, we are more conscious of the natural wealth that lies embedded in the Andaman and Nicobar group of Islands. The resources, with which nature has endowed these islands and those introduced and naturalized in the region, are so rich now that their proper utilization/exploitation cannot only sustain life well but also give a standard of living to the people inhabiting them.

Whereas, the detailed programme for eco-development of the Andaman and Nicobar group of islands would vary from place to place, island to island according to prevailing conditions, some broad suggestions can be made for the eco-development of the region in context of agro-biodiversity and their proper exploitation. Although with the establishment of Central Agricultural Research Institute (CARI), research in the field of agriculture attained momentum and much have been accomplished, yet necessity for conducting more extensive research work through a chain of experimental centres in the important islands, is all the more important, because wide range of conditions exist in different islands even within a short distance. In the scientific transformation of the rural economy of the Andaman and Nicobar group of islands, more emphasis is to laid on the introduction of superior high yielding cultivars, so as to boost the agricultural production/potential of the region.

The ecological diversity in habitats ideally provides a venue for the introduction of newer germplasm of wide variety of agri-horticultural economic types. Particularly, the change in the growing of agricultural crops, forest species with that of crops most suited to the zone is desired. Introduction of oil palm plantation by Forest -and Plantation Development Corporation (FPDC) at Hut Bay (Little Andaman), is a right step. The FPDC has plans to enlarge oil palm plantation more extensively. It seems that the region is ideally suited for oil palm plantation. Rubber was also introduced in a large scale in Katchall island. Spices and condiments also add good returns. In Camorta islands, cashew plantations have been established. Areca nut and *Cocos nucifera* (coconut) have proved boon to the Nicobar group of islands. It showed variation in the size and colour of nut, kernal weight, and yield. Coconut grows as wild population unattended in several Nicobar islands. Coconut of these islands, despite the association with many insect and termites etc., are not infested with any of the major diseases and pests, which affect the plantations elsewhere in the world. It is probably due to presence of some gene complexes, that wild population with a magnitude of variations survived so long. More areas at present under forests needs replacement by plantation crops, medicinal plants, cash crops such as cardamom, cinnamon, ginger and turmeric, and pepper. Areas under coconut and oil palm plantations also need to be enlarged to a great extent.

Finally, the maximization of efforts towards efficient and economic land use would be required. Silvi-agricultural needs of the terrain/region would demand raising of quick growing food (*Echinochloa frumentacea, Eleusine coracana, Panicum miliaceum, Brassica campestris, Vigna unguiculata, Lablab purpureus, Lagenaria siceraria, Cyamopsis tetragonoloba, Luffa cylindrica, Manihot esculenta, Pisum sativum, Colocasia esculenta*) fuel, M & AP (*Calophyllum filiformis, Myristica elliptica, Vitex negundo* etc.) and plantation crops (*Elaeis guineansis, Cocos nucifera, Piper betle* etc.), fodder trees (*Brachiaria distachya, Crotolaria retusa, Paspalum scrobiculatum, Panicum miliaceum, Heteropogon contortus*). Lot of hue and cry has been raised about manifold problems in these islands, exploitation of setllers and aboriginals and backwardness of these tribes. Eco-conservation and integrated rural enhancement may be launched by way of involving government officials and

active manpower of the region. It is high time now that scientists/technocrats and administrators specializing in microdimensional features of eco-development, social workers and grass-root activists, educationists and visionaries, all sit together to arrive at solution to eco-developmental problems in the Andaman and Nicrobar group of Islands and act accordingly.

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QUALITY EVALUATION OF RAINFED RICE (*Oryza sativa* L.) GENETIC RESOURCES

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Proper evaluation of germplasm is a pre-requisite for its effecient utilization. A vigorous programme of evaluation of traditional cultivars and land races for yield, qualtiy and major biotic stresses has been underway since 1986 and many useful accessions were indentified. The present paper discusses the current status of quality evaluation programme. From 1988-96, three hundred and eighty four accessions were evaluated for 12 quality traits. In general, low variability (CV %) was recorded for hulling, milling recovery, volume expansion, amylose content, kernel breadth, cooked kernal length, and kernel linear elongation, Alkali value exhibited the highest variabilitity (CV 32 %) followed by rice recovery (21.5%). Variation for grain size (kernel length) and shape (L: B ratio) and water uptake was moderate (CV head-10-18%). The grouping of accessions is also presented. The potential accessions for various quality traits and accessions possessing multible desirable traits are also listed.

Key words : *Oryza sativa* L, quality, rainfed rice, genetic resources

The constant updating of the cultivars is essentail to avoid genetic uniformity which may prove disastrous (Khoshoo, 1987). Crop genetic resources play a pivotal role in the cultivar development programme by continuosly providing new genes to evolve better varieties with high level of tolerance of major biotic and abiotic stresses and high crop yield and quality. In rice, considerably high genetic erosion had occured due to fast replacement of land races/traditional cultivars by high yielding varieties, which occupies nearly 74 per cent of the cropped area which could be even higher in irrigated areas. Still impressive land race diversity persists especially in stress environments such as rainfed agro-ecology and areas inhabited by the tribals and various ethnic groups. In view of such enormous genetic erosion, the collection and conservation programme at Central Rainfed Upland Rice Research Station has been intensified since 1985. The exploration and collection programme was reorganized systematically in a phased manner in collaboration with other institutes operating in the plateau region of Bihar and resulted in the collection/acquisition of 2091 accessions from the Bihar, adjoining areas of Uttar Pradesh, West Bengal and Orissa, IRRI, (Philippines) (Chauhan *et al*, 1995). The genetic potential of an accession remains unknown until it is systematically evaluated and screened; only then it may become an important gene source for utilization in the breeding programme. A vigorous programme of

evaluation of traditional cultivars and land races for yield and its components, quality and major biotic stresses has been underway since 1986 and several useful germplasm accessions have been identified (Varier *et al.*, 1990; Sinha *et al.*, 1990; Chauhan *et al.*, 1991; Shukla *et al.*, 1995; 1996). This paper presents the status of quality evaluation programme.

MATERIALS AND METHODS

Three hundred eighty four accessions from diverse agro ecologies and origin were evaluated from 1988 to 1996 in the wet crop season (Table 1). They were grown in 3-row 3-5 plots; 3-5 in. long rows spaced 20 cm apart . The crop was raised at 40 N : 8.7 P : 16.6 K kg/ha. Except for rainfall, the other agronomic and plant protection practices were identical. A composite sample from the central row was used to record observations on brown rice colour, milled rice length, breadth and L : B ratio, hulling milling head-rice recovery, abdominal white, alkali value, amylose content; water uptake, volume expansion, cooked kernel length and kernel linear elongation.

Table 1. Rice accessions evaluated for quality traits (1988-96).

Type	Accessions (Number)
Indigenous upland	
Traditional	109
Improved varieties	42
Improved breeding lines	16
Total	167
Medium and low land	
Traditional	136
Improved	5
Total	141
Total (Indigenous)	308
Exotic upland	
Traditional	64
Improved varieties/breeding lines	5
Total	69
Medium and low lands	
Traditional	2
Improved varieties/breeding lines	5
Total	7
Total (Exotic)	76
Grand Total	384

Using Satake dehusker and Kett T-2 polisher, 100 g representative paddy sample was hulled and milled. Milling was done for 90 seconds. The method of Govindaswamy and Ghosh (1969) was followed to compute hulling, milling and head-rice recovery. Milled rice length and breadth were recorded by digital micrometer (Mitutoyo Japan). Standard methods were used to estimate alkali value (Little *et al.*, 1958) and amylose content (Juliano, 1971). The sample was cooked following the method of Beachell and Stansel (1963). Kernel linear elongation was computed as suggested by Azeez and Shafi (1966).

The range, mean and coefficient of variation (CV) were calculated to assess the variability for each character using standard statistical methods. The accessions were grouped by the frequency distribution for each character.

RESULTS AND DISCUSSION

Hulling, milling and head-rice recovery

The commercial success of the varieties is largely determined by the high hulling milling out-turn and head-rice recovery. Of these hulling and milling, recovery had very low variation (Table 2). The hulling and milling recovery ranged form 65.5 (Ambemohar, HRC 26) to 87.2 per cent (IRAT 240, HRC 1075) and 58.2 (Nagpur 22, HRCI 1) - 76.7 per cent (Gora Malti, NIC 105699), respectively. Similar results were reported by Chauhan *et al.*, (1991), and Malik *et al.*,

Table 2. Range, mean and coefficient of variation (CV) for quality characters in rice

Character	Range	Mean Sem	CV(%)
Hulling recover (%)	65.65-82.2	76.6±0.15	3.7
Milling recovery (%)	58.2-76.6	71.7±0.19	5.2
Head-rice recovery (%)	21.3-74.0	56.0±0.61	21.5
Kernel length (mm)	3.89-7.43	5.77±0.03	10.0
Kernel breadth (mm)	1.82-3.07	2.44±0.01	9.2
L : B ratio	1.68-3.91	2.38±0.02	14.3
Alkali value	2.50-7.00	4.00±0.07	32.0
Amylose content (%)	1.25-26.1	20.6±0.13	9.3
Water uptake (ml)	165.0-415.0	285.2±2.62	18.0
Volume expansion	3.5-4.3	3.9 ± 0.01	4.1
Cooked kernel length (mm)	7.0-12.4	9.85 ± 0.05	9.1
Kernel linear elangation	1.35-2.05	1.71 ± 0.01	6.1

(1994). Majority of the accessions (241) had hulling recovery between 75.1-80 per cent (Fig 1a). Nevertheless, 31 accessions (8.1%) had more than 80 per cent hulling recovery. The majority of the accessions showed total milling out-tum between 68.1-73.0 per cent followed by those having more than 73 per cent (Fig 1b). But the present collection showed substantial variation for head-rice recovery (CV 21.5%). The accessions were fairly well distributed for this trait (Fig 1c). A good number of accessions (44.8%) exhibited 60.1-70.0 per cent head-rice yield. Eight accessions had more than 70 per cent head rice recovery (Fig 1c). Accession BR 19-23 (HRC 680) had the lowest headrice recovery whereas, Shyamjeera (HRC 701), being the highest. Thus, there is a scope for improving this trait by selection. In earlier studies also similar results were reported (Chauhan *et al.*, 1991). Jennings *et al.*, (1979) also suggested that instead of total milled rice yield, emphasis should be given to improving head-rice yield because it varied more.

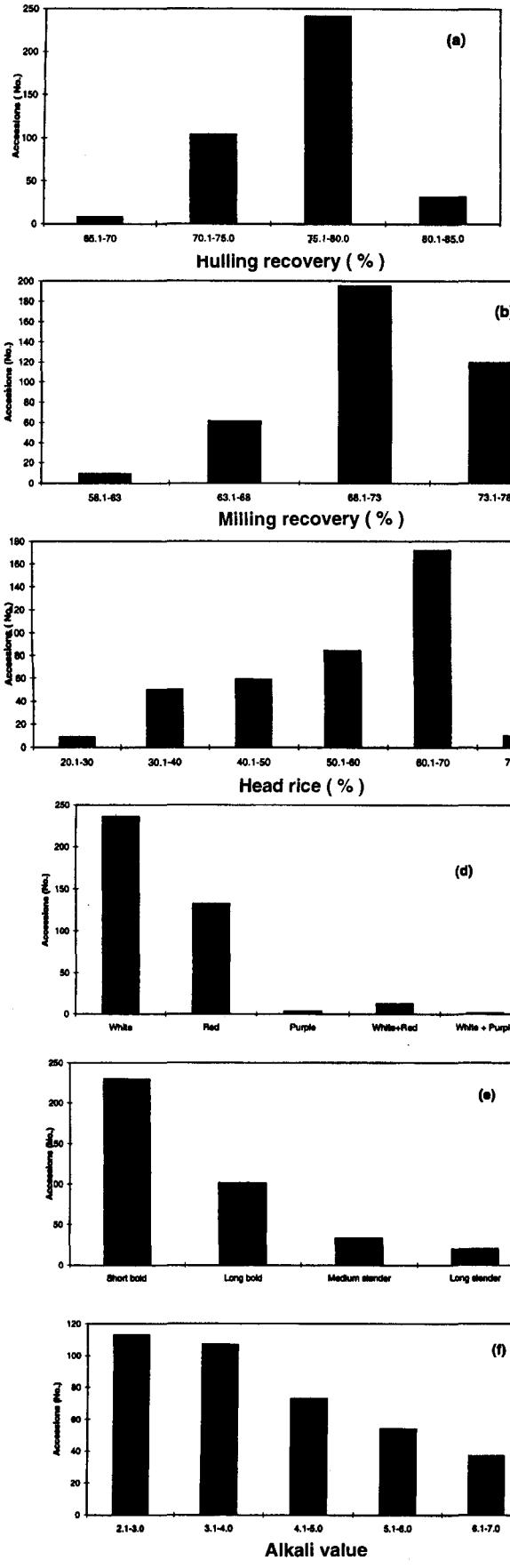
In the present collection, the environmental influence on head-rice recovery could not be ruled out fully as the accessions were evaluated in different seasons.

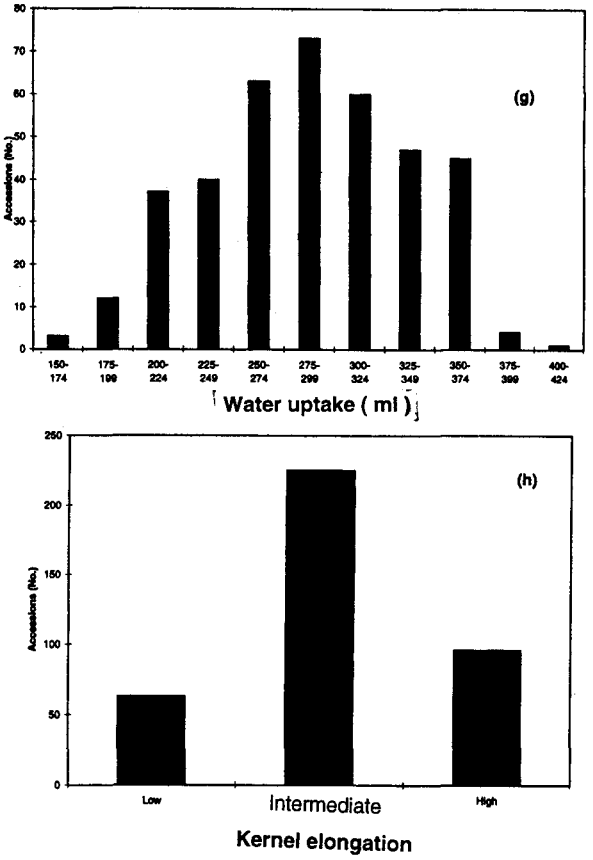
Kernel colour, size and shape

These are the important accession identifying traits. Further, size and shape also determine the commercial value of the crop. Most of the accessions had white kernel (61.5%) followed by those with red (35.4%). Only 3 accessions showed purple colour (Fig 1d). Apart from accessions having distinct colours, 13 exhibited mixed colour. Probably these accessions were not selected for kernel colour and continued to grow as a mixed populations, as phenotypically there was no difference in their grain size and shape. The variation for kernel size and shape was moderate (Table 2). The range and mean for kernel length were 3.89 (Satalchini, NIC 105815)-7.43 mm (A 08-391, HRC 1003) and 5.78 ± 0.03, respectively. Accessions A08-391 (HRC 1003), CNA 5166 (HRC 1032), IRAT 144 (HRC 106 1), Kalamkata (HRC III 0) and Kalamdani (HRC 212) showed kernels as long as 7.0 mm or more (Table 3). The L : B ratio which determines the grading of rice varieties varied from 1.68 (Charamuni, HRC 467)-3.91 (Kalamkata, HRC 1110). (Table 2). The accessions showing the high L : B ratio are listed in Table 3. The accessions with narrow kernels are of the desired type because kernel breadth is negatively related to L:B ratio. Accession Kalamkata (HRC 1110) had the minimum kernel breadth (1.82 mm) and IRAT 115 (HRC 1058) the maximum (3.07 mm). Several accessions having narrow kernels were identified from the present collection (Table 3). Of the 384 accessions, 230 were short bold (59.9%), only 20 accessions (5.2%) had long slender grains (Fig 1e.).

Chalkiness

The endosperm opacity or amount of chalkiness determines appearance of the milled kernel. Nevertheless, it does not affect eating or





nutritional quality but is important from the consumers point of view. The varieties with chalkiness have been reported prone to breakage during milling, hence varieties with clear endosperm are preferred. Only 41 accessions (10.8 %) had chalkeiness in kerenels, whereas 329 accessions (85.2%) showed clear endosperm. The rest showed occasional presence.

Gelatinization temperature and amylose content

Starch is the principal constituent of the rice grain. The properties of starch as exemplified by gelatinzation temperature and amylose content are the major determinant of rice quality, especially cooking and eating. Therefore, choice of suitable donors with these two traits is the pre-requisite for the success of rice quality improvement programme. The premium quality rice of India-Basmati possess long slender and transluscent grains, intermediate amylose content (20-25 %) intermediate gelatinization temperature (5-6 alkali value) aroma and high kernel linear elongation.

Table 3. Useful rice accessions for various quality traits for utilization in the hybridization

Character	Accessions
Hulling recovery (81.0%)	63-83A (HRC 1001), Arroz - De Producto (HRC 1008), CNA 4744 (HRC 1027), IAC 025 (HRC 1044), IRAT 240 (HRC 1027)
Milling recovery (76.0%)	Arroz De Producto (HRC 1008), Gora Malti (NIC 105699), IRAT 233 (HRC 1027), CNA 5164 B (HRC 103 1), CNA 4125 (HRC 1020)
Head- rice recovery (70 %)	Shyamjeera (HRC 701), IRAT 115 (HRC 1058), Satalchini (NIC 105815), Gora Malti (NIC 105699), CNA 5164B (HRC 1031).
Kernel length (7.0 mm)	A 08-391 (HRC 1003), CNA 5166 (HRC 1032) IRAT 144 (HRC 1061), Kalamkata (HRC II 10)
Kernel breadth (1.98 mm)	Kalamkata (HRC 1110), Raskadam (HRC 29), Improved Raskadam (HRC 30), Delhi Sathi (HRC 453), Kalamdani (HRC 212), Kalamkadhi (NIC 105784)
L : B ratio (3.19)	Kalamkata (HRC 1110)
Intermediate alkali value (5-6)	Aditya (HRC 756),A08-391 (HRC 1003), Kalamdan (NIC 105814), Kadamkudhi (NIC 105791), Badnasall (NIC 105783)
Intermediate amylose content	Aus 454 (HRC 1013), Badshabhog (NIC 105510), ARC 7046 (HRC 432), Bagya (HRC 762), Black gora (HRC 362), Ajondholi (NIC 105703)
Intermediate amylose content and gelatinization temperature	Ambemohar (HRC26), Badshabhog (NIC105598and Bangani (NIC 105598), Black gora (HRC 370), Brown gora (HRC 371)
Water uptake (380ml)	Laloo 14 (HRC 457), Bhattadhan (HRC 19), Improved Raskadam (HRC 30), Sathi 34-36 (HRC 35), Shyamjeera (NIC 105806)
Volume expansion (4.2)	Tupijhinga (NIC 105719), White gora (HRC 303), Pathri (HRC 205), Kalamdani (HRC 212), IRAT 144 (HRC 1061)
Cooked kernel length (11.6mm)	Maghidhan (NIC 105752), Kalamdani (HRC 212), IRAT 240 (HRC 1075), IRAT 144 (HRC 1061), Brown gora (HRC 407)
Kernel linear elongation (1.94)	White gora (HRC 318), Sudha (HRC 432), Salumpikit (HRC 20), Marto (HRC 741), Deeptisall (NIC 105758)

HRC Hazaribag Rice Collection Number, CRURRS, Hazaribag.
NIC National Indigenous Collection Number, NBPGR Base Centre, Ranchi.

Alkali digestion value gives an indication of gelatinization temperature. Alkali value ranged from 2.5 (ARC 11775, HRC 429) to 7.0 (ADT 33, HRC 766) and varied the most. Two hundred and twenty (57.3 %) accessions had high gelatinization temperature (1-3 alkali score). About 14.1 per cent of the accessions had intermediate gelatinizatiuon temperature (Fig If). A wide variation for this trait has also been reported earlier (Chauhan *et al.*, 1990; 1991). Of the 219 accessions analysed for amylose content, only Aditya and Neela, two rained upland varieties showed high amylose content (25%). Predominance of accessions (63.0%) with intermediate amylose content was observed in the present collection. Low amylose content (%) was observed in 79 accessions. Thirty five accessions had the desirable combination of both intermediate gelatinization temperature (4.5-5.5 alkali score) and intermediate amylose content.The range for this character being 12.5 (IRAT 133, HRC 1059)-26.1 % (Aditya, HRC 756).

Water uptake and volume of expansion

The basmati rices have high volume of expansion and water uptake. These two characters determine the cooking quality of rice. Fluffiness of cooked rice, is primarily due to water uptake and volume expansion. Water uptake exhibited considerable variation (CV 18%). Accession (Laloo 14) had the highest water uptake (415 ml). The accessions were fairly well distributed for this character (Fig 1g). Fifty accessions (13.0%) had the water uptake 350 ml. Two hundred and twenty eight accessions had less than 300 ml of water uptake. The accessions with high water uptake are listed in Table 3. Volume expansion did not show appreciable variation in this collection. The range being 3.5 (Raria, HRC 268)-4.3 (Pathri, HRC 205). In previous studies also, this character was observed to vary the least (Chauhan *et al.*, 1990; 1991).

Table 4 : Characterization of rice accessions with multiple desirable quality traits

Accession	Hulling recovery (%)	Milling recovery (%)	Head rice recovery (%)	Kernel length (mm)	L:B ratio	Akali value	Amylose content (%)	Water uptake (ml)	Volume expansion	Kernel elongation
Kalamdani (HRC212)	76.0	70.5	65.9	7.02	3.54	3.5	22.1	340	4.3	1.77
A08-391 (HRC1003)	80.0	74.8	66.0	7.43	2.80	5.5	-	370	4.0	1.48
Arroz-De product (HRC1008)	81.6	76.1	67.2	6.76	2.70	3.5	-	300	4.0	1.68
CNA 5164 B (HRC 1031)	81.6	76.1	70.7	6.37	2.19	2.5	-	230	4.0	1.63
I RAT 144 (HRC 1061)	79.6	74.1	68.3	7.13	2.55	3.5	-	225	4.2	1.63
IRAT 233 (HRC 1072)	81.7	76.3	53.4	6.48	2.39	5.5	-	265	4.0	1.66
Kalamkata (HRC 1110)	77.9	72.1	65.4	7.11	3.91	6.5	19.3	300	4.0	1.66
Gora Malti (NIC 105699)	80.0	76.7	72.8	5.52	2.41	6.5	19.8	305	3.7	1.77
Kalamkadhi (NIC 105784)	79.2	74.1	67.8	6.76	3.41	4.5	-	365	4.0	1.57

Underline values indicate desirable trait(s).

Table 5. Characterization of rice accessions with a) high kernel elongation, b) intermediate amylose content and gelatinzation temperature

Accession	Hulling recovery (%)	Milling recovery (%)	Head rice recovery (%)	Kernel length (mm)	L: B ratio	Alkali value	Amylose content	Water uptake (ml)	Volume expansion	Kernel elongation
(a) Linear elongation										
Salumpikit (HRC 20)	74.1	68.5	65.6	5.18	1.90	3.5	19.1	365	4.0	2.05
Whitegora (HRC 318)	76.3	70.7	40.0	5.03	1.72	3.1	21.5	295	4.0	1.95
Sudha (HRC 432)	77.3	72.6	66.4	5.32	2.08	5.5	21.5	330	4.0	2.03
Marto (HRC 741)	79.8	74.0	63.5	5.06	2.05	6.5	21.0	295	3.7	1.94
Deeptisall (NIC 105758)	78.0	72.5	68.0	5.10	1.90	4.5	360	4.0	1.96	
(b) Intermediate amylose content and gelatinization temperature										
Birsadhan 201 (HRC751)	77.0	68.5	58.0	5.49	2.06	4.5	21.7	265	4.0	1.86
Browngora (HRC 379)	80.1	75.2	56.4	5.41	2.05	5.5	21.5	220	4.0	1.81
Chaingora (NIC105534)	78.5	71.0	55.0	5.23	2.00	4.5	23.0	280	4.0	1.80
Jhilidhan (HRC 703)	80.0	75.0	68.3	6.09	3.01	4.5	21.0	280	4.0	1.84
Prakash (HRC 87)	73.0	68.8	43.3	5.17	2.23	4.5	20.5	315	3.7	1.93
Marto (HRC 741)	79.8	74.0	63.5	5.06	2.05	6.5	21.0	295	3.7	1.94

Underined values indicate desirable trait (s).

Kernel elongation

This is the most prized character in the high quality rice besides aroma. Cooked kernel length varied from 7.0 (Raskadam, HRC 29)-12.4 mm (Kalamdani, HRC 212) and exhibited low variability (Table 2). The average length was 9.85 + 0.05 mm. Kernel linear elongation although showed a wider range of 1.35 (Gaharadhan, HRC 1106) 2.05 (Salumpikit, HRC 20) but the character did not vary much (CV 6.1%). Most

of the accessions (225; 58.6 %) exhibited intermediate linear elongation (1.62 - 1.77). Ninty nine accessions showed high (1.77) kernal linear elongation (Fig 1h). Several potential accessions with multifile desirable quality traits were identified and characterized (Tables 4 and 5) among this collection for utilization in the quality improvement of rice.

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GENETIC DIVERGENCE FOR YIELD AND ITS COMPONENT TRAITS IN CULTIVATED *MICROSPERMA* LENTILS (*Lens culinaris* MED.)

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Forty one genotypes of lentil belonging to microsperma group of *Lens culinaris* were grouped into six clusters following non-hierarchical Euclidean cluster analysis utilizing data on a set of eleven characters related to yield and its contributing traits, Number of pods and seeds and leaves per plant, grain yield and biological yields per plant and harvest index were mainly responsible for the genetic divergence. Based on statistical distance and cluster mean values, five genotypes namely LL-19, LL-61, LL-117 and PL-7712 (from cluster IV) and K80 (from cluster V) were found to be most promising and hence, these genotypes may be used in future hybridization programmes to evolve desirable segregants.

Key words: Lentil, germplasm, genetic divergence, cluster analysis

Lentil (*Lens culinaris* Med.) is one of the important pulse crops of Indian sub-continent and ranks fifth on the production map of India with an area of 1.15 million hectares and production of 0.79 million tons with an average yield of 6.81 q/ha (Sharma, 1995). The Indian sub-continent is by far the largest lentil producing region of the world. The majority of the lentils grown throughout the world are local land races and only a few released cultivars are available to farmers (Sardana *et al.*, 1998). The improvement in the crop is limited, though a wide range of genetic diversity is available in collections of lentil (Solth and Erskine, 1981). Genetic diversity is an essential requirement for any crop improvement program, because genetically diverse parents when crossed, can bring together diversity of gene combinations either to exploit heterosis or to obtain superior recombinants. The genetic divergence between populations can be quantified by using several available statistical methods, of which multivariate analysis has been found to be most appropriate (Murty, 1965; Joshi and Dhawan, 1966). Therefore, an attempt was made to evaluate the magnitude of genetic diversity among 41 genotypes of lentil with the help of nonhierarchical Euclidean cluster analysis.

MATERIALS AND METHODS

The experimental material consisted of 41 genotypes of lentil (mostly cultivars) belonging to microsperma group of *Lens culinaris* Med. procured from different research institutes/universities of Uttar Pradesh. All the 41 genotypes were grown in a randomized block design with 3 replications at the Department of Agricultural Botany Research Farm, Ch. Charan Singh University, Meerut during rabi 1997-1998. Each genotype was evaluated in a plot of two rows of 5 in length. Observations were recorded on five random plants per genotype in each replication for 11 quantitative characters. The data were subjected to non-hierarchical Euclidean cluster analysis to measure genetic divergence following Beale (1969)

and Spark (1973). F test was utilized for assigning appropriate number of clusters.

RESULTS AND DISCUSSION

The analysis of variance indicated significant differences between genotypes for most of the metric characters studied except internode length, no. of seeds per pod and 100 seed weight. All the 41 genotypes were grouped into six clusters (Table 1). The cluster III had maximum number of 14 genotypes followed by clusters VI and II with 11 and 10 genotypes, respectively. Clusters I and V contained the minimum number of genotypes i.e. one genotype each. In lentil, it was observed that genetic drift and selection in different environments have caused greater genetic diversity than geographical distance (Bhatt, 1970; Chahota *et al.*, 1994).

Table 1. Distribution of 41 lentil genotypes in different clusters

Cluster No.	No. of genotypes	Name(s) of genotypes
I	1	JL-81
II	10	L-94, L-103, L-145, L-812, L-271, L-848, L-1205, L-130, LL-1269, P-570
III	14	JL-54, K-75, L-59, LL-75, LL-79, LL-97, LL-153, P-75, P-259, P-293, P-406, P-589, P-872, PL-639
IV	4	LL-19, LL-61, LL-117, PL-7712
V	4	K-80
VI	11	L-1282, LG-108, LL-175, LL-189, LL-1258, P-38, P-67, P-276, P-631, P-641, P-870

The intra- and inter-cluster divergence among the material studied was of varying magnitude (Table 2). Intra-cluster D^2 values ranged from a minimum of 1.897 in cluster II to a maximum of 3.175 in cluster IV. The maximum inter cluster D2 was obtained between clusters IV and V (8.728), followed by clusters I and IV (8.545), clusters I and V (8.055), clusters II and V (7.647) whereas inter cluster D^2 value was found to be minimum (2.307) between clusters II and VI suggesting close relationship between the clusters. The maximum inter-cluster distance observed between the clusters IV and V indicate that their members are far apart and it would be useful to attempt crosses among them. The magnitude of heterosis largely depends on the degree of genetic diversity in the parental lines.

Table 2. Estimates of average intra- and inter-cluster D 2 for six clusters constructed from 41 genotypes of lentil

Clusters	I	II	III	IV	V	VI
I	**0.000**	6.333	5.137	8.545	8.055	6.230
II		**1.897**	3.749	3. 960	7.647	2.304
III			**2.097**	6.269	5.951	2.789
IV				**3.175**	8.728	4.830
V					**0.000**	6.749
VI						**2.283**

Figures in bold print indicate intra-cluster D^2 values.

The cluster mean values for eleven quantitative characters presented in Table 3, provided an interesting picture of the nature of diversity. Crosses among divergent parents are likely to yield desirable combinations. Therefore, a crossing programme should be initiated between the genotypes belonging to different clusters. For this purpose following points are to be considered: (1) choice of clusters whose genotypes are separated by maximum inter-cluster distance, (ii) selection of those genotypes that showed good performance in the selected clusters. Based on these facts, genotypes LL-19, LL-61, PL-7712 and LL-117 of cluster IV (having maximum cluster means for all characters except days to maturity and number of pods per plant) and K-80 of cluster V (with maximum mean value for days to maturity) are expected to give promising transgressive segregants. These genotypes can be utilized in hybridization programmes aimed at yield improvement in lentil.

Table 3. Mean values of different characters in various clusters

Character		Cluster					
		I	II	III	IV	V	VI
1.	Plant height (cm)	4.90	36.39	35.55	41.22	34.58	39.30
2.	Internode length (cm)	2.18	2.29	2.16	2.34	2.14	2.29
3.	No. of leaves/plant	109.60	108.61	102.56	125.65	94.73	115.11
4.	Days to maturity	142.67	147.23	148.07	151.08	153.33	147.24
5.	No. of pods plant	59.07	92.01	61.58	87.13	51.07	76.63
6.	No. of seeds plant	83.07	130.77	89.94	134.18	74.33	111.65
7.	No. of seeds pod	1.47	1.43	1.47	1.56	1.50	1.46
8.	Grain yield/plant (g)	1.46	2.57	1.25	3.69	0.83	1.97
9.	Biological yield/plant (g)	6.26	8.71	5.56	10.86	4.04	5.66
10.	100 seed weight (g)	1.75	1.96	1.43	3.07	1.40	1.77
11.	Harvest index	23.20	29.50	22.86	33.79	20.48	35.73

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GENETIC DIVERGENCE IN LATE SOWN WHEAT (*Triticum aestivum* L. em Thell)

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Forty nine genotypes of wheat (*Triticum aestivum* L. em Thell) suited for late sown irrigated conditions were studied for their genetic divergence for a set of seven characters using Mahalanobis D^2 statistic. The genotypes could be grouped into seven clusters. The genetic diversity among genotypes did not show any relation to geographical diversity. Based on genetic divergence and superior cluster means, it is predicted that crosses between genotypes from clusters II, IV, VI and VII may result in superior types.

Key words : Wheat, genotypes, genetic divergence, hybridization

Choosing genetically diverse parents is a pre-requisite for any plant breeding programme because it enables the expansion of genetic base and there from development of superior types. The use of Mahalanobis' D^2 statistic based on quantitative traits to estimate genetic divergence has been emphasized by many workers (Bhatt, 1973; Jatasara and Paroda, 1983; Dasgupta and Das, 1984; Kuruvadi, 1988) to formulate the hybridization programme before effecting the actual crosses. Besides, the present status of wheat cultivation in North Indian wheat belt includes very few number of wheat cultivars like HD 2285, UP 2338, PBW 373, UP 2425, Raj 3765 and Raj 3077 (Tondon and Sethi, 1998). Of these, many are going to be obsolete. Hence, the genetic diversity of cultivars for late sowings is going to be very narrow. This situation demands diversification of genotypes at cultivar level which needs the availability of the genetic diversity in wheat germplasm which is going to contribute towards the development of late sown wheat.

MATERIALS AND METHODS

The experimental material consisted of 49 elite genotypes of wheat suited for late sowing and contributed by different wheat breeders of IARI, New Delhi and its regional stations located in different mega-environments of wheat cultivation. The experiment was laid out in a randomized block design with three replications during rabi season of 1997-98 under late sown irrigated conditions. Each genotype was planted in a plot having a gross area of 6 m × 1.08 m, with 6 rows at 18 cm apart. The recommended cultural and agronomical practices for late sown irrigated conditions were followed to raise the crop with respect to seed rate, fertilizer and irrigation requirement. Observations were recorded for seven yield contributing characters viz. plant height (cm), relative leaf water content (%), total chlorophyll content (mg/g of flag leaf sample), days to physiological maturity, number of seeds/spike, 1000-grain weight and grain yield/100 tillers. The mean values were subjected to Mahalanobis D^2 statistic to measure genetic divergence as suggested by Rao (1952) and the

clusters were formed by Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance exhibited highly significant differences among the genotypes for all the seven characters. On the basis of D^2 values, all the 49 genotypes were grouped into seven clusters (Table 1). The maximum number of genotypes were in cluster II (10 genotypes) while cluster V included the minimum number of genotypes (5 genotypes). It was interesting to note that the genotypes belonging to different eco-geographical areas were included in the same cluster. This indicated that there is no association between clustering pattern and eco-geographical distribution of genotypes. Hence, it seems that geographical diversity is not necessarily related to genetic diversity. These findings are on consonance with Bhatt (1970), Thete *et al.* (1987) and Garg and Gautam (1988). The clustering of genotypes from different eco-geographical locations into one cluster could be attributed to possible free exchange of breeding materials or even varieties from one place to another (Sharma and Hore, 1997). This may also be due to the fact that the unidirectional selection practised for a particular trait in several places produced similar phenotypes which were aggregated in one cluster irrespective of their geographic origin (Somayajulu *et al.*, 1970). On the other hand, many genotypes originating from one place were scattered over different clusters. Such genetic diversity among the genotypes of common geographic origin could be due to factors like heterogeneity, genetic architecture of the populations, past history of selection, developmental traits and degree of general combining ability (Murty and Arunachalam, 1966).

Table 1. Group constellation of the genotypes

Cluster	No. of genotypes	Genotypes included
I	6	PS 458, DL97-11, PS 463, GW 173, PS 460, Ind 98-34
II	10	DW 1093, PS 465, DW 1092, DW 1104, DL 97-8, PBW 373, DL 97-12, DW 1119, DW 1111, DW 1118
III	6	DW 1105, PS 456, PS 469, DW 1118, PS 466, Ind 98-32
IV	8	DL 97-9, DW 1120, PS 467, Ind 98-36, DL 97-10, DW 1097, WR 821, PS 464
V	5	Ind 98-35, Ind 98-33, DW 1123, DW 1106, DW 1115
VI	6	PS 461, DW 1114, HW 2045, DW 1102, PS 462, DW 1117
VII	8	PS 470, NIAW 34, PS 468, PS 459, HP 1744, PS 457, PS 455, DW 1122

Sources of genotypes:
IARI, Regional Station, Pusa (Bihar) : PS series
IARI, Regional Station, Indore (MP) : Ind Series
Rust Genetics Group, IARI, N. Delhi : DL series
High Fertility Irrigated Group, IARI, N. Delhi : DW series
Interspecific Programme, IARI, N. Delhi : WR series
Miscellaneous and Standard Checks : GW,HP,NIAW,HW series

The intra- and inter-cluster divergence among the genotypes was of varying magnitude (Table 2). It can be seen that intra-cluster distance was maximum for cluster II while cluster I showed minimum intra-cluster distance. The highest inter-cluster distance was noted between cluster I and II. The distance between cluster III and VII was minimum indicating close relationship between these clusters. The greater the genetic distance between clusters, wider is the genetic diversity between genotypes. The cluster means for each character are presented in Table 3. Cluster VI showed the highest mean for plant height, relative leaf water content, days to physiological maturity and grain yield/100 tillers. The highest mean for total chlorophyll content was observed for cluster II. Cluster IV exhibited the highest mean number of seeds/spike. The maximum mean for 1000-grain weight was observed for cluster III. The lowest mean for plant height, total chlorophyll content, number of seeds/spike and grain yield/100 tillers was observed for cluster I. Cluster VII showed minimum mean for relative leaf water content.

Table 2. Inter and intra cluster distances (D^2 and $\sqrt{D^2}$ values) for 7 characters

Cluster		I	II	III	IV	V	VI	VII
I	D^2 $\sqrt{D^2}$	236.49 (15.38)	674.95 (25.98)	427.32 (20.67)	609.17 (24.68)	299.90 (17.32)	644.48 (25.39)	435.28 (20.86)
II	D^2 $\sqrt{D^2}$		369.61 (19.22)	576.67 (24.01)	461.32 (21.48)	583.79 (24.16)	469.77 (21.67)	510.40 (22.59)
III	D^2 $\sqrt{D^2}$			2567.90 (16.06)	379.24 (19.47)	373.41 (19.32)	437.13 (20.91)	281.64 (16.78)
IV	D^2 $\sqrt{D^2}$				336.06 (18.33)	671.98 (25.92)	373.56 (19.33)	501.46 (22.39)
V	D^2 $\sqrt{D^2}$					244.98 (15.65)	618.37 (24.87)	530.73 (23.89)
VI	D^2 $\sqrt{D^2}$						296.27 (17.21)	367.36 (19.17)
VII	D^2 $\sqrt{D^2}$							270.70 (16.45)

Table 3. Cluster means of 49 genotypes for 7 characters

Cluster	Plant height (cm)	Relative leaf water content (%)	Total chlorophyll content (mg/g)	Days to physiological maturity	Number of seeds/spike	1000-grain weight (g)	Grain yield/100 tillers (g)
I	81.19	56.13	1.74	116.50	37.72	40.67	155.60
II	83.13	57.57	2.96	120.17	45.67	39.78	189.27
III	85.07	58.27	2.35	114.94	38.22	45.66	183.96
IV	84.02	64.49	2.01	117.67	49.92	40.01	196.88
V	87.66	55.20	1.96	120.73	41.40	37.50	155.83
VI	89.80	70.02	2.17	121.06	45.78	42.53	198.78
VII	87.82	51.56	2.09	119.03	40.83	44.13	189.49

Cluster III had the lowest mean for days to physiological maturity. Cluster V exhibited the lowest mean for 1000-grain weight.

On the basis of divergence and grain yield and components of grain yield, it is suggested that maximum heterosis and good recombinants could be obtained in crosses between genotypes of clusters II, IV, VI and VII. This information may be useful to the breeders engaged in varietal improvement programmes of late sown irrigated wheat.

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GENETIC DIVERGENCE IN MULBERRY GERMPLASM

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The analysis of variance for nine characters of 124 accessions of mulberry (*Morus* L.) germplasm indicated the significant differences due to genotypes, seasons and their interactions. The heritability coefficients for fresh weight of leaves, internode length and plant height were high (> 0.7). The 124 accessions were grouped into 11 clusters, indicating the existence of considerable diversity. Maximum number of genotypes were included in cluster I (114) and other clusters contained one genotype each. The genetic diversity and geographical distribution were not related. Fresh weight of leaves, plant height, lamina-petiole ratio by weight and internode length were the most potential characters contributing to the total genetic divergence. Intra-cluster D^2 values were 0-4.95 and inter-cluster 2.963-17.24. The cluster IX and cluster XI were highly divergent. Highest mean performance was observed for more number of characters in cluster XI, followed by cluster IV. The inter-cluster divergence was also more between these two clusters (14.341) and accessions from these clusters can be used as promising parents, for varietal improvement through hybridization.

Key words: Mulberry, germplasm, divergence, cluster analysis

Mulberry (*Morus* L.) is the most important component of the sericulture industry as its leaf is the sole food source of the silkworm (*Bombyx mori* L.). Since area of mulberry cultivation is spreading to different climatic conditions in the country, it is imperative to emphasize the need to develop superior as well as location-specific mulberry cultivars. To cater to these demands, large scale long-ranging breeding programmes are necessary. As a back up, an adequately conserved broad genetic base of mulberry and its systematic evaluation for various desirable characters is a prerequisite.

For the choice of diverse parents, and their utilization in hybridization programmes, multivariate analysis by Mahalanobis D^2 statistics has been extensively used in quantifying the degree of genetic divergence among parents in numerous crops (Bartual *et al.*, 1985). It appears that relatively little information is available on mulberry (Susheelamma *et al.*, 1997). The present study was undertaken to measure the genetic diversity among mulberry genotypes to identify the suitable parents for hybridization, for its improvement.

MATERIALS AND METHODS

The 124 mulberry genotypes evaluated were acquired by field collections, genetic exchange and through visiting scientists. These genotypes were maintained in the field genebank (Mallikarjunappa *et al.*, 1995). Data were recorded on propagation parameters like sprouting and rooting of cuttings, growth and yield parameters like plant height, number of branches per plant, internode length, fresh weight of 100 leaves, lamina-petiole ratio by weight and quality parameters like leaf water

content and leaf water loss at six hours after harvest (from five plants per accession), for nine trials covering different seasons, from 1989-1994.

The mean values were subjected for analyses of variance. Multivariate analysis was carried out using Mahalanobis D^2 statistics (Mahalanobis, 1936). The genotypes were grouped into different clusters following the Tocher's method as described by Rao (1952). The relative contribution of different characters towards divergence was estimated.

RESULTS AND DISCUSSION

The analysis of variance showed highly significant differences between the genotypes and the environments (seasons) for all the nine characters, indicating the existence of genetic variability in the genotypes studied. Heritability coefficients indicated that characters like fresh weight of leaf, internode length and plant height were highly heritable (> 0.7) and rooting, number of branches per plant and lamina-petiole ratio by weight were having moderate heritability of 0.61-0.63 (Table 1).

Based on the relative magnitude of D^2 values, the 124 genotypes were grouped into 11 clusters (Table 2). The maximum genotypes (114) were included in cluster I. Whereas, clusters II to XI were unique with only single genotype each. The grouping pattern indicated that the clusters were heterogenous with respect to geographical origin of the genotypes. It indicated that the genotypes from different geographic regions, do not necessarily give good recombinants, and therefore genotypes should be evaluated on the basis of their individual merit and genetic diversity (Joshi and Rana, 1997). According to Murty and Arunachalam (1966), the genetic drift and selection in different environments could cause greater diversity than the geographic distance.

The intra-cluster divergence was zero for all the clusters except cluster I (4.95). Minimum inter-cluster distance was observed between cluster III and cluster V (2.963), followed by cluster V and cluster VII (3.754), indicating the close relationship among these clusters (Table 3). Maximum inter-cluster distance was found between cluster IX and cluster XI (17.24). This indicated that the genotypes included in these clusters had maximum divergence (Sardana et al., 1998). These clusters were followed by cluster VI and Cluster XI (14.961) and cluster IV and cluster XI (14.341).

The contribution of different characters towards genetic divergence was calculated by using Mahalanobis D^2 divergence (Table 1). The character fresh weight of leaf contributed maximum (35.85%), followed by plant height (15.57%), lamina-petiole ratio by weight (15.38%), internode length (13.30%) and rooting (10.12%). The least contribution was from leaf water content (0.18%), followed by leaf water loss (0.37%). The potent variables such as fresh weight of leaves, plant height, lamina- petiole ratio by weight, internode length and rooting can be given greater importance in selection of potential parents for hybridization.

The existence of diversity among the genotypes was also supported by the considerable amount of variation in cluster means for different characters (Table 3). Cluster XI ranked first for plant height (197.73), fresh weight of leaf (909.01) and internode length (8.04). cluster X recorded the highest value for rooting (56.33). Cluster VIII has shown highest value for lamina-petiole ratio by weight (14.70), whereas cluster IV consisted the highest value for number of branches per plant (30.78). Since the inter- cluster distance between cluster IX and cluster XI has been the highest, the maximum number of mean values for the characters was found to be only three, viz., plant height, internode length and the fresh weight of leaves. The inter-cluster distance between clusters VI and XI has been the second highest, the number of characters with higher mean values were again found to be above mentioned three

Table 1. Mean squares from analysis of variance for nine characters, heritability and contribution of different characters to the diversity in mulberry

Character	Mean	Trials (d.f. 8)	Genotypes (d.f. 123)	Error (d.f. 984)	Heritability (h^2)	Contribution (%)
Plant height (cm)	173.9	49971.01**	14113.63**	618.78	0.7079	15.57
No. of branches/plant	21.42	2093.71**	415.11**	27.39	0.6113	7.78
Internode length (cm)	4.56	3.87**	5.65**	0.19	0.7538	13.3
Fresh wt. of 100 leaves (g)	412.53	68582.49**	194668.09**	4938.75	0.8102	35.85
Lamina-petiole ratio by wt. (%)	8.37	39.89**	19.46**	1.24	0.6203	15.38
Leaf water content (%)	74.57	66.94**	30.60**	8.54	0.2229	0.18
Leaf water loss (%)	12.65	309.02*	70.98**	18.57	0.2388	0.37
Sprouting (%)	65.64	25633.94**	3570.43**	698.84	0.3135	1.46
Rooting (%)	31.35	12427.70**	4134.99**	245.80	0.6374	10.12

Table 2. Distribution of 124 mulberry genotypes in 11 clusters based on D^2 values

Cluster	No. of genotypes	Genotypes with origin
I	114	Indigenous-78
		Exotic - 46 (from 7 countries)
II	1	Ooshima (Japan)
III	1	Rymenokuwa (Japan)
IV	1	*M. multicaulis* (China)
V	1	Daimyo Nishiki (Japan)
VI	1	Tokiyutaka (Japan)
VII	1	Acc. no. 246 (Japan)
VIII	1	Chigimikawa (Japan)
IX	1	Acc. no. 175 (Japan)
X	1	Cemeintero (venenzuela)
XI	1	*M. laeviqata* (India)

Table 3. Average intra- (in bold) and inter-cluster values of D^2 in 11 clusters of mulberry germplasm

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**4.95**	6.737	7.782	6.412	8.712	8.054	9.345	7.953	10.516	8.516	12.008
II		**0**	4.591	9.917	4.737	4.178	5.131	6.695	6.514	8.246	11.621
III			**0**	11.693	2.963	6.464	3.913	8.036	8.955	6.05	9.562
IV				**0**	12.483	10.543	13.302	8.359	12.719	11.707	14.341
V					**0**	6.47	3.754	8.368	8.281	6.417	10.557
VI						0	4.827	7.625	3.98	11.149	14.961
VII							**0**	9.433	6.564	9.175	13.159
VIII								**0**	0.946	9.821	11.255
IX									**0**	13.47	17.24
X										**0**	6.186
XI											**0**

Table 4. Cluster mean values for nine characters in mulberry

Character	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
Plant height (cm)	179.54	90.60	120.72	196.90	67.44	65.03	70.11	87.38	27.10	173.33	197.73
No. of branches/plant	22.30	7.22	13.33	30.78	8.79	8.57	5.56	9.89	3.22	13.22	13.22
Internode length (cm)	4.60	3.79	4.21	4.66	4.02	2.16	2.82	4.30	1.10	6.40	8.04
Fesh wt. of 100 leaves (g)	398.35	466.00	760.87	141.06	745.62	416.10	722.14	376.32	355.44	848.34	909.01
Lamina-petiole ratio by wt. (%)	8.27	7.83	8.49	10.72	8.54	8.83	7.81	14.70	7.69	8.53	11.16
Leaf water content (%)	74.61	73.46	77.51	70.21	75.50	74.98	77.82	73.74	66.24	76.67	75.15
Leaf water loss (%)	12.71	12.54	9.35	22.43	8.09	15.44	7.50	15.48	11.65	8.78	8.43
Sprouting (%)	67.90	13.49	34.26	67.44	45.10	28.45	54.85	29.43	31.09	66.50	28.59
Rooting (%)	32.80	1.27	0.56	45.83	28.44	3.81	5.60	4.64	1.67	56.44	0.00

characters. Further, the inter-cluster distance between cluster IV and cluster IX was found to be third highest and the number of characters with higher mean values were found to be four, viz., number of branches per plant, in addition to above mentioned characters. Also, the characters with second higher mean values were found to be more between these two clusters. Hence, genotypes of the cluster XI (Accn. no. 181) and cluster IV (Accn. no. 188), would be the better parents for hybridization programmes (Singh *et al.*, 1998). In addition, the genotypes with outstanding mean performance from the other clusters could also be involved as potential parents in interspecific hybridization, for developing superior mulberry cultivation.

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GENETIC DIVERGENCE AMONG FIELD BEAN (*Lablab purpureus* L Sweet) CULTIVARS OF SOUTHERN KARNATAKA

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A total of 144 collections of field bean belonging to southern Karnataka revealed considerable diversity. The accessions were grouped into 15 clusters. The genetic diversity observed was not related to geographic diversity. Grain yield, pods per plant, inflorescence per plant, branches per plant and days to 50% flowering were the most potential traits contributing to the total divergence. Clusters XV and VIII were important because they comprised accessions with high yield, pod number, inflorescence per plant and branches per plant (cluster XV) and early duration and photoinsensitivity (cluster VIII). By utilizing these accessions desirable segregants may be evolved through hybridization.

Key words : Field bean, *Lablab purpureus*, divergence, clusters

Lablab purpureus L. Sweet, commonly referred to as field bean or Dolichos bean or Lablab bean is an important legume crop of Karnataka grown for both grain and fodder purpose. Southern Karnataka is by far the largest field bean producing region of the India. The majority of field bean grown are local land races and only a few released cultivars available to farmers. Attempts are therefore, being made for developing desirable high yielding field bean genotypes for increased productivity and production under the agroclimatic conditions of Southern Karnataka. In the present study, an attempt has been made to identify genetically divergent parents which can be utilized in hybridization programme.

MATERIALS AND METHODS

The experimental material comprised of 144 germplasm collections of field bean from Southern Karnataka. The accessions were grown in a 12 × 12 simple lattice design with two replications during Kharif 1998 at GKVK Farm, University of Agricultural Sciences, Bangalore. Each germplasm line of 5.0 metre length was sown with spacing of 90 cm between rows and 20 cm with in the row. Observations were recorded on five plants choosen at random in each replication for 14 growth and yield component characters viz., days to 50% of flowering, days to maturity, plant height (cm), branches per plant, inflorescence per plant, fruiting nodes per inflorescence, pods per plant, pod length (cm), pod width (cm), seeds per pod, pod weight (g), grain yield per plant (g), 100 seed weight (g) and shelling per cent. Genetic divergence was determined using Mahalanobis D^2 statistics (Mahalanobis, 1936) and the genotypes were grouped into clusters according to Tocher's method (Rao, 1952). The inter and intra cluster distances were also calculated following the method of Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the 14 characters studied. Based on D^2 values,

the 144 field bean genotypes were grouped into 15 clusters by Tocher's method (Table 1). The cluster I included maximum number (78 genotypes). Among other clusters, 16 genotypes were grouped in cluster II, 15 in cluster III, 8 in cluster IV, 6 each in cluster VI and VIII, 4 in cluster VII, 3 in cluster V and 2 in cluster X, respectively. The remaining six clusters are mono genotypic. The clustering pattern of cultivars, as they are of the same geographical origin, might have resulted from genetic drift followed by selection (Murthy and Arunachalam, 1960). Similar observations were also made by Baswana *et al.* (1980), Pandey *et al* (1983), Nayar (1984) and Singh (1991) in field bean. As a consequence, the character constellation that might be associated with particular region, in nature loose their individually under human interference. This suggested to choose diverse parents based on D^2 analysis rather geographical isolation for hybridization.

Table 1. Distribution of 144 field bean genotypes in different clusters

Cluster No.	No. of Genotypes	Accession Number (GA numbers)
I	78	GA 49, 54, 31, 41, 34, 122, 130, 130, 102, 94, 46, 51, 127, 58, 33, 55, 115, 134, 105, 91, 135, 95, 133, 131, 99, 136, 109, 22, 120, 29, 53, 63, 8, 68, 72, 64, 67, 37, 132, 36, 35, 93, 92, 59, 38, 17, 21, 89, 77, 90, 103, 126, 9, 86, 42, 108, 57, 90, 74, 16, 47, 12, 116, 26, 65, 52, 28, 15, 106, 48, 137, 100, 40, 25, 96, 18 and 32.
II	16	GA 43, 129, 14, 88, 87, 111, 39, 113, 114, 128, 27, 84, 119, 104, 112 and 24
III	15	GA 62, 83, 82, 66, 75, 73, 125, 50, 3, 6, 1, 123 and 56, 14 and 78.
IV	8	GA 11, 124, 110, 118, 45, 85, 69 and 76
V	3	GA 60, 23 and 121
VI	6	GA98, 79, 13, 10, 70 and 2
VII	4	GA 5, 71, 61 and 7
VIII	6	GA 143, 144, 139, 141, 142 and 140
IX	1	GA 117
X	2	GA 107 and GA 20
XI	1	GA 4
XII	1	GA 97
XIII	1	GA 138
XIV	1	GA 101
XV	1	GA 19

The intra and inter D^2 values on pooled basis are presented in Table 2. The clusters IX, XI, XII, XIII, XIV and XV showed zero magnitude of intra-cluster distance being solitary. The cluster VI had maximum intra-cluster divergence (160.90). The other intra-cluster differences lying between these two values. Genotypes grouped into the same cluster would diverge very little than those grouped in different clusters. Therefore, it would be desirable to attempt crosses between genotypes belonging to different clusters for getting desirable recombinations. In the present study, the inter cluster distance was maximum between cluster VIII and XV (2313.60), suggesting that the genotypes from these clusters were highly divergent from each other. Similarly cluster XI and XV were also quite diverse (2046.1). The minimum intercluster distance was observed between cluster II and V (150.00) indicating close relationship among the genotypes contained in them.

The cluster means for 14 characters on pooled basis (Table 3) indicated that the solitary cluster CV with genotype GA 19 had the highest mean in respect of grain yield per plant, branches per plant and pods per plant. The cluster VIII exhibited lowerst means for days to 50 per cent flowering, days to maturity and inflorescence per plant. Hence, it could be concluded that significant genetic diversity exist among 144 genotypes for most of the important characters. This could be attributed to long term selection in different directions by both natural and human forces. In

Table 2. Inter-cluster (above diagonal) and intra-cluster (diagonal) D2 values for 15 clusters in field bean

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	115.97	213.49	165.57	223.76	162.5	182.53	280.78	744.63	229.24	547.47	390.03	497.14	498.68	617.3	1001.12
II		120.68	295.97	394.43	150	341.02	573.41	1084.5	500.78	208.32	767.77	531.51	802.84	316.88	558.59
III			103.35	216.93	236.52	172.68	259.18	535.43	399.48	621.05	358.08	430.14	325.49	616.54	966.09
IV				136.39	318.85	280.07	422.4	904.36	496.1	321.87	283.09	501.09	501.96	647.87	1081.92
V					136.73	257.95	398.19	872.46	302.29	356.14	558.74	605.81	658.96	525.04	801.49
VI						160.9	393.36	797.82	437.48	603.62	522.59	377.15	501.96	820.7	811.91
VII							102.86	329.48	208.67	1096.35	171.42	938.5	239.47	1312.69	1759.68
VIII								115.1	797.59	1643.99	397.63	1508.99	221.12	1904.34	2313.6
IX									0	1001	349.86	913.82	632.42	1239.3	1718.1
X										141.31	1374.85	854.48	1370.19	256.51	353.13
XI											0	785.93	269.45	1458.65	2046.17
XII												0	959.69	388.77	841.94
XIII													0	1415.16	1804.54
XIV														0	215.86
XV															0

Table 3. Means for 14 quantitative characters of 15 clusters in field bean

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Inflorescence per plant	Fruiting nodes per inflorescence	Pods per plant	Pod length (cm)	Pod width (cm)	Seeds per pod	Pod yield per plant (g)	Grain yield per plant (gm)	100 seed weight (g)	Shelling per cent
I	102.12	141.38	56.95	7.21	15.85	6.47	62.11	4.40	1.65	3.72	62.25	43.83	25.41	70.52
II	107.12	146.72	58.93	7.15	16.58	6.70	78.86	4.56	1.71	3.77	81.41	49.16	26.78	59.88
III	87.97	136.07	61.25	7.00	15.57	7.22	69.52	4.48	1.67	3.74	65.75	44.81	24.96	71.49
IV	105.25	144.43	59.89	7.65	14.61	7.61	68.71	4.37	1.29	3.78	63.96	42.88	25.05	69.09
V	109.33	147.16	60.60	6.65	16.00	6.30	65.19	4.54	1.69	3.75	73.49	45.52	25.53	60.79
VI	99.58	141.25	62.45	7.10	15.91	7.71	84.26	4.49	1.68	3.72	80.17	61.78	26.86	74.12
VII	86.12	133.12	62.18	6.29	13.28	7.30	32.65	4.72	1.69	3.69	33.97	26.84	26.06	78.73
VIII	49.83	113.08	57.23	6.68	7.91	6.99	28.72	4.46	1.68	3.80	33.03	26.72	23.02	80.80
IX	118.00	158.00	51.80	6.32	16.35	6.95	30.30	4.50	1.68	3.64	33.57	25.93	27.99	77.09
X	108.75	149.75	59.55	7.32	17.12	7.-5	94.25	4.79	1.76	3.91	103.20	56.20	27.04	54.48
XI	81.50	130.00	72.20	6.20	13.90	6.65	27.55	4.49	1.32	3.34	23.16	16.38	23.40	70.55
XII	113.00	153.50	73.20	8.80	16.30	6.25	105.10	4.39	1.34	3.76	87.07	63.14	21.25	72.50
XIII	62.00	122.00	92.40	9.70	13.00	8.15	47.35	4.48	1.67	3.61	44.92	34.93	25.23	77.77
XIV	113.00	157.00	61.50	6.90	18.10	8.00	123.00	4.45	1.65	3.67	116.56	72.20	24.69	61.91
XV	103.00	143.00	66.85	12.20	29.35	6.42	157.40	4.48	1.65	3.80	169.22	117.64	27.92	67.43
Mean	96.44	141.03	64.79	7.00	15.99	7.05	17.66	4.51	1.61	3.71	71.45	48.53	25.41	66.28
SE	5.05	3.25	2.49	0.41	1.14	0.16	9.66	0.03	0.04	0.03	9.89	6.37	0.46	3.80
CV (%)	20.30	8.93	15.12	21.12	27.61	8.65	52.19	2.93	9.32	3.23	53.61	50.37	7.03	23.04

this context, grain yield, pods per plant, inflorescence per plant, branches per plant and days to 50% flowering are the important characters contributed substantially to the genetic divergence.

Crosses among genetically diverse genotypes are likely to yield desirable recombinants. Therefore, a crossing programme between the genotypes belonging to divergent clusters might be useful for identifying such recombinants. Among the six possible crosses between cluster VIII and XV, three crossing programmes viz., GA141 × GA19, GA142 × GA19 and GA143 × GA19 appeared to be most promising to combine duration and high yield potential as the D^2 value between these clusters was very high. All the three genotypes, GA 141, GA 142 and GA 143 from cluster VIII were characterized by early duration and photo insensitiveness, the two most important characters for developing varieties for growing field bean throughout the year. Moreover, GA 19 from the cluster XV was characterized by high pod number, inflorescence per plant and branches per plant, the most important yield components in field bean. Therefore, it is possible that, the three crossing programmes involving parents material on the basis of genetic divergence might lead to an overall improvement in yield combining with early maturity and photo insensitivity in field bean.

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GENETIC DIVERSITY IN TRADITIONA AROMATIC RICE ACCESSIONS FROM MADHYA PRADESH

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Genetic diversity among 300 traditional aromatic rice accessions was worked out using non-hierarchical Euclidean cluster analysis. Based on genetic distance, these accessions were grouped into 16 different clusters, of which cluster II with 61 genotypes was the largest. The maximum intra-cluster distance was observed in cluster XII (D = 1.911) followed by cluster XI (D = 1.676) and cluster XV (D = 1.610). Cluster XII and XIII were identified as genetically the most divergent. The inter-cluster distances indicated the greater divergence between cluster XII and XIII followed by clusters XI and XII, clusters V and XII, clusters IX and XII, clusters I and XII. The average genetic distance for all possible pairs of combinations ranged from 1.165 (II, VI) to 6.475 (XII, XIII). The highly diverse and superior germplasm accessions viz., H:41 I, S:715, D:1017 and T:150 of cluster XII, A:367 II, W:48, B:801 and A:283 of cluster XIII, U:78 II, B:2354, C:340 and B:1209 of cluster XI, L:1238 II, B:1094 II, B:323 II, B:2604, B:1717 and B:2402 of cluster V, A:328 I, B:1693, B:323 I, B:2495 and C:751 of cluster IX, U:69 II, B:1322, B:1389, B:2461, B:2812 and V:9 of cluster I, were selected and appeared the most promising. These selected accessions may be utilized as donors in rice breeding programme for developing semidwarf, high yielding, early aromatic rices with good grain quality.

Key words : Rice, *Oryza sativa*, divergence, quality, yield

Genetic improvement mainly depends upon the amount of genetic variability present in a population. In any crop, germplasm serves as a valuable source of base population and provides scope for wide variability. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parents for breeding programme (Vivekanandan and Subramanian, 1993).

In respect of the rice germplasm, Chhattisgarh, India can be considered as a centre of divergence where approximately at every 250 ha, the germplasm pattern changes (Richharia, 1979). With increase in rice production, greater emphasis is being given to aromatic rices with good grain quality and has been of major concern to rice breeding programme in recent years. The development of improved high yielding germplasm with superior grain qualities along with aroma is one of the most important objectives.

The spectrum of variability in segregating generations for grain yield and other traits depends on the genetic diversity of the combining parents. Hence, estimation of genetic diversity for grain yield and other traits among genotypes is important for planning the future crossing programmes. Characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures, such as D^2 statistic (Mahalanobis, 1936) and non-hierarchical

Euclidean cluster analysis (Beale, 1969; Spark, 1973). These potent tools for estimation of divergence has been emphasised by many workers (Murty and Arunachalam, 1966; Anand and Murty, 1968; Arunachalam, 1981; Rahaman *et al.* 1997; Mehetre *et al.* 1998; Sarawgi *et al.* 1998; Sharma *et al.* 1998; Soni *et al.* 1999). Understanding the genetic diversity for grain yield and other components in traditional rice accessions and its utilization for selection of desirable parents, either for exploitation of hybrid vigour or to get desirable recombinants is important for developing high yielding, aromatic, semidwarf, multiple resistant with good grain quality varieties.

In India, farmers mostly grow traditional aromatic rice varieties. Eventhough these varieties are well adapted to the local conditions, they are tall, scented and poor yielders (Sinha *et al.* 1991). The knowledge of available genetic diversity in traditional aromatic rice accessions pave the way to success for varietal improvement programme. The present investigation was carried out to ascertain magnitude of genetic diversity present in the traditional aromatic rice accessions with the objectives to develop high yielding export quality variety.

MATERIALS AND METHODS

The material for the study consisted of 300 geographically diverse aromatic accessions of *indica* rice collected from various places of Madhya Pradesh state in India (Table 1). The material was grown in a randomized complete block design with two replications. Direct seeded line sowing method was used for establishment of seedling. Each accession was grown in plots of four rows at a spacing of 20 cm between rows. The experiment was conducted during the wet season. The nutrients (N:P:K) were applied at the rate of 80, 50 and 30 Kg ha^{-1} asurea, super phosphate and muriate of potash, respectively. No plant protection measures were applied. Observations

Table 1. Details of rice accessions

S. No.	Accession Number	Area of collection (State Madhya Pradesh)		
		District	Block	Village
1.	B:372	Raipur	Kurud	Bhothli
2.	:996	Sarona	Devena	Dhunsing
3.	B:1589	Raipur	Dharsenwa	Banarsi
4.	B:2357	Raipur	Mainnpur	Idagaon
5.	B:13 II	Bastar	Bastar	Chiralpadar
6.	B:25	Bastar	Jagdalpur	Dhaniatur
7.	B:173 I	Bilaspur	Malharoda	Malkharoda
8.	B:173 II	Bilaspur	Malkharoda	Malkharoda
9.	B:173	Bilaspur	Malkharoda	Malkharoda
10.	B:189 III	Bilaspur	Pandaria	Pandaria
11.	B:497 II	Bastar	Jagdalpur	Kohkapal
12.	B:1049 III	Durg	Dhamda	Hirri
13.	M:1 A III	Raipur	Bilaigarh	Purgaon
14.	C:72 II	Bilaspur	Pandaria	
15.	C:395 B	Seoni	Kewlari	Ugli
16.	C:606	Bilaspur	Mungeli	Jamkor
17.	C:839	Raipur	Dharsinwa	Pawni
18.	D:812	Shahdol	Kotma	Kotma
19.	D:19 I	Raipur	Devbhog	Amlipatar
20.	D:202	Raipur	Balodabazar	Lavan
21.	D:297	Hoshangabad	Piparia	Nagpura
22.	D:339	Rajnandgaon	Bodla	Odekera
23.	D:378	Jabalpur	Patan	Barodaghidi
24.	D:452	Seoni	barghat	Sarekha
25.	D:459	Raipur	Tilda	Nagpura
26.	D:672	Durg	Saja	Ballootola
27.	D:675	Durg	Bemetara	Navagaon
28.	D:684	Sidhi	Sidhi	Jamodi
29.	D:691	Rajnandgaon	Chhuikhadan	Khurmudi
30.	D:692	Rajnandgaon	Chhuikhadan	Dhodra
31.	D:693	Durg	Dhamdha	Birjhapur
32.	D:699	Mandla	Bichhia	Ajania
33.	D:712	Raipur	Kasdol	Tundra
34.	D:725	Raipur	Devbhog	Kodobhanta
35.	D:727	Raipur	Devbhog	Sargimuda
36.	D:741	Shahdol	Pali	Ladera
37.	D:751	Mandla	Mandla	Patpara

38.	D:753	Mandla	Mainpur	Chichgaon
39.	D:762 I	Raipur	Tilda	Tarashiv
40.	D:773	Balaghat	Baihar	Kukurra
41.	D:776	Balaghat	Waraseoni	Koste
42.	D:777	Balaghat	Bissa	Nevargaon
43.	D:777 II	Balaghat	Bissa	Nevargaon
44.	D:809	Balaghat	Kirnapur	Hirg
45.	D:833	Bastar	Sarona	Danwarkhar
46.	D:864	Rajnandgaon	Rajnandgaon	Dharregaon
47.	D:874	Balaghat	Waraseoni	Tegawela
48.	D:875	Balaghat	Waraseoni	Tegawela
49.	D:889 I	Balaghat	Kirnapur	Kakodi
50.	D:893 II	Balaghat	Kirnapur	Seoni
51.	D:896 I	Balaghat	Kirnapur	Pathri
52.	D:904	Balaghat	Calbarra	Beori
53.	D:908 II	Bilaspur	Masturi	Nargoda
54.	D:914	Raipur	Fingeshwar	Sorip
55.	D:921 II	Raipur	Devbhog	Amlipadar
56.	D:929	Raipur	Devbhog	Kukhurd
57.	D:934	Raipur	Magarlod	Bhainsmudi
58.	D:939	Raipur	Magarlod	Dhaniabora
59.	D:940	Raipur	Magarlod	Bhainsmudi
60.	D:942	Raipur	Magarlod	Bhainsmudi
61.	D:951	Raipur	Bhatapara	Niyania
62.	D:952	Raipur	Bhatapara	Tikulia
63.	D:959	Raipur	Simga	Kesada
64.	D:968	Bilaspur	Mungeli	Karahi
65.	D:1017	Bastar	Kanker	Bevratti
66.	D:1020	Rajnandgaon	Kawardha	Jhalmala
67.	D:1024	Shahdol	Suhagpur	Chewani
68.	D:1024	Shahdol	Suhagpur	Chewani
69.	D:1071	Raigarh	Tapkara	Lawakera
70.	D:1075	Bilaspur	Pamgarh	Bhaisa
71.	D:1090	Raipur	Fingeshwar	Patseoni
72.	D:1098	Raipur	Saraipali	Banigirdol
73.	D:1100	Raigarh	Dharamgaigarh	Kadga
74.	D:1119	Bilaspur	Chanda	-
75.	D:1123	Raipur	Mahasamund	Sirpur
76.	D:1126	Raipur	Basna	Chhote temri
77.	D:1214	Raigarh	Tamnar	Bhuikurri
78.	D:1216	Raigarh	Tamnar	Darama
79.	D:1230	Raipur	Devbhog	Chichiya
80.	D:1246 II	Raipur	Devbhog	Dhanora
81.	D:1276	Bastar	Lohandiguda	Matwar
82.	D:1289	Bastar	Jagdalpur	Bademurma
83.	D:1284	Bastar	Kanker	Muddongori
84.	D:1293	Bastar	Antagarh	Bulawand
85.	D:1310	Bastar	Durgkondal	Pudomichgaon
86.	D:1348	Bastar	Narayanpur	Bakulbadi
87.	D:7 III	Raipur	Nagri	Sirsida
88.	B:2875	Raipur	Saraipali	Sagarpali
89.	B:2738	Bastar	Sarona	Danwarkhar
90.	B:2739	Baster	Sarona	Bhawlipara
91.	D:1173	Raigarh	Saranggarh	Dansara
92.	D:1041	Rajnandgaon	Dongargarh	Diwanbhedi
93.	D:1362	Bastar	Sarona	Simanpur
94.	D:1366	Bastar	Sarona	Dhanesara
95.	H:41 I	Raipur	Simga	Lanja
96.	M:576 I	Sarguja	Masturi	Ralila
97.	D:668 II	Bastar	Sarona	Sarona
98.	D:1404	Raipur	Mahasamund	Kosrangi
99.	D:839 I	Sarguja	Lakhanpur	Lahori
100.	G:1035	Rajnandgaon	Chowki	Metepar
101.	J:450	Raigarh	Gharghoda	Pulsada
102.	S:227	Bilaspur	Gorella	Bacharwar
103.	R:169 II	Raipur	Fingeshwar	Rajim
104.	R:171 IV	Raipur	Fingeshwar	Rajim
105.	D:1543	Raipur	Fingeshwar	Rajim
106.	T:102 I	Sargeya	Odagi	Kalamjan
107.	T:103	Raipur	Arang	Jugesar
108.	B:562	Durg	Bemetara	Mohtara
109.	C:539	Raigarh	Bagicha	Sanna
110.	G:583	Raigarh	Bahicha	Gaylunga
111.	M:873	Raipur	Fingeshwar	Kirwai
112.	B:728 I	Raipur	Gariyaband	Mohanda
113.	B:1380	Raipur	Dharsenwa	Banarsi
114.	C:43	Jabalpur	Badpara	Amdi
115.	C:56	Jabalpur	Sehora	Junnani
116.	C:195	Jabalpur	Shahpura	Surai
117.	C:265	Damoh	Jabera	Kariakheda
118.	C:389 I	Shahdol	Pali	Barkoda
119.	C:611	Bilaspur	Takhatpur	Sankri
120.	G:3	Raipur	Palari	Datan
121.	K:1295	Bhind	Mehgaon	Jugekapura
122.	K:2533	Bhind	Gohad	Dhimka
123.	L:88	Bastar	Makdi	Jarandi
124.	S:1250	Bilaspur	Masturi	Luthera

125.	S:1332	Bilaspur	Gorela	Ropanhand
126.	S:1072	Raigarh	Gharghida	Puri
127.	T:150	Durg	Dondi	Bharritola
128.	S:715	Shahdol	Sohagpur	Jodhpur
129.	T:186	Bastar	Kanker	Badebhata
130.	C:194	Jabalpur	Katni	Khirhani
131.	C:2671	Damoh	Jabera	Melithana
132.	C:808	Seoni	Barghat	Takhlakala
133.	K:216	Durg	Saja	Parasbod
134.	K:1374	Raipur	Simga	Kesada
135.	K:1890	Raipur	Mahasamund	Birkoni
136.	B:728	Raipur	Gariaband	Mohanda
137.	C:459	Bastar	Sarona	Saletola
138.	Bd:444	Gwalior	Dabra	Dabra
139.	Bd:153	Raipur	Basna	Basna
140.	Bd:384 A	Bilaspur	Jaijaipur	-
141.	Bd:8	Raipur	Arang	Arang
142.	A:319	Mandal	Bichhia	Bhua
143.	A:349	Balaghat	Baihar	Powdilar
144.	A:26	Bastar	Chhindgarh	Leda
145.	A:274	Bastar	Keshkal	Adega
146.	A:283	Bastar	Chhindgarh	Leva
147.	A:328 I	Bastar	Dantewara	Badped
148.	A:543	Raipur	Tilda	Kharora
149.	A:625	Bastar	Lohandiguda	Harikodar
150.	A:644	Bastar	Bastar	Nehrani
151.	A:367 II	Sarguja	Sitapur	Sontai
152.	A:593	Raigarh	Dharamjaigarh	Siyra
153.	B:480 II	Bastar	Baderajpur	Tenwsa
154.	B:1728	Bastar	Bastar	Mundagaon
155.	B:1689	Seoni	Barghat	Dharnakula
156.	B:1358	Bastar	Kanker	Bewarti
157.	B:361	Raipur	Arang	Umaria
158.	W:48	Sidhi	Majholi	Khadora
159.	B:1166	Raipur	Deobhog	Kodevan
160.	A:647	Bastar	Bastar	Selemata
161.	B:1209	Shahdol	Jaithari	Bargawan
162.	B:801	Bastar	Lokapal	Sonarpal
163.	B:42 I	Bastar	Bakawand	Dodiapal
164.	B:54 II	Raipur	Devbhog	Amlipadar
165.	B:54	Raipur	Devbhog	Amplipadar
166.	B:214 III	Durg	Durg	Tirga
167.	B:220	Durg	Dondi	Salhaitan
168.	B:220 II	Durg	Dondi	Salhaitan
169.	B:254	Raipur	Tilda	Chhatod
170.	B:323	Bastar	Gidam	Kasoli
171.	B:323 I	Bastar	Gidam	Kasoli
172.	B:323 II	Bastar	Gidam	Kasoli
173.	B:381	Raipur	Bhatapara	Mirgi
174.	B:381 II	Raipur	Bhatapara	Mirgi
175.	B:405	Bilaspur	Gorela	Dhanoli
176.	B:440 II	Raipur	Dharseva	Chirhuldih
177.	B:484	Bastar	Bakawand	Borpadar
178.	B:497	Bastar	Jagdalpur	Kohkapal
179.	B:528	Rajnandgaon	Kawardha	-
180.	B:562	Durg	Bemetara	Mohtara
181.	B:562 II	Durg	Bemetara	Mohtara
182.	B:799 I	Bastar	Tokapal	Mirga
183.	B:799 II	Bastar	Tokapal	Mirga
184.	B:973	Bastar	Geedam	Ronge
185.	B:1005	Bastar	Baderajpur	Madokikhargaon
186.	B:1010	Bastar	Baderajpur	Kargaon
187.	B:1209	Shahdol	Jaithari	Badgaon
188.	B:1307	Sarguja	Bharatpur	Janakpuri
189.	B:1322	Sarguja	Sitapur	Pratapgarh
190.	B:1340	Bastar	Narayanpur	Narayanpur
191.	B:1370	Bastar	Farargaon	Bade Dongar
192.	B:1389	Bastar	Narayanpur	Kodia
193.	B:1427	Rajnandgaon	rajnandgaon	Bharregaon
194.	B:1693	Bastar	Antagarh	Sarandi
195.	B:1727	Bastar	Bastar	Kalchur
196.	B:1731	Bastar	Bastar	Baniagaon
197.	B:2094	Bastar	Durgkondal	Chihro
198.	B:2297	Raipur	Pithora	-
199.	B:2354	Raipur	Devbhog	Usarijor
200.	B:2355	Raipur	Devbhog	Usarijor
201.	B:2402	Bastar	Bakawand	Bajabandh
202.	B:2461	Bastar	Abujmand	Ader
203.	B:2495	Bastar	Lohandiguda	Mardum
204.	B:2812	Bastar	Bakawand	-
205.	B:2814	Bastar	Lohandiguda	Kothiaguda
206.	B:1092	Durg	Gunderdehi	Arjunda
207.	B:1717	Bastar	lohandiguda	Taragaon
208.	B:2604	Bastar	Antagarh	Antagarh
209.	B:2669	Bastar	Lohandiguda	Taragaon
210.	B:380 II	Bastar	Pithora	Girna

211.	B:1094 II	Durg	Dhamda	Hirri
212.	B:1094 IV	Durg	Dhamda	Hirri
213.	L:1238 II	Raigarh	Kunkuri	Hastanpur
214.	R:509	Bastar	Baderajpur	Forgaon
215.	V:9	Bilaspur	Gorela	Tifarkala
216.	V:26 I	Sarguja	Bhaiyath	Sirsi
217.	B:525 III	rajnandgaon	Kawardha	-
218.	U:78 II	Jabalpur	Kargi	Dhanpuri
219.	U:69 II	Seoni	Barghat	Keshala
220.	C:165 II	Raigarh	Lelunga	Sarega
221.	C:30 II	Shahdol	Budhar	Pakariha
222.	C:340	Bastar	Bhanupratappur	Jampara
223.	C:236	Seoni	Barghat	Sajanwada
224.	C:334 I	Raipur	Dhamtari	Dhamtari
225.	C:392	Seoni	Barghat	Taklakhurd
226.	C:494 II	Balaghat	Waraseoni	Piparia
227.	C:604	Shahdol	Suhagpur	-
228.	C:828	Raipur	Mahasamund	-
229.	C:751	Bastar	Lohandiguda	Ermur
230.	C:705	Bastar	Bakawand	Bakawand
231.	D:625	Bastar	Jagdalpur	Bagbohar
232.	D:18	Raipur	Devbhog	Jakharpara
233.	D:18 I	Raipur	Devbhog	Jakharpara
234.	D: 18 II	Raipur	Devbhog	Jakharpara
235.	D:26	Raipur	Pallari	Ghotia
236.	D:27	Raipur	Pallari	Telasi
237.	D:33 A	Bastar	Bijapur	Ghanora
238.	D:76	Bastar	Kondagaon	Sukurpal
239.	D:80	Bastar	Charama	Haradula
240.	D:81	Bastar	Charama	Mahud
241.	D:90	Bilaspur	Baloda	Kamrid
242.	D:90 II	Bilaspur	Baloda	Kamrid
243.	D:119	Durg	Dongargarh	Sevtatola
244.	D:130	Durg	Durg	Karjabhilai
245.	D:136	Durg	Dondi	Solha
246.	D:137	Durg	Bhanpuri	Bawsa
247.	D:143	Durg	Dondilohara	Sanjari
248.	D:156	Balaghat	Lalbarra	Miregaon
249.	D:181	Raipur	Tilda	Tulsi
250.	D:181 II	Raipur	Tilda	Tulsi
251.	D:185 I	Raipur	Basna	Mithli
252.	D:191	Raipur	Basna	Rasoda
253.	D:194 I	Raipur	Bagbahara	Bhatgaon
254.	D:202	Raipur	Balodabazar	Lavan
255.	D:204	Raipur	Simga	Sankari
256.	D:1131	Bilaspur	Bilha	Madanpur
257.	D:1132	Raigarh	Lelunga	Madanpur
258.	D:1135	Bastar	Bastar	Ritaband
259.	D:226	Bastar	Tokapal	Bharkot
260.	D:268 II	Raipur	Arang	Nagpura
261.	D:297	Hoshangabad	Piparia	Simar
262.	D:311	Raipur	Dharsivan	Chirhuldih
263.	D:318	Raigarh	DHarmjaigarh	Shahpur
264.	D:320	Raigarh	Kausabel	Bagia
265.	D:329 I	Raigarh	Lelunga	Beskimuda
266.	D:329 II	Raigarh	Lelunga	Beskimuda
267.	D:360	Rajnandgaon	Dongargarh	Dhordah
268.	D:421	Rajnandgaon	Chhuikhadan	Borai
269.	D:423	Rajnandgaon	Chhuikhadan	Chakmar
270.	D:424	Rajnandgaon	Chhuikhadan. Bundeli	
271.	D:428	Rajnandgaon	Chhuria	Sitakasa
272.	D:433	Raipur	Devbhog	Amlipadar
273.	D:436	Mandla	Nainpur	Joharmau
274.	D:440	Raipur	Bhatapara	Maldi
275.	D:459	Raipur	Tilda	Nagpura
276.	D:482	Bilaspur	Jaijapur	Amgaon
277.	D:519	Raipur	Gariaband	Shobha
278.	D:610 II	Rajnandgaon	Dongargarh	Meregaon
279.	D:657 II	Bastar	Sukma	Sonakukanar
280.	D:659	Bastar	Koilibeda	Koylibeda
281.	D:665	Bastar	Durgkondal	Sukhai
282.	D:666 I	Bastar	Burgkondal	Kodekurse
283.	D:666 II	Bastar	Burgkondal	Kodekurse
284.	D:684	Sidhi	Sidhi	Jamodi
285.	D:731 I	Bastar	Usur	Usur
286.	D:734 II	Raipur	Chura	-
287.	D:742	Shahdol	Jaithari	Barbaspur
288.	D:749	Seoni	Kedari	Vimari
289.	D:750	Mandla	Mandla	Bapsa
290.	D:766	Rajnandgaon	Mohla	Mahewa
291.	D:780	Balaghat	Katangi	Lakhanwara
292.	D:781	Balaghat	Katangi	Agari
293.	D:806	Raipur	Kurud	Gogi

294. D:817	Bastar	Narayanpur	Narayanpur
295. D:819	Raipur	Nagri	Amgaon
296. D:828	Bastar	Keshkal	Gatka
297. D:843	Raipur	Bagbahara	Khamaria
298. D:862	Rajnandgaon	Manpur	Chhidivadi
299. D:875	Balaghat	Waraseoni	Tegabela
300. D:902	Balaghat	Lalbarra	Nilji

were recorded on five randomly selected plants from the central rows of each plot of each accession per replication except grain yield recorded on plot basis. The observations recorded on days to 50 per cent flowering, plant height, panicle length, hundred grain weight and spikelet sterility percentage. Ten whole milled kernels were used to measure kernel length and breadth. Then length:breadth ratio was calculated. The non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973) was followed to estimate the intra- and inter-cluster distances and to group the genotypes into different clusters.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences within the rice germplasm accessions for all the traits studied. Based on non-hierarchical Euclidean cluster analysis, the 300 cultivars were grouped into sixteen clusters (Table 2). The average genetic distance for all possible pairs of combinations ranged from 1.165 (II, VI) to 6.475 (XII, XIII) which indicated considerable amount of genetic diversity among the strains studied (Table 3). Amongst sixteen clusters, cluster II consisted of large number of cultivars (61) followed by cluster VI (45); XIV (33), V(26), I(23) and cluster X included 21 accessions. Minimum number of 4 cultivars accomodate in cluster XII. The maximum intra-cluster distance was observed in cluster XII (D = 1.911) followed by cluster XI (D = 1.676) and cluster XV (D = 1.610). The cluster XII consisted of 4 accessions, cluster XI of 7 accessions and cluster XV of 10 accessions. The above grouping indicates existence of wide

Table 2. Distribution pattern of 300 rice accessions into 16 clusters

Cluster No.	No. of genotypes	Accession numbers
I	23	B:1358, B:361, B:54, B:381 II, B:484, B:562 II, B:799 II, B : 973, B:1010, B:1209, B:1322, B:1340, B:1370, B:1389, B:1727, B:2297, B:2355, B:2461, B:2812, V:9, B:525 III, U:69 II, C:165 II
II	61	B:25, D:297, D:452, D:459, D:675, D:684, D:699, D:725, D:741, D:751, D:753, D:773, D:776, D:777, D:777 II, D:809, D:875, D:921 II, D:940, D:951, D:1024, D:1090, D:1126, D:1348, B:2875, B:2738, B:2739, B:2739, D:1362, D:1362, :576 I, D:668 II, D:1404, D:839 I, C:392, C:494 II, D:18, D:18 II, D:181 II, D:191, D:204, D:1131, D:1132, D:1135, D:297, D:423, D:424, D:436, D:436, D:440, D:610II, D:666 I, D:666 II, D:734 II, D:742, D:750, D:780, D:781, D:806, D:817, D:819, D:828, D:843, D:862
III	12	B:372, B:996, C:539, G:583, M:873, B:728 I, C:611, L:88, S:1250, S:1332, K:1890, BD:8
IV	9	B:562, C:43, C:56, C:389 I, C:194, C:808, C:459, Bd:444, Bd:384 A
V	26	B:1166, B:54 II, B:220, B:220 II, B:254, B:323, B:323 II, B:381, B:405, B:497, B:562, B:1005, B:1307, B:1427, B:2402, B:2814, B:1092, B:1717, :2604, B: 1094 II, L:1238 II, R:509, V:26 I, C:30 II, C:604, C:751
VI	45	B:1589, B:13 II, B:173 I, B:173 II, B:173, B:189 III, M:1A III, C:72 II, C:606, D:378, D:672, D:691, D:692, D:693, D:712, D:874, D:959, D:1020, D:1024, D:1075, D:1098, D:1100, D:1289, D:1293, G:1035, B:480 II, B:380 II, C:828, C:705, D:625, D:26, D:136, D:156, D:194 I, D:202, D:360, D:421, D:428, D:433, D:459, D:482, D:519, D:665, D:684, D:731I
VII	6	B:497 II, T:102 I, B:214 III, B:1094 IV, C:334 I, D:33A
VIII	7	B:2357, D:1230, S:227, D:1543, T:103, K:1374 II, B:728

IX	14	A:274, A:328 I, A:593, B:1728, B:42 I, B:3231, B:528, B:7991, B:1693, B:1731, B:2094, B:2495, B:2669, C:751
X	21	D:727, D:833, D:864, D:904, D:908 II, D:939, D:942, D:7 III, B:1689, D:27, D:76, D:80, D:81, D:90, D:119, D:130, D:137, D:239 II, D:749, D:875, D:902
XI	7	A:319, A:349, A:647, B:1209, B:2354, U:78 II, C:340
XII	4	D:1017, H:41 I, T:150, S:715
XIII	9	A:26, A:283, A:543, A:625, A:644, A:367 II, W:48, B:801, B:440 II
XIV	33	B:1094 III, C:395 B, D:812, D:191, D:202, D:339, D:762 I, D:889I, D:893 II, D:896 I, D:914, D:929, D:934, D:952, D:1071, D:119, D:1123, D:1310, D:1173, D:1041, C:236, D:18 I, D:90 II, D:143, D:181, D:185 I, D:226, D:268 II, D:311, D:318, D:329 I, D:659, D:766
XV	10	B:1380, C:195, C:265, G:3, K:1295, K:2533, S:1072, T:186, C:267 I, K:216
XVI	13	C:839, D:968, D:1214, D:1216, D:1246 II, D:1276, D:1284, D:1366, J:450, R:169 II, R:171 IV, Bd:153, D:320

genetic divergence among constituent genotypes. Such high degree of divergence was found in local collections (Rahaman *et al.* 1997; Sardana *et al.* 1997; Sarawgi *et al.* 1998; Soni *et al.* 1999) as well as in International collections (Usha Kumari and Rangaswamy, 1997). The minimum intra-cluster value (D = 1.000) exhibited by cluster II containing 61 acceesions, indicated limited genetic diversity among the constituent genotypes (Table 3). The unidirectiona selection practiced in the past might have resulted in uniform features with less divergence between these genotypes. The relative divergence of each cluster from other clusters (inter-cluster distances) indicated greater divergence between cluster XII and XIII followed by clusters XI and XII, clusters V and XII, clusters IX and XII, clusters I and XII (Table 3). In all the above inter-cluster distances, cluster XII was more distantly placed. It indicates that the accessions of cluster XII were genetically more diverged from accessions of rest of the clusters. Due emphasis for breeding programme should be given to four accessions of cluster XII: nine

Table 3. Mean intra-cluster (diagonal and bold) and inter-cluster distances among sixteen clusters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	**1.313**	3.956	3.671	4.703	1.493	3.732	3.837	3.992	1.508	4.460	2.596	6.164	2.841	4.489	5.056	4.735
II		**1.000**	3.904	4.094	4.169	1.165	3.683	3.431	4.374	1.535	5.523	4.043	5.004	1.639	4.992	2.723
III			**1.529**	2.256	4.261	3.911	3.792	1.910	4.270	4.013	3.847	4.495	4.377	4.147	3.000	4.568
IV				**1.363**	4.882	3.968	3.774	2.317	5.141	4.264	4.885	3.050	4.796	3.953	2.248	3.951
V					**1.198**	3.686	3.155	3.944	1.700	4.585	3.055	6.401	2.157	4.204	4.772	4.130
VI						**1.243**	2.925	3.096	4.275	2.407	5.548	4.494	4.641	1.625	4.766	1.933
VII							**1.530**	2.604	3.868	4.036	4.970	5.567	2.948	3.084	3.370	2.250
VIII								**1.545**	4.503	3.521	4.553	4.495	4.184	2.988	2.334	3.127
IX									**1.163**	5.524	2.351	6.381	1.959	4.690	5.070	4.967
X										**1.483**	5.383	3.890	5.051	1.632	4.691	3.239
XI											**1.676**	6.428	2.990	5.690	4.610	6.132
XII												**1.911**	6.475	4.053	4.430	4.632
XIII													**1.504**	4.795	4.115	4.582
XIV														**1.135**	4.241	1.720
XV															**1.610**	4.146
XVI																**1.406**

accessions of cluster XIII; seven accessions of cluster XI; twenty six accessions of cluster I. The selection of divergent genotypes from above clusters would produce a broad spectrum of variability for yield and other traits studied which may enable further selection and development of aromatic high yielding, good grain quality varieties. The hybrids developed from the selected genotypes within the limits of compatibility of these clusters may produce high magnitude of heterosis or desirable transgressive segregants which would be rewarding in varietal improvement programme. Bhatt (1973), Roy and Panwar (1993), Vivekanandan and Subramanian (1993), Rahaan *et al.* (1997), Sarawgi *et al.* (1998) and Soni *et al.* (1999) also found similar degree of diversity in rice.

The cluster mean values for all the traits under study are furnished in Table 4. There was a wide range of variation in the cluster mean values for all the characters under study. The maximum and minimum mean values for characters viz., days to 50 per cent flowering, 108.23 (XVI) and 94.89 (IV); plant height, 137-91 (XIII) and 107.90 (VI); panicle length 30.37 (XI) and 21.13 (II); hundred grain weight, 2.88 (XII) and 1.08 (V); grain yield, 632.90 (X) and 205.00 (VII); spikelet sterility %, 39.30 (XV) and 16.06 (I); kernel length, 6.78 (XII)and 4.34 (IX); length: breadth ratio, 3.14 (VIII) and 2.00 (XI), respectively were observed. This indicates that while planning hybridization programme to achieve early flowering germplasm accessions viz., C:56, C:194, C:808, C:459 and Bd:444 from cluster IV and C:195, C:265 and C:267 I from cluster XV should be included; for breeding dwarfness accessions C:72II, B: 1589, D : 519, D : 731, D : 380 II and B : 189 III from cluster VI hold promise; higher panicle length, germplasm accessions namely U: 78 II, C : 340, B : 1209 and A : 647 from cluster XI having longest panicle; for improvement in hundred grain weight, accessions T : 150, S : 715 and D : 1017 from

Table 4. Cluster means for different characters

Cluster	No. of genotypes included	Days to 50% fowering	Plant height (cm)	Panicle length (cm)	100-grain weight (g)	Grain yield (g/plot)	Spikelet sterility (%)	Kernel length (mm)	L : B ratio
I	23	103.00	120.07	25.31	1.10	286.09	**16.06**	4.53	2.22
II	61	107.92	111.81	**21.13**	1.74	471.98	17.84	5.96	2.97
III	12	97.50	124.83	28.56	1.50	326.83	17.27	6.23	3.08
IV	9	**94.89**	124.24	25.82	2.14	277.44	25.59	6.27	3.07
V	26	103.88	119.02	24.42	**1.08**	281.75	27.61	4.42	2.14
VI	45	107.97	**107.90**	21.37	1.65	360.20	23.18	5.87	2.94
VII	6	106.83	123.62	24.23	1.39	**205.00**	37.88	5.83	2.89
VIII	7	100.71	116.91	27.88	1.52	350.00	30.08	6.34	**3.14**
IX	14	105.50	132.09	25.14	1.13	337.71	20.02	**4.34**	2.09
X	21	107.38	119.81	21.99	1.74	**632.90**	21.10	5.98	3.03
XI	7	98.86	134.40	**30.37**	1.22	407.00	18.92	4.42	**2.00**
XII	4	99.00	122.58	23.30	**2.88**	510.00	20.03	**6.78**	2.83
XIII	9	105.78	**137.91**	26.68	1.27	240.44	32.93	4.53	2.23
XIV	33	107.11	112.46	21.49	1.76	519.11	30.59	6.05	3.01
XV	10	94.90	133.19	27.24	1.80	352.70	**39.30**	6.13	3.03
XVI	13	**108.23**	110.37	21.61	1.84	327.88	37.93	6.08	2.95

Bold figures indicate maximum and minimum cluster mean for a particular character

cluster XII hold promise; to minimise spikelet sterility, accessions B : 54; B : 799 II; B : 1209; B : 1727, B : 2297 and B : 2461 from cluster I should be included; for higher kernel length, accessions D : 1017; T : 150 and S : 715 from cluster XII hold promise; for length : breadth ratio accessions D : 1543; B : 728 and S : 227 from cluster VIII should be used; for improvement in grain yield accessions D : 875; D : 902, D : 904, D : 908 II; D : 864, D : 833 and D : 90 from cluster X should be used as donors in hybridization programme for improvement of individual traits.

The highest divergence between clusters are useful in heterosis as well as in recombination breeding since highly divergent genotypes would throw a wide spectrum of variability enabling further selection. The highly diverse and superior germplasm accessions viz., H : 41 I, S : 715, D : 1017 and T : 150 (XII), A : 367 II, W : 48, B : 801 and A : 283 (XIII), U : 78 II, B : 2354, C : 340 and B : 1209 (XI), L : 1238 II, B : 1094 II, B : 323 II, B : 2604, B : 1717 and B : 2402 (V), A : 328 (I), B : 1693, B : 323 (I), B : 2495 and C : 751 (IX), U : 69 (II), B : 1322, B : 1389, B : 2461, B : 2812 and V : 9 (I) were selected and appeared the most promising. These selected accessions may be utilized as donors in rice breeding programme for developing semidwarf, high yielding, early aromatic rices with good grain quality.

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VARIETAL PERFORMANCE AND FOLIAGE YIELD IN VEGETABLE AMARANTH

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The present investigation was carried out to evaluate the foliage yield and its component characters of different level of cuttings in vegetable amaranth. The 10 cultivars were grown in RBD with three replications and foliage cutting was started after 3rd week of sowing and subsequent cuttings were done at the interval of 10 days. Data on plant height, branches/plant, leaves/plant and leave size were taken of each cutting. The cultivar 'AV-190' (285.24 q/ha) was found the most promising cultivar for foliage yield followed by 'AV-45' (270.66 q/ha) and 1AV-35/1' (218.75 q/ha). It was observed that foliage yield enhanced in subsequent cuttings. The component characters noticed were mainly responsible for the enhancement of foliage yield.

Key words : Amaranth, selection, foliage, regeneration

Amaranths are hardy, fast growing pseudo-cereals and cheap source of protein rich seed and carotene rich leafy vegetables. The leaves as pot herbs of many amaranth species are widely consumed as food in the developing countries. Its fliage is particularly rich in vitamin 'A' as well as in protein, iron and calcium (Devadas and Saroja, 1980; Prakash and Pal, 1991). It also has a considerable amount of vitamin C which is an important water soluble antioxidant and plays a significant role in maintaining the preferred oxidation-reduction potential in human tissues (Kutsky, 1973). For nutritional quality, the selection of genotypes for high foliage yield in different cuttings and stages is necessary. The information on this aspect in vegetable type amaranth is meagre. Therefore, keeping importance of green leafy vegetables, present investigation was undertaken to evaluate the promising strains for foliage yield and its component characters in different cuttings in summer season.

MATERIAL AND METHODS

The seeds of 10 cultivars namely 'AV-35', 'AV-45', 'AV-35/1', 'AV-63', 'AV-64', 'AV-77', 'AV-151', 'AV-N-3', 'AV-190' 'AV-76' selected from large germplasm maintained at the NBRI, Lucknow, were sown in randomized block design with three replications in the year 1997-98 at NBRI, Lucknow on sandy loam soil under uniform cultural and climatic conditions. The distance between plant to plant and row to row were kept 45×10 cm^2 respectively. The net plot size was 5.76 M^2. The first cutting was done after 3rd week of sowing and subsequent cuttings were done at the interval of 10 days. The data on foliage yield (kg/plot) and its components traits i.e. plant height (cm), leaves/plant, leaves size (cm^2) and branches/plant were recorded for each cutting.

Statistical analysis was done in factorial design according to Panse and Sukhatme (1978).

RESULTS AND DISCUSSION

Analysis of variance for individual cutting showed significant differences among treatments for all the characters (Table 1). Pooled analysis of variance due to cuttings and cultivars also showed significant differences for different characters except branches/plant due to cultivars. The variances due to cutting × cultivars were significant for all the traits.

Table 1. Pooled ANOVA for different characters over different cuttings in vegetable amaranth

Source	df	Plant height (cm)	Leaves/plant	Leaves size (cm^2)	branches/plant	Foliage yield (kg/plot)
Cuttings	4	426.63**	981.18**	193.87*	22.72**	22.11**
Cultivars	9	75.63**	143.32*	547.22**	7.47	2.31*
Cutting × cultivar	36	10.48**	56.90**	66.78**	5.83**	0.72**
Pooled Error	100	3.68	15.11	16.71	2.38	0.18

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

Considering the total foliage yield/ha, the cultivar 'AV-190' (285.24 q/ha) was most promising followed by 'AV-45' (270.66 q/ha) and 'AV-35/1' (218.75 q/ha) (Table 3). The 'AV-190' and 'AV-45' were significantly higher yielder than all the cultivars. In general, foliage yield enhanced in subsequent cuttings may be due to higher regeneration in component characters viz. plant height, branches per plant, leaves per plant and leaves size in successive cuttings. However, in strains 'AV-77' and 'AV-151' the foliage yield declined in Vth cutting due to loss in plant growth per population.

Generally the plant height increased in subsequent cuttings in all the strains and was maximum in Vth cutting (Table 2). The overall mean showed maximum height in the strain 'AV-64' (24.35 ± 3.81) followed by 'AV-190' (23.42 ± 3.19) and 'AV-63' (21.15 ± 2.38) respectively. The branching pattern was found very irregular. On the overall mean basis the cultivar 'AV-64' (11.80 ± 1.89) followed by 'AV-190' (10.60 ± 0.96) and 'AV-151' (10.41 ± 0.57) showed maximum number of branches per plant.

The leaves per plant generally enhanced in subsequent cutting and maximum in IVth cutting with some exception. The maximum number of leaves per plant was observed in 'AV-151' (37.46 ± 5.90) followed by 'AV-190' (35.98 ± 8.26) and 'AV-77' (34.53 ± 6.15). In general leaves size was larger in IInd to IVth cuttings. On the overall mean basis maximum leave size was found in the cultivar 'AV-151' (53.46 ± 5.07) followed by 'AV-N-3' (47.27 ± 2.63) and 'AV-64' (37.17 ± 5.96). The characters plant height, branches per plant, leaves per plant and leaves size are the main components for the enhancement of foliage yield. Selection based on these components need to be made for breeding superior varieties. The cultivar 'AV-190', 'AV-45', 'AV- 35/1' and 'AV-64' were found most promising. These may be hybridized for component breeding and selection of genotypes for foliage yield and contributing characters will be rewarding to isolate better plant types in vegetable amaranth.

Table 2. Stages of different cultivars in different traits at different cuttings of vegetable amaranthus

Cultivars/ cuttings	Plant height (cm)					Mean ± SE	Leaves/plant					Mean ± SE	Leaves size (cm^2)					Mean ± SE	Branches/plant					Mean ± SE
	Ist	IInd	IIIrd	IVth	Vth		Ist	IInd	IIIrd	IVth	Vth		Ist	IInd	IIIrd	IVth	Vth		Ist	IInd	IIIrd	IVth	Vth	
AV-35	10.00	14.50	20.84	16.84	32.00	18.84±3.73	11.15	28.67	38.17	24.50	20.67	24.63±4.46	20.92	32.44	42.17	26.66	29.11	30.26±3.52	10.00	8.33	13.34	8.50	4.50	8.93±1.43
AV-45	6.74	15.17	16.34	20.67	30.50	17.88±3.88	14.07	25.33	25.67	31.17	37.17	26.68±3.82	6.11	14.08	20.29	22.04	23.92	17.29±3.25	5.83	8.67	9.50	8.17	11.84	8.80±0.97
AV-35/1	8.12	15.70	14.67	19.67	33.67	18.37±4.25	11.37	17.00	28.67	33.71	57.17	29.58±7.97	10.11	29.54	28.46	45.67	31.96	29.15±5.67	7.27	7.84	9.33	10.84	13.17	9.69±1.07
AV-63	12.90	20.75	22.25	22.17	27.67	21.15±2.38	13.24	24.00	26.17	36.34	25.67	25.08±3.67	26.67	32.29	40.91	36.75	31.67	33.66±2.42	12.34	7.67	13.67	7.67	5.00	9.27±1.62
AV-64	15.33	16.92	31.84	23.50	34.17	24.35±3.81	15.67	16.33	39.50	27.33	34.67	26.70±4.78	21.75	24.43	43.12	52.04	44.50	37.17±5.96	15.17	6.00	16.67	10.34	10.83	11.80±1.89
AV-77	6.34	20.17	20.17	18.17	22.84	17.54±2.90	13.00	29.00	41.00	42.83	46.83	34.53±6.15	19.93	46.46	40.00	36.17	33.62	35.24±4.40	6.16	8.05	12.17	10.50	9.67	9.31±1.03
AV-151	9.95	14.50	17.17	18.33	24.34	16.86±2.36	15.64	40.33	36.00	48.33	47.00	37.46±5.90	45.65	65.70	66.04	44.46	45.46	53.46±5.07	9.99	9.23	12.34	9.50	11.00	10.41±0.57
AV-N-3	13.65	16.34	21.67	18.67	33.17	20.70±3.39	17.50	25.50	31.16	35.00	25.50	26.93±2.97	55.25	50.58	41.33	41.96	47.21	47.27±2.63	15.05	7.84	13.17	8.67	7.00	10.35±1.59
AV-190	12.42	21.50	25.00	26.67	31.50	23.42±3.19	12.37	20.84	44.00	46.83	55.84	35.98±8.26	33.42	35.25	26.20	29.87	26.80	30.31±1.78	11.97	8.17	9.17	10.17	13.50	10.60±0.96
AV-76	6.27	12.00	11.84	9.52	12.92	10.51±1.20	10.15	18.16	30.00	23.83	38.67	24.16±4.88	32.04	35.17	32.17	33.67	40.6	34.73±1.58	7.17	6.50	9.67	7.34	9.67	8.07±0.67
Mean	10.17	16.76	20.18	19.42	28.28		13.42	24.52	34.03	34.99	38.92		27.18	36.39	38.07	36.93	33.49		10.09	7.83	11.90	9.17	9.62	
S.E.	1.04	0.98	1.80	1.44	2.10		0.73	2.28	2.07	2.77	4.03		4.78	4.58	3.99	2.94	2.64		1.10	0.30	0.78	0.40	1.00	
CD 5%	3.38	3.19	5.85	4.68	6.83		1.65	5.15	4.68	6.26	9.11		15.54	14.89	12.97	9.56	8.58		3.58	0.98	2.54	1.30	3.25	
CD 1%	2.35	2.21	4.07	3.25	4.75		2.37	5.40	6.73	9.00	13.10		10.80	10.33	9.02	6.64	5.97		2.49	0.68	1.76	0.90	2.26	

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

Table 3. Foliage yield of different cultivars in different cuttings in vegetable amaranth

Cultivars	Cuttings					Total yield (Kg)	Yield (q/ha)
	Ist	IInd	IIIrd	IVth	Vth		
AV-35	0.41	1.00	1.16	2.40	2.06	7.03	122.05
AV-45	0.54	1.30	3.50	4.40	5.85	15.59	270.66
AV-35/1	2.00	0.90	1.30	3.40	5.00	12.60	218.75
AV-63	1.12	1.07	2.30	2.70	4.30	11.49	199.48
AV-64	0.87	0.90	1.80	6.00	3.33	12.15	210.94
AV-151	0.83	1.46	2.10	4.00	2.20	10.59	183.85
AV-N-3	0.31	0.50	0.51	2.01	2.60	5.93	102.95
AV-190	0.43	1.70	3.00	5.80	5.50	16.43	285.24
AV-76	0.55	0.90	0.78	2.00	4.25	8.48	147.22
Mean	0.72	1.06	1.89	3.64	3.97	11.27	195.64
S.E.	0.17	0.11	0.30	0.46	0.43	1.07	18.65
CD 5%	0.55	0.36	0.98	1.50	1.40	2.42	42.19
CD 1%	0.38	0.25	0.68	1.04	0.97	3.48	60.61

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GENETIC DIVERGENCE IN HIMALAYAN CHENOPOD

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Fifty three genotypes of Himalayan chenopod (*Chenopodium album* L.) including 3 exotic introductions (*C. quinoa*) were grouped into eleven clusters following multivariate analysis on a set of ten characters related to yield and its contributing characters. The multivariate analysis studies indicated that geographical isolation might not be the only factor causing genetic diversity. Leaf length, days to maturity, leaves on main shoot and leaf width were the most potnetial traits contributing to the total genetic divergence. Clusters IV, V and VII were important because they comprised genotypes with high grain yield/plant, high inflorescence length, high number of leaves on main shoot, long leaf length and bold grain types. Utilizing genotypes from these clusters, there is a sufficient scope for varietal improvement through hybridization.

Key words : Chenopod, geographical isolation, genetic divergence, multivariate analysis

Chenopod (*Chenopodium album* L.) is the most important under-utilized food crop of Indian Himalayas and *C. quinoa* is an important crop of the Andean region, which originated near Lake Titicaca in the Andean region. Chenopod local land races account for all the produce in the Himalayan region and no improved variety is available for cultivation to the farmers. The grain yield improvement work in this crop is meager in the Himalayan region, though a wide range of genetic diversity is available in chenopod collections (Joshi, 1991 and Partap, 1990). The utility of these collections in genetic improvement programme is limited unless they are systematically evaluated. An attempt has been made to evaluate and group fifty-three genotypes of chenopod germplasm based on their genetic distance.

MATERIALS AND METHODS

The experiment was conducted with fifty accessions of chenopod originating from Kulu, Shimla, Chamba, Kinnaur (Himachal Pradesh); Jammu and Kashmir; Uttarkashi, Almora (Uttaranchal) and Lucknow (Uttar Pradesh); Darjeeling and three accessions originating from Bolivia, Mexico and Guatemala. These 53 accessions were sown during Kharif season of 1993 and 1994 in an augmented design (Federer, 1956). The seeds were drilled in rows 50 cm apart first followed by thinning and plant to plant distance was kept 20 cm within rows. Five competitive plants of each accession were selected at random. Data were recorded on ten characters viz. plant height (cm), number of branches, number of leaves on main shoot, inflorescence length (cm), leaf length (cm), leaf width (cm), days to flower, days to mature, 1000-grain weight (g) and yield per plant (g). The average values of 5 plants for each character were subjected to multivariate analysis, using Mahalanobis (1949) generalized distance D^2. The genotypes were grouped into different clusters according to Tocher's method as described by Rao (1952). The contribution of different characters towards divergence was estimated.

RESULTS AND DISCUSSION

Fifty-three accessions of chenopod collections were grouped into eleven clusters (Table 1). Cluster I was largent, comprising 15 accessions and clusters IX, X and XI were the smallest with one accession only. Among others clusters cluster II with 9 accessions, cluster III with 8 accessions, cluster IV and V having 5 accessions each, cluster VI with 4 accessions all originating from South America except one from Chamba. Cluster VII and VIII with 2 accession each both originating from NBRI, Lucknow. The exotic material received from Mexico, Bolivia and Guatemala got grouped together with one Himalayan collection from Chamba in cluster VI. All the exotic introductions maintained their geographic isolation by falling together in one and the same cluster. falling of one accessions in cluster VI from Chamba suggested that there is no firm relationship between genetic divergence and geographical distance. genetic drift and selection under diverse environment could cause greater diversity than geographical distance. While classifying the large germplasm of chenopod into different ecotypes according to information on their origin, Risi and Galwey (1989) reported a considerable overlap with respect to the origin between ecotypes. The results therefore, suggest that genotypes belonging to the same location may yield better transgressive segregates than the genotypes originating from different areas. There is also a need to evaluate the genotypes originating from different areas. There is also a need to evaluate the genotypes on the basis of their individual merit and genetic diversity and only those genotypes, which stand top and highly diverse, should be chosen for breeding work.

Intra and inter-cluster D^2 values are presented in Table 2. Intra cluster values ranged 0.00 to 15.47. The highest intra-cluster value was recorded in cluster VI (15.47) followed by cluster I (12.32) and cluster VIII (12.10). Inter cluster D^2 values ranged from 16.62 to 55.08. Highest inter-cluster D^2 value was observed between XI and X (49.70) indicating that these clusters are highly divergent. The least inter-cluster D^2 value was recorded between these two clusters.

Table 1. Cluster composition based on D^2 values in chenopod

Clusters	No. of Genotypes	Name of genotypes	Geographical origin
I	15	IC108088, IC108089, IC109025, IC109480, IC109732, IC109734, IC109736, IC109738, IC109740, IC109758, IC100355, P1123, P1171, P1212, CH/LKW-10	Kulu, Chamba, Uttarkashi, Shimla
II	9	T45-87, T87, TP30, T2-87, CH/LKW-16, CH/LKW-49, IC109739, T3-87, CH/LKW-5	Almora, Kulu, Lucknow, Shimla
III	8	NC58224, NC58229, NC58230, NC58230, NC58231, NC58232, IC15022, CH/LKW-16, CH/LKW49	Chamba, Kinnaur, Darjeeling
IV	5	IC107297,IC107854,IC107808,IC109733,IC109737	Kulu,Shimla
V	5	IC107185,IC107263,IC107295,IC107396,IC108086	Shimla
VI	4	NC58233,EC180010,EC180011,EC180012	Chamba,Bolivia,Gautamala,Mexico
VII	2	CH/LKW-66,CH/LKW-100	Lucknow
VIII	2	CH/LKW-60,CH/LKW-62	Lucknow
IX	1	NC58014	Jammu & Kashmir
X	1	T-87	Kulu
XI	1	CH/LKW-6	Lucknow

Table 2. Average intra and inter cluster D^2 values

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	12.32	27.43	25.32	37.31	34.10	29.00	30.00	20.45	29.62	32.50	37.46
II		**11.19**	19.42	32.72	27.30	27.32	31.56	33.70	31.95	37.97	39.35
III			**8.39**	16.62	27.50	32.76	22.83	37.37	21.97	26.14	32.10
IV				**10.97**	47.62	48.02	38.26	25.60	44.60	50.69	40.14
V					**9.31**	39.30	24.39	24.63	40.72	30.81	36.32
VI						**15.47**	30.00	28.73	37.43	31.27	31.44
VII							**10.03**	39.21	40.20	42.54	39.77
VIII								**12.10**	39.64	23.46	37.75
IX									**0.00**	49.70	55.08
X										**0.00**	41.03
XI											**0.00**

Table 3. Average cluster means of 53 genotypes belonging to different clusters

Traits/ Cluster	Plant height	Branches/ plant	No. of leaves on main shoot	Inflore-scence Length	Leaf length	Leaf width	Days to flower	Days to mature	1000 seed weight	Yield/plant
I	107.23	26.22	32.36	17.48	5.25	4.28	62.15	119.20	0.73	7.40
II	118.83	32.16	33.41	7.59	4.20	5.21	60.75	125.08	0.72	7.01
III	123.40	24.20	34.61	18.49	5.54	4.00	60.00	123.70	0.67	8.39
IV	106.40	67.90	89.58	29.30	7.98	6.51	38.40	99.10	0.99	10.25
V	205.90	36.00	27.56	25.29	4.52	3.13	61.40	38.40	99.10	0.99
VI	97.00	45.62	50.50	8.53	6.50	4.58	37.25	97.57	0.87	5.91
VII	88.00	27.75	28.25	8.10	8.20	3.85	34.75	59.06	1.01	8.35
VIII	84.24	31.50	37.75	8.15	8.10	4.12	49.50	148.00	0.94	6.45
IX	194.00	52.45	34.00	9.10	8.25	4.10	40.50	98.51	0.81	8.25
X	107.50	22.30	24.50	9.45	3.75	4.60	65.00	133.00	0.60	8.60
XI	79.00	32.24	38.26	16.40	4.62	4.42	56.50	119.40	1.77	7.20

The inter-cluster distance was higher than the intra-cluster distances in all the cases indicating more divergence of genotypes between the clusters. The maximum cluster mean (Table 3) was observed in cluster IV for yield per plant, number of branches/plant, number of leaves on main shoot, inflorescence length and leaf width; cluster VII for 1000-grain weight, leaf length, early maturity and plant height. These clusters could be regarded as useful sources of genes for different traits and there is sufficient scope for varietal improvement through hybridization. These results also indicate that if we take one representative genotype from each cluster and make a diallel, then in the progeny we can get better heterotic effects and more variability in F_2 population which will be helpful in selection and breeding programme of chenopod for the Himalayan region.

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EVALUATION OF CRAB APPLES FOR POLLINATION

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Eight flowering crab apples namely *Malus robusta, Malus, floribunda, Malus georgious, Malus* E M Wilson, Snowdrigt, Manchurian, Redflush and Golden Hornet were tested in various apple growing situations of Kotkhai area for their growth, flowering and fruit set responses to Delicious cultivars. All the crab apples under study, except *Malus robusta* and *Malus* E M Wilson were observed slow growing with compact and spreading habit. In branch grafting of *M. robusta* on primary or secondary branches, it was found to overgrow the main tree. In respect to flowering behaviour, Manchurian and Redflush are very early in flowering but their bloom often coincides with king bloom of Delicious. Snowdrift is an excellent annually flowering crab with pronounced effect on fruit set, though it is also little early in bloom. *M. georgious, M.* E M Wilson, *M. floribunda* have the bloom period almost coinciding with the Delicious, whereas Golden Hornet is late like Golden Delicious. Golden Hornet and Snowdrigt had high flower bud intensity (0.86 and 0.70 respectively). Highest fruit set (152.2 per 100 spurs) was recorded in Snowdrift pollinated Delicious trees. It was followed by Manchurian (104 per cent). *Malus robusta* and *M. floribunda* had the least response on fruit set.

Key words : Crab apples, pollinisers, flowering, pollination, fruit set

Due to irregular bearing of present apple pollinising varieties and production of low value crop, the modern trend in pollinisers is being shifted world over to crab apples as these are becoming important in apple pollination (Crasswellar *et al.*, 1980). The advanrages of crab apples as pollinisers for apple cultivars are seen as source of abundant flower production and prolonged flowering period, production of large open flowers attractive to bees and high pollen viability and fertilizing ability (Georgiev and Blagov, 1988). Keeping this in view the eight crab apple species/varieties were evaluated for their growth behaviour, flowering period and pollination responses to select appropriate polliniser.

MATERIALS AND METHODS

Eight crab apple varieites/species namely Manchurian, Snowdrift, Golden Hornet, Redflush, *M.* E M Wilson, *Malus georgious, M. floribunda, M. robusta* were planted in various apple orchards having inadequate polliniser proportion in different placement systems. These crabs were studied for their growth behaviour under different systems of placement systems. These crabs were studied for their growth behaviour under different systems of placements, flowering behaviour with respect to Delicious, flower bud intensity and fruit set responses on Delicious as per standard procedures.

RESULTS AND DISCUSSION

1. Growth behaviour - Two crab apple species namely *Malus robusta* and *Malus E M Wilson* were semivigorous to vigorous in growth of trees. However later was comparatively slow in branch top grafting. In branch top working of *M. robusta* on primary or secondary branches, it was found to overgrow the main tree which is the behaviour

of Red Gold variety. Such vigorous growth habit of crabs is not desirable since we have only to plant these for pollination. All other varieties/species were slow growing with spreading type of growth habit (Table 1).

2. Flowering

i) *Flowering period and duration* : *Malus georgious, M. E M* Wilson, and *M. floribunda*, had their bloom almost coinciding with Starking Delicious behaviour but differentily under different

Table 1. Growth behaviour of various pollinisers in different placement systems

Name of pollinisers/placement systems	Standard plants	Branch top working on Delicious	
		Basal Periphery	Mid periphery
Manchurian	Slow growing, spreading type.	Slow growing, spreading type	Slow growing, spreading type
Snowdrift	Slow growing, spreading type	Little vigorous and spreading type	Slow growing, compact
M. robusta	Vigorous, upright, spreading	Vigorous	Semi vigorous, spreading
Golden hornet *Malus floribunda*	Slow growing, erect and compact	Slow growing and erect	Slow growing
M. E M Wilson	Semi vigorous, spreading	Slow growing and erect	Slow growing
M. georgious	Semi dwarf, spreading	Slow growing	Slow growing
Red flush	Very slow growing (abundant powdery mildew attack)	Slow growing and spreading	Slow growing
Control (Commercial pollinisers)			
Golden Delicious	Semi vigorous, spreading	Semi vigorous, spreading, Slow growing	
Red Gold	Very vigorous spreading	Very vigorous spreading	Slow growing and spreading

Table 2. Flowering behaviour to different crop pollinisers at different situations and aspects with respect to Delicious

Name of pollinisers	Flowering period with respect to Delicious			
	1800M SW	1800M N	2800M SW	2100M N
Manchurian	5-6 days early	4-5 days early	almost coinciding	2- 3 days early
Snowdrift	3-4 days early	3-4 days early	2-3 days early	almost coinciding
M. robusta	3-4 days early	coinciding	coinciding	coinciding
Golden Hornet	2-3 days late	2-3 days late	3-4 days late	2-3 days late
M. E M Wilson	2-3 days late	coinciding	coinciding	coinciding
M. georgious	coinciding	coinciding	coinciding	coinciding
M. floribunda	coinciding	2-3 days early	almost coinciding	coinciding
Redflush	3-4 days early	3-4 days early	almost coinciding	2-3 days early
Control (Commercial pollinisers)				
Golden Delicious	4-5 days late	2-3 days late	2-3 days early	1-2 days coinciding
Red Gold	coinciding	2-3 days early	2-3 days early	coinciding

systems of placements and altitudes/aspects. The flowering duration in Snowdrift, Manchurian and Golden Hornet is quite prolonged. Though earlier two flowers little early but they also cover the full bloom of Delicious there by having beneficial effect on its fruit set.

ii) *Flower characters* : The data on different flower characters of these crabs are given in Table 3. It is evident from the persual of table that crab apple generally have high flower bud intensity. Golden Hornet has the highest flower bud intensity (0.86) followed by Snowdrit (0.70) and least was in our commercial varieties like Golden Delicious and Red Gold. Manchurian and Snowdrift also had higher numbers of flower buds (7 to 10) in a spur, number and weight of anthesis per flower.

Table 3. Flower bud intensities and other characteristics of crab flower parts

Name of pollinisers	Flower bud intensity (per inch shoot length)	No. of flower per spur	Wt of anthers per flowers (mg)	No. of anthers per flower
Manchurian	0.50	9-10	16-0	20.0
Snowdrift	0.70	7-8	14-0	20.0
Malus robusta	0.45	5	11-0	19.0
Golden Hornet	0.86	5-6	8-0	20.0
Malus floribunda	0.65	5-6	4-0	19.0
M. E M Wilson	0.40	5-0	15-0	11.0
Redflush	0.40	5-0	15-0	11.0
Malus georgious	0.60	5-0	9-0	12.0
Control (Commercial pollinisers)				
Golden Delicious	0.80	5-0	12-0	18.0
Red Gold	0.48	5-0	18-0	20.0

3. Effect on fruit set of Delicious

The data on fruit set is given in Table 4. The fruit set was higher with Manchurian, Snowdrift in comparison with commercial varieties as well as other crabs.

Table 4. Effect of different crab pollinisers on fruit set of Delicious

Sr. No.	Name of polliniser	Mean fruit set (in 100 spurs)		
		Site I 1800 M (SW)	Site II 100M (NE)	Mean
1.	Manchurian	57.0	152.0	104.0
2.	Snowdrift	114.2	190.2	152.2
3.	Golden Hornet	50.4	98.0	74.2
4.	Red flush	25.0	55.0	40.0
5.	*M. georgious*	56.0	96.2	71.2
6.	*M. E M* Wilson	72.0	102.7	87.3
7.	*M. floribunda*	35.0	60.0	47.5
8.	*M. robusta*	15.0	45.0	30.0
Control (Commercial pollinisers)				
1.	Red Gold	10.0	125.0	69.5
2.	Golden Delicious	8.4	70.0	39.2

Two crab apple species namely *M. robusta* and *M. E M Wilson* were found vigorous in growth habit. These types of pollinisers are generally not desirable due to their occupying more space without commerical fruit production. In respect of flowering behaviour, Manchurian and Red flush were early in their flowering but Manchurian have given pronounced effect fruit set. *M. georgious, M. E M* Wilson and *M. floribunda* have the bloom period almost coinciding with Delicious, whereas Golden Hornet was late like Golden Delicious. Golden ornet and Snowdrift also have the highest flower bud intensity.

Wild apple species have been reported to cause 50 to 80 per cent fruit set compared to open pollinated Golden Delicious (Blasse and Schrotter, 1985; Selli and Montalti, 1985 and Gautam et al., 1994). Manchurian crab has been reported tohave the advantage of flower shape which abstract more top workers (Mayer, 1987)

Vigorous growth behaviour of *M. robusta* and *M. E M* Wilson makes them unfit for apple pollination use. Manchurian and Redflush are very early in flowering, however Manchurian due

to prolong flowering duration has beneficial effect on fruit set of Delicious. Snowdrift with high flower bud intensity, prolong flowering period and annual flowering habit has been observed as excellent crab polliniser for Delicious. This was however closely followed in some locations by Manchurian. *Malus florobunda*, Red flush, *M. robusta* and Golden Hornet had resulted in poor performance on fruit set of Delicious apple.

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COLLECTING TARO AND OTHER TUBER CROPS FROM NORTH EASTERN HILL REGION OF INDIA

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A germplasm collection mission to North Eastern hill region of India was undertaken to collect taro and other tuber crops during 1996. The area showed wide distribution of taro. This supports the theory that this region is the Centre of Origin of taro. In all, 42 accessions of taro and 50 accessions of other tuber crops were assembled from Garo hills, Khasi hills and Jawai hills of Meghalaya. The collection contains high yielding varieties, acid free cultivars and leaf blight free types. The collected germplasm will be very useful in the breeding programme.

Key words: Taro, collection, tuber crops, leaf blight

Taro (*Colocasia esculenta* L. Schott) is a tuber bearing herbaceous plant belonging to the family Araceae of Monocotyledons. It is a large family of about 110 genera and over 2000 species widely distributed in tropical and subtropical regions of the world. Taro is estimated to be cultivated in an area of 1.07 million hectares producing 6.5 million tons of tubers (FAO, 1997). However, it is an underestimate, as taro is a backyard crop and estimates are not available from many countries including India. Eventhough taro is cultivated in many countries of Asia, and South America it is in the South Pacific that the crop has gained economic, social and national importance (Pena, 1970). Taro is a staple food in most of the pacific Islands and in many countries such as Tonga, Western Samoa and Papua New Guinea, it is a prestigious crop playing an important role in the gift giving ceremonies (Clark, 1977; Thaman, 1977).

Taro is considered to be one of the most ancient tuber crops domesticated by man, perhaps much before grains. It is believed to have originated in the South East Asia including India and Malaysia (Watt, 1889; Chang, 1958; Keleny, 1962). From there it has spread to Taiwan. The Solomon Islands and to Japan (Spencer, 1966; Kumasava *et al.*, 1966). Later work of Kuruvilla and Singh (1981), Velayudhan *et al.* (1991), Medi *et al.* (1994) and Pandey *et al.* (1993) have confirmed the assumption that North Eastern India is the primary centre of origin of taro.

MATERIALS AND METHODS

Considering the importance of the collection of taro from the North Eastern hill region of India, a germplasm collection trip was arranged under the aegis of an ICAR sponsored Ad hoc scheme on taro and the Crop Improvement Division of the Central Tuber Crops Research Institute (CTCRI), Thiruvananthapuram, India. This trip was taken up during October-November 1996 in collaboration with the regional centre of the National Bureau of Plant Genetic Resources, Umiam (Barapani), Meghalaya.

The state of Meghalaya represents two distinct agro-climatic zones, namely mild tropical hill zone and sub-tropical hill zone. Similarly different soil types also are available; black, red and laterite. The collections were made mostly from cultivated fields, market places and road sides. Taro is mostly found as mixed crop along with rice, legume, ginger etc. in a typical jhum cultivation system of the region (Jhum is an old traditional way of cultivation by the hill tribes, where an area of the forest is cleared, burned and mixed cultivation is done there for a few years till the soil fertility lasts. Thereafter they look for other pasture/forest area.

RESULTS AND DISCUSSION

Forty two accessions of taro and more than 50 accessions of other tuber crops like cassava (12), sweet potato (5), yams (5), swamp taro (4), tannia (9), elephant foot yam (4) and other minor tuber crops (22) were collected (Fig. 1-2). Most of the collections of taro were obtained from Garo hills, Khasi hills and Jowai hills. Details regarding the collections made from each region along with their soil type and agro-climatic conditions are given in table 1. Wide variability with regard to colour, shape and size of tubers was noticed (Fig. 1-4). This great diversity is in conformity with the assumption that North Eastern India is the centre of origin of taro.

Majority of the collections were dasheen type, consisting of corm only (Fig. 3-4). This is in contrast to the situation in South India where majority of the accessions are eddoe or mixed type. Flowering and seed setting are rarely noticed in this region. Out of 42 collections, only one was found to flower whereas in South India a good number of diploid accessions flower and set seed (Thankamma Pillai and Unnikrishnan, 1993; Sreekumari, 1992).

Taro is a popular crop in Meghalaya and as such it forms an inevitable item of daily food. Cultivars like "Garokatchu" and "Tha'h" are known for their high yield, early maturity, low acridity and good cooking quality. One particular cultivar "Wang Panaii" is said to be non-acrid and it is eaten fresh as salad with lime juice added for flavour. However, other tuber crops did not show much variability in this region. Swamp taro is favourite dish here. Cassava might have infiltrated into this area from Burma. Amorphophallus (elephant foot yams) are of two distinct type, the big commercial type and a small type, as small as potato. Minor tuber crops belonging to Zingiberaceae family also are found. "Saflong" a minor tuber crop, the small tubers of which are eaten fresh, is a speaciality of this area.

Table 1. Two collection from North Eastern Hill region

Place of collection	No acce-ssions	Soil type	Zone
Garo hills	6	Black	NEH-5 (mild tropical hill zone)
Tura	3	Black	NEH-5
Bhagmara	3	Black	NEH-5
Bhalphakrum	3	Black	NEH-5
Khasi hills	1	Red + Laterite	NEH-3 (tropical hill zone)
Barapani	6	Red	NEH-3
Umroi	3	Red	NEH-3
Jawai	4	Laterite	NEH-3
Kanduli	2	Laterite	NEH-3
Laitkore	5	laterite	NEH03
NBPGR (R.S.)	2	Red	NEH-3
Konjoi	4	Red	NEH-3

Utility

Acridity is a major problem in the breeding of taro. Even when low acrid varieties are hybridized a number of high acrid progenies are thrown out. Cultivars like "Wang panaii" should be a great significance in breeding low acrid varieties as well as for basic studies on the pattern of inheritance of acridity.

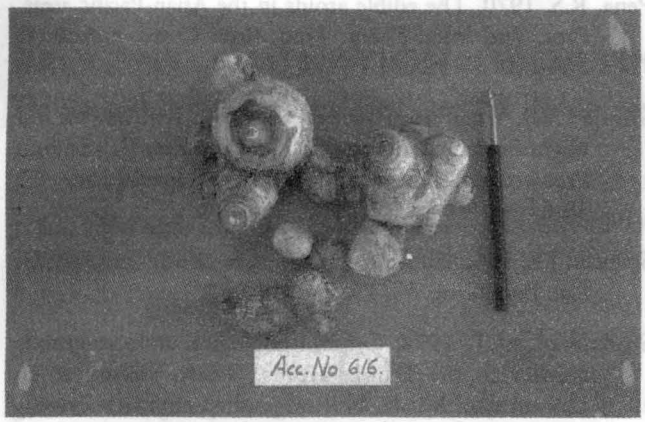

Fig. 1. Round corm and many cormels

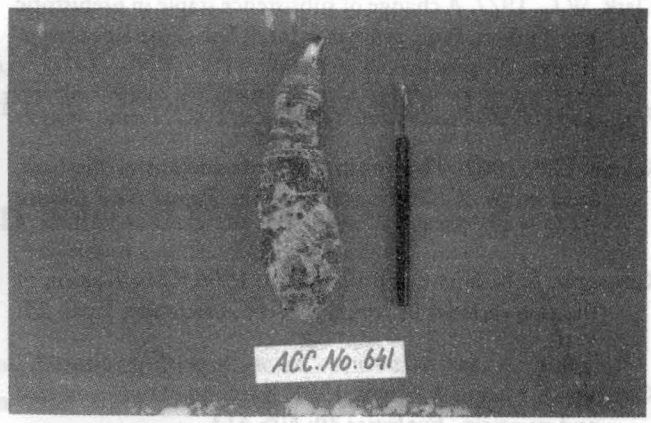

Fig. 3. Oblong corm only (dasheen type)

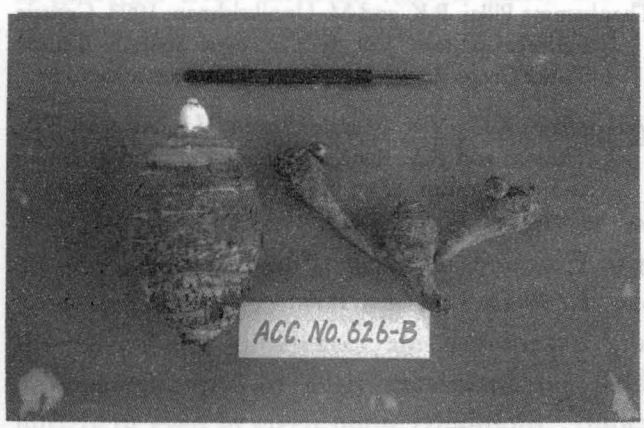

Fig. 2. Conical corm and few cormels

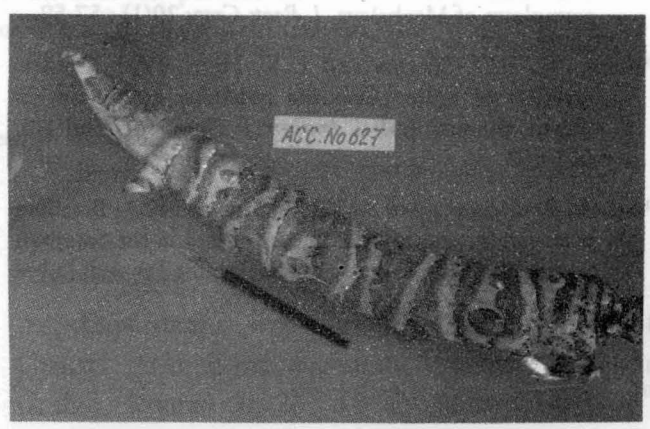

Fig. 4. Oblong, large corm only (dasheen type)

Leaf blight disease was not apparent in this region. Blight caused by *Phytophthora colocasiae* is one of the serious diseases of taro in all taro growing countries including India (Santha Pillai *et al.*, 1991). Taro plantations in a number of Pacific Islands were completely damaged by leaf blight. Recently 90 per cent of the taro plantations in Western Samoa was destroyed by the epidemic of leaf blight. Patel *et al.* (1993) have suggested that leaf blight resistant varieties from India, the center of origin of taro, should be used in resistance breeding. So far no cultivar was found to be completely resistant to leaf blight. The leaf blight free cultivars can be screened in hot spots and tolerant ones can be used in the resistance breeding program.

It is expected that cultivars collected from NEH region will be of immense use is genetic studies and breeding of tuber crops.

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PROGENY EVALUATION OF LATIN AMERICAN *Prosopis pallida* (Humboldt ex Bonpland ex Willdenow) H.B.K. IN INDIAN ARID TRACT

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Twenty two accessions of *Prosopis pallida* of Latin American origin were evaluated at 4 years growth for plant height and collar diameter in Indian arid tract. Shifting of accession rank order occured with advancement of growth; accession No. 418, 420 and 424 performed consistent and relatively better for both plant height and collar diameter upto the age of four years. Variability at genotypic level, hertibility (broad sense) and genetic advance as percent of mean were maximum at 2-year stage, indicating thereby the scope of improvement through selection at this stage.

Key words : *Prosopis pallida*, collar diameter, non-hirerchical eucleadian cluster analysis

Heritable differences among genotypes of different populations (Provenances "Sources") have been well recognised for many commercial tree species. These differences are demonstrated in designed provenance trials conducted on field, nursery or even in green house conditions. Burley *et al.*, (1984) opined that when provenance trials are carried out at a particular location, it is possible to detect some heritable differences in the provenances of same species collected from different habitats. These differences are particularly important to identify and select a suitable provenance for maximum productivity.

Importance of *Prosopis* species in and regions has been widely recognised (Muthana and Arora 1983; Felker, 1984; Sharma *et al.*, 1993, 94 and Sharma, 1995) but very little information is available regarding genetical aspects of exotic accessions on this species (when tried in India). Present Investigation was carried out on twenty two accessions of *Prosopis pallida* of Latin American origin with objectives to study the variability for plant height and collar diameter and to identify fast growing accession(s).

MATERIALS AND METHODS

Experimental site

Experiment was conduced at Silvatum of Central Arid Zone Research Institute, Jodhpur (India), located at 26° 18' N latitude and 73° 08' longitude. The climate of the area is typically arid, characterised by exceptionally hot dry summer, sub-humid monsoon and cold dry winters. The climatic details recorded at experimental site during the period of investigation are set in Fig. 1. The soil of the site is sandy-loam

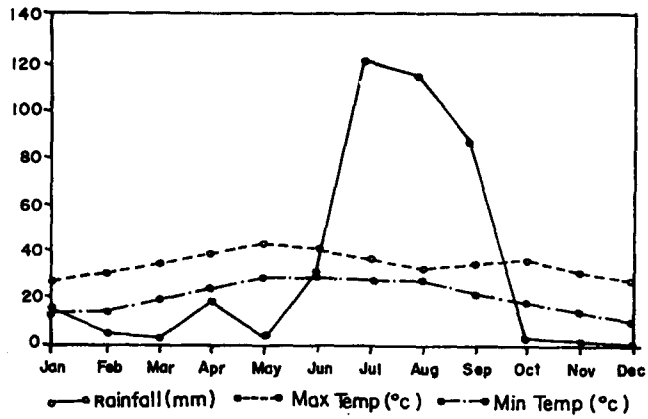

Fig. 1. Ombrothermic diagram for the study site. Data represents average of four years i.e., during course of experimentation

(Camborthid) with pH 8.1, and poor in nutrients having 0.23 per cent organic Carbon, 0.33 per cent nitrogen and 0.02 per cent phosphorus (Dhir 1984),

Field experimentation

Twenty two accessions of *Prosopis pallida* of Peruvian origin (procured from Caesar Kleberg Wildlife Research Institute, Texas A & M University, Kingville, USA) were used for the study, Except EC 308213 (US acc. no. 423) and 308214 (US acc. no. 424), all the accession belonged to Trujillo province of Peru. The EC 308213 (US. acc. no. 423) and 308214 (US acc. no. 424) owed their origin to Contumaza province. Here after only US accession numbers are used in further discussion which are simply indicated as accession number (acc. no.). The term accession is used to describe seeds from single tree representative of one location. Seeds were first scarified with conc. H_2SO_4 for 15 minutes and then washed with running tap water, and sown in Polythene bags (25 cm x 10 cm in 1:2:1) during the month of March (i.e. the onset of spring season). Five months old seedlings were then outplanted to field in the month of July (i.e. the onset of rainy season). Planting was done at the spacing of 2.5 x 4.0 in in randomised complete block design with four replications, each having five plants. Plants were veriguled fortnightly in summer and once in a month during winter (g 15 liter per plant in first year of planting only. Two hoeing (in a year) were carried out to control the weeds.

Quantitative analysis

Observations on survival, plant height and collar diameter of all the accessions were recorded in yearly interval up to four years age by following standard silvicultural measurement procedure. Replication means were used for statistical analysis using a computer software "SPAR 1" developed by Doshi and Gupta (1991).

RESULTS AND DISCUSSION

During the period of investigation, on an average, across all the accessions introduced, there was gradual increase in plant height from 89 cm per plant, at one year to 276 cm per plant, at four year age and in collar diameter from 0.88 cm per plant at one year to 3.8 crn per plant at four year age (Table 1). The characters, however, did not exhibit uniform growth in progenies of different accessions.

After one year, accessions no. 420 registered maximum plant height (128 cm/plant) as well as collar diameter (1.22 cm/plant) followed by acc. no. 418 for plant height (120 cm/plant) and acc. no. 421 for collar diameter (1.13) cm/plant). After 4 years, plant height was maximum in acc. no. 442 (387 cm/plant) followed by acc. no. 424 (373 cm/plant) and collar diameter was maximum in acc. no. 424 (6.05 cm/plant) followed by acc. no. 442 (5.35 cm/plant). For plant height, acc. no. 417, 418, 420, 424 and 4'13-, and for collar diameter, acc. no. 417, 418, 420, 421, 423 and 424 performed consistently better during all the four years. The performance of acc. no. 418, 420 and 424 was relatively better and consistent for both the characters. Therefore, these accessions may prove to be highly useful for raising plantations in the areas having similar climatic and edaphic conditions as that of experimental site.

Non-hirarchical eucleadian cluster analysis placed all the 22 accessions in four clusters across all the four years (Table 2). The cluster IV includes the accessions having comparatively higher mean values of plant height and collar diameter. Clustering pattern of accessions changed with growth. Among all 22 accessions, only acc. no. 424 found a place in cluster IV across all the four years. Inter- and intra-cluster distances revealed the presence of considerable variability in the material studied. The intra-cluster distances were less than inter-cluster distances and

Table 1. Means of plant height and collar diameter of 22 accessions of *Prosopis pallida* across four years (at early interval)

S. No.	EC no.*	US acc. no.**	Plant height (cm)				Collar diameter (cm)			
			1st yr.	2nd yr..	3rd yr.	4th yr.	1st yr.	2nd yr.	3rd yr.	4th yr.
1	3080207	417	63	134	209	266	1.01	2.32	3.04	4.53
2	3080208	418	120	269	279	323	0.94	3.56	3.99	4.65
3	3080210	420	128	288	232	326	1.22	3.74	3.60	3.85
4	3080211	421	103	227	216	271	1.13	3.03	3.09	4.38
5	3080213	423	79	162	213	289	1.03	3.29	4.48	4.46
6	3080214	424	108	235	264	373	1.08	3.31	5.09	6.05
7	3080218	428	89	156	245	315	0.81	2.32	3.60	4.57
8	3080219	429	73	126	161	189	0.67	1.26	1.66	1.99
9	3080220	430	90	146	144	228	0.90	1.65	1.54	2.81
10	3080221	431	80	126	181	256	0.77	1.67	3.19	3.52
11	3080222	432	80	104	178	227	0.77	1.32	1.74	2.58
12	3080223	433	97	164	230	301	0.85	2.05	3.57	4.10
13	3080224	434	81	124	187	260	0.81	1.41	2.84	3.31
14	3080225	435	87	122	230	311	0.88	1.57	3.41	4.62
15	3080227	437	95	163	204	254	0.88	1.89	2.88	3.56
16	3080228	438	82	124	166	236	0.75	1.80	2.04	2.80
17	3080229	439	75	114	191	215	0.78	1.47	2.05	2.90
18	3080230	440	93	152	191	247	0.68	1.75	2.58	3.34
19	3080231	441	89	143	187	254	0.91	1.89	2.58	2.89
20	3080232	442	87	132	292	387	0.75	2.23	3.81	5.35
21	3080233	443	86	162	234	296	0.96	2.13	2.74	3.78
22	3080236	446	132	196	250	0.70	1.77	2.97	3.54	
Mean			89	159	210	276	0.88	2.16	3.02	3.80
± SE			15	29	51	70	0.12	0.38	1.13	1.28
CV %			24	26	35	36	19.37	25.16	52.84	47.52
CD (5%)			30	57	-	-	0.24	0.76	-	-
CD (1%)			-	76	-	-	0.32	1.01	-	-

* EC no: Exotic collection number (EC No.) given by NBPGR, New Delhi to the seed lots received for the present study from donor agency
**US acc. no: The number given by donor agency for seed material used in the present study

inter-cluster distances were found to be to maximum between cluster I and cluster IV (Table 3).

Analysis of variance revealed that significant differences existed only during first two years of growth for plant height and collar diameter and these significant values are set in Table 4. In third and fourth years, differences were not significant for either character. In initial years, significance of differences may be attributed to

Table 2. Clustering pattern of 22 accessions of *Prosopis pallida* in four different years using non-hirerical eucleadian analysis

Years	Cluster No.	No. of obser-vation	Serial no. of accesions*	Cluster mean (cm)	
1st	I	9	8, 10, 11, 13, 16, 17, 18, 20, 22	81.87	0.74
	II	2	1, 5	70.88	1.02
	III	7	7, 9, 12, 14, 15, 19, 21	90.29	0.88
	IV	4	2, 3, 4, 6	114.50	1.09
2nd	I	9	8, 9, 10, 11, 13, 14, 16, 17, 22	124.06	1.55
	II	8	1, 7, 12, 15, 18, 19, 20, 21	150.47	2.07
	III	1	5	162.25	3.29
	IV	4	2, 3, 4, 6	254.75	3.41
3rd	I	5	8, 9, 11, 16, 17	168.00	1.81
	II	7	3, 4, 5, 7, 12, 14, 21	227.00	3.50
	III	7	1, 10, 13, 15, 18, 19, 22	193.39	2.87
	IV	3	2, 6, 20	278.33	4.30
4th	I	11	8, 9, 10, 11, 13, 15, 16, 17, 18, 19, 22	237.68	3.02
	II	6	2, 3, 7, 12, 14, 21	311.83	4.26
	III	3	1, 4, 5	275.25	4.46
	IV	2	6, 20	379.75	5.70

*Refer Table 1 for serial no. of accessions

maternal effects (due to differential seed reserves) because some accessions may have bolder seeds and some have smaller seeds, as accessions were collected from different habitats of wider locations having different climatic conditions and soil types. It is quite possible the seeds having different vigour may also vary in genetic constitution. Bolder seeds having more food reserve generally provide better nourishment to growing seedling, therefore, it is expected to give better plant type as compared to the cases of smaller seeds. The

Table 3. Average distances of cluster members from cluster centroid (diagonal) and distances between cluster centroids of four cluster during four different years in 30 accessions of *Prosopis pallida*

Years	Cluster	I	II	III	IV
1st	I	0.49	-	-	-
	II	2.02	0.55	-	-
	III	1.12	1.60	0.39	-
	IV	3.23	2.96	2.14	0.96
2nd	I	0.33	-	-	-
	II	0.88	0.36	-	-
	III	2.44	1.63	0.00	-
	IV	3.59	2.73	1.85	0.61
3rd	I	0.47	-	-	-
	II	2.44	0.62	-	-
	III	1.35	1.13	0.34	-
	IV	4.02	1.62	2.75	0.69
4th	I	0.64	-	-	-
	II	1.97	0.44	-	-
	III	1.66	0.77	0.21	-
	IV	3.98	2.02	2.41	0.39

Table 4. Analysis of variance and genetic parameters for plant height and collar diameter in *Prosopis pallida* across four years at yearly interval

Source of variation	d.f.	Mean Squares			
		Plant height		Collar diameter	
		1yr.	2 yr.	1 yr.	2 yr.
Replications	3	97.44	3040.4	0.10	0.99
Accessions	21	893.46*	10084.4**	0.09**	2.26**
Error	63	443.97	1641.2	0.03	0.29
GCV		11.87	28.87	14.01	32.48
PCV		26.41	38.49	23.90	41.08
Heritability (%)		20.20	56.30	34.30	62.50
Genetic advance (GA)		9.81	70.99	0.15	1.14
GA as % of mean		10.98	44.60	17.05	52.78

maternal effect (food reserve) will not influence the growth and development of genotypes after certain time period. Further development of plant will depend on genotypes (G), environment (E) and G x E interactions. In such cases, where variability was more at initial stage but decreased in advance stage, the accessions showing relatively better and consistent performance may be used for future course of plantations in the areas having similar climatic and edaphic conditions as that of experimental site.

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VARIATION IN *Berberis lycium* Royle POPULATIONS FOR BERBERENE CONTENTS

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In the present study, roots from sixty eight phenotypically superior shrubs comprising seventeen provenances (four superior shrubs from each provenance) from wide altitudinal range of Himachal Pradesh were collected and analyzed for within and between provenance variation for berberine. Berberine ranged from 1.28 to 6.36 per cent and provenance mean from 2.54 to 4.91 per cent. Maximum berberine content was found in Rajgarh, followed by Palampur, Gohar and Jamta provenances. Whereas, one of the shrub of Palampur provenance gave the highest berberine content of 6.36% and showed significant superiority over all other shrubs.

Key words : *Berberis*, provenance, shrubs, berberine variation

Berberis lycium is a spiny shrub belonging to family Berberidaceae. It is found gregariously between 600-3000m altitude. Genus *Berberis* consists of about 280 species spread world wide, of which 14 are reported from Indian Himalaya (Osmaston, 1927). Wood and bark extract of these spacies is used as febrifuge. A yellow dye obtained from wood and root is used in leather processing. Berberine, an alkaloid of iso-quinoline nature is obtained from its root and is exploited extensively for its commercial value (Anon, 1976). Berberine also act as good intestimal astringent, cure for cough, chest, throat troubles, eyesores, eyeitch, piles and chronic diarrhoea. Leaves are administered for jaundice in Baluchistan. In Indo-China, fruit is administered as tonic for kidney troubles (Kirtikar and Basu, 1975). Eyedrops of berberine chloride (0.2%) is reported to cure active trichoma lesions (Babber *et al.*, 1982). Berberine has also been found to inhibit auto-reproduction of influenza virus and the activity of reverse transcriptase of HIV-1 virus responsible for AIDS (Kedzia, 1992). The present study covering the part of its distribution across Himachal Himalaya was conducted with the objective of understanding the variation in different provenances for berberene content.

MATERIALS AND METHODS

Roots of *Berberis lycium* were collected from seventeen provenences representing the entire range of its distribution in Himachal Pradesh (600-3000m) for the present study. Each provenance comprised four selected shrubs. The provenances selected were located in Solan, Shimla, Sirmour, Bilaspur, Mandi, Kullu, Kangra and Chamba districts of the state ranging from 30° 25' to 32° 18' N latitude and 75° 45' E to 79° 04' E longitude. Root samples from the selected shrubs of each provenance were cleaned and dried in over at 80°C till constant weight, crushed, powdered and sieved through 0.1 mm sieve to prepare the sample for alkaloid estimation. The method adopted for estimation was standardized

based on lines of Snell and Snell (1970). Absorbance curve for qualitative estimate was standardized using berberine chloride as reference compound. Powdered root was refluxed in ethyl alcohol for two hours.

Extract was condensed and thin layer chromatography was employed to separate berberine from it. Quantification of berberine was determined using Spectronic-20 based on absorbance at 426 nm. Data so obtained was analyzed in compact family block design which delineated between and within provenance variation (Narain, 1990). Bartlett's test was performed to test the homogeneity of between and within provenance error variance.

RESULTS AND DISCUSSION

Statistical analysis showed significant to highly significant variation in berberine content between provenances. Within provenance, the variation was found significant except for Darlaghat and Sarahan provenances. The Bartlett's test also established that provenances were heterogeneous as depicted by significant Chi-square value (31.91).

The average berberine content between provenances ranged from 2.54 percent (Shimla) to 4.91 percent (Rajgarh) (Fig. 1). Rajgarh was followed by Jamtah (4.69%) and Gohar (4.66%). Minimum berberine content of Shimla was in proximity to Solan (2.79%) and Sarahan (3.11%). Other provenances with intermediate values were viz; Dharamsala (3.89%), Kullu (3.41%) and Joharji (3.94%) etc. The individual plant performance showed highest berberine content of 6.36 per cent to lowest of 1.28 per cent. The mean content of alkaloid was found to be 3.88 per cent. Whereas, the mean content of berberine in Pakistan was reported to be 1.75 per cent (Hussain *et al.*, 1984) which seems to be quite low in comparison to our present study.

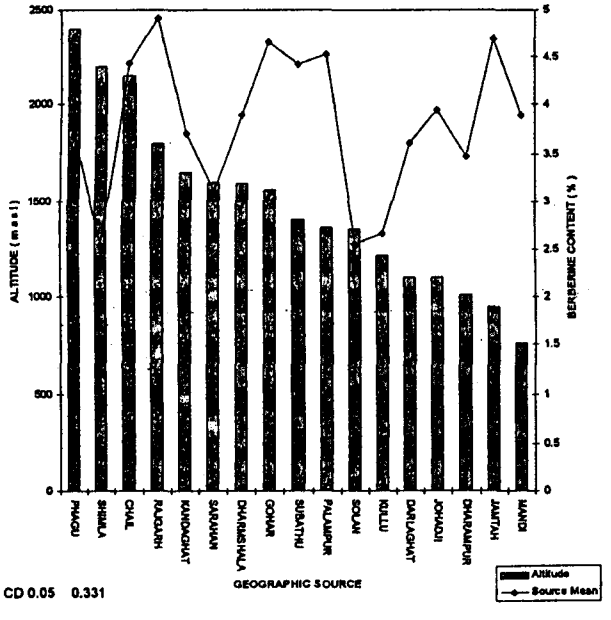

Fig. 1. Geographic variation of berberine content in *Berberis lycium* along altitude

The detailed pattern of statistically significant differences between individual populations is delineated in Fig. 2. Palampur and Rajgarh showed promising results worth immediate conservation. Populations with at par performances clustered around middle and at lower altitudes. Diversity increased on edges of distributions; therefore, suggesting an increase in variation at fringes of distribution. So suitable increase in the sampling intensity in fringes can be structured based on this information.

	PHG	SML	CHL	RJG	KND	SRN	DMS	GHR	SBT	PMP	SLN	KLU	DRL	JDJ	DMP	JMT	MND
PHAGU (PHG)					X		X					X	X		X		X
SHIMLA (SML)											X						
CHAIL (CHL)								X	X	X							
RAJGARH (RJG)								X								X	
KANDAGHAT (KND)							X					X	X		X		X
SARAHAN (SRN)											X	X					
DHARAMSHALA (DMS)													X			X	X
GOHAR (GHR)									X					X		X	
SUBATHU (SBT)										X						X	
PALAMPUR (PMP)																	
SOLAN (SLN)																	
KULLU (KLU)															X		
DARLAGHAT (DLG)																X	X
JOHADJI (JDJ)																	
DHARAMPUR (DMP)																	
JAMTAH (JMT)																	X
MANDI (MND)																	

X - Statistically No Significant differences

Fig. 2. Matrix showing pattern of statistically similar geographic sources of *Berberis lycium* for berberine content

Scrutiny of best populations (Rajgarh, Jamtah, Gohar and Palampur) showed the following order of individual shrub performances as presented in Fig. 3. Expect for Gohar, even populations with

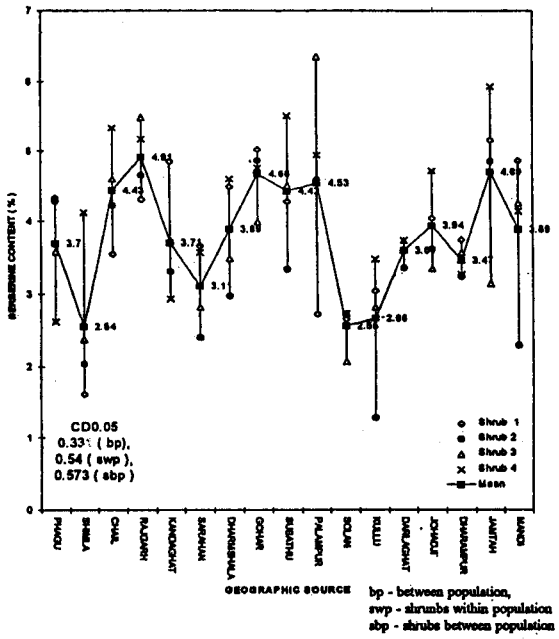

Fig. 3. Between and within source variation for berberine content in berberis lycium

low berberine content (Phagu and Joharji), depicted significant within provenance variation. Highest berberine content estimated was in Palampur shrub (6.36%). Shrubs with berberine levels close to Palampur, Rajgarh, Chail and Subathu etc. deserve necessary screening.

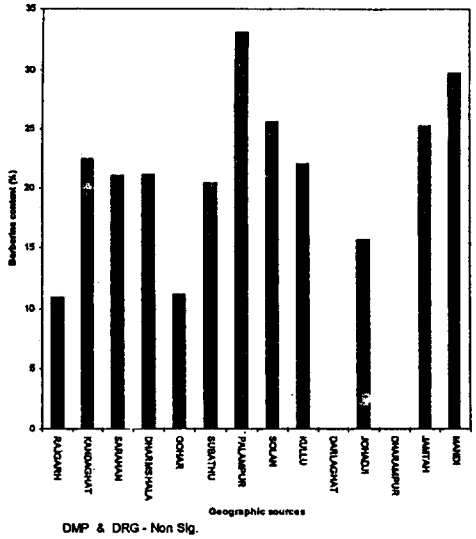

Fig. 4. Phenotypic variability estimates for different provenances in berberine content fo *Berberis lycium*

Phenotypic variability based on parent (half-sib) performance Shimla was found to be highly variable population. However, comparative understanding between higher chemical contents and variability suggests that Palampur and Mandi may be best possible choice for the establishment of long term gene base. High degree of adaptive variation at genetic and biochemical levels within species range, associated with fast colonizing abilities of *Berberis lycium* may be a key driving factor. Further studies for estimation of genetic components to quantify the heritability of berberine would enable sustainable exploitation.

Maximum content of berberine available in Palampur's individual shrub along with wide range and phenotypic variability may be recommended for overall improvement of berberine production. Rajgarh along with Gohar and Jamtah which are promising provenances also needs further delineation of variability.

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GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN GERMPLASM OF INDIAN-MUSTARD (*Brassica juncea* (L) Czern & Coss.)

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Variability, correlation and path analyses were carried out for eleven agro-morphological characters of Indian-mustard [*Brassica juncea* (L) Czern & Coss]. The highest coefficient of variation (CV) was found for secondary branches/plant (67.0%) and seed yield/plant (47.0%) while, the least for days to maturity (2.0%). Rest of the characters had moderate variation (CV ranged from 6.6 to 19.3%). Seed yield had significant and positive correlation with all the characters except for days to maturity. Hioghest correlation was recorded with siliquae on main shoot (0.5) and secondary branches (0.5). Days to maturity had negative but non-significant correlation with all characters except plant height and seed yield. Siliquae on main shoot had the highest direct effect (0.344) on seed yield, followed by primary branches/plant (0.223), secondary branches/plant (0.189), 1000-seed weight (0.159) and siliqua length (0.147). Therefore, these characters are the main yield components and greater emphasis must be laid on them while, selecting plants in segregating generation.

Key words : Indian mustard, variability, interrelationship

Indian mustard is the predominant crop among the *Brassica* oil seeds occupying nearly 85 per cent of the total hectarage (7.0 m. ha). The productivity is low and there is further scope for improvement in productivity. Evaluation for available variability is prerequisite for planning the breeding programmes. The present study was undertaken to analyze the variability and interrelationship of components of productivity in Indian mustard germplasm.

MATERIAL AND METHODS

Three hundred and eleven germplasm accessions of Indian mustard was grown with standard checks in augmented design during *rabi* 1998-99 under irrigated conditions at National Research Centre on Rapeseed-mustard, Bharatpur. Each line was sown in paired row in plot size of 5.0m × 0.6 m with all recommended package of practices and the crop geometry (10 cm., plant to plant, 30 cm row to row space) was maintained by thinning at 25 days after sowing. Observations were recorded on a sample of 10 plants selected randomly from each plot for eleven agro-morphological traits viz., maturity, plant height (cm), primary and secondary branches per plant, main shoot length (cm), siliquae on main shoot, siliqua length (cm), seeds per siliqua, 1000- seed weight (g), seed yield (g) and oil content (%). The seeds were counted by an electronic seed counter and oil content was measured by NMR (Oxford, 5000). Correlation and direct and indirect effects were computed by using standard statistical methods (Dewey and Lu, 1959).

RESULTS AND DISCUSSIONS

The evaluated germplasm showed considerable variability for majority of traits as

indicated by coefficients of variation (CV) presented in Table 1, which is prerequisite for further improvement. Secondary branches per plant and seed yield per plant had the highest variability (CV 67%) and (CV 47%) respectively. The seed yield per plant in the present collection ranged from 1.0 to 22.1 g. Most of the accessions (75.5%) ranged from 3.6 to 10.0 g. while, only seven accessions had more than 17.6 g. seed yield (Fig. 1). On the other hand, secondary branches per plant showed variability ranged from 3.0 to 29.0 branches which is also a good sign for yield improvement because it is one of the main yield contributing characters. Most of accessions (54.3%) had 5 .to 10 branches while, twelve accessions had more than fifteen branches (Fig. 2). Number of primary branches and 1000-seed weight showed moderate magnitude of variability (CV 19.3 and 19.2%, respectively). Selection of plants with more primary branches and bold seed are highly required for increasing the yield. The frequency distribution pattern for these characters showed that majority of accessions (90.3%) had 4 to 8 primary branches per plant (Fig. 3), and (79.1%) had 3 to 5g. 1000-seed weight nevertheless, 13.8 per cent of the accessions showed more than 5 g. seed weight (Fig. 4). Variability for main shoot length and siliquae on main shoot was also moderate (Table 1). Main shoot length ranged from 22.6-91.4 and 79.1 per cent accession had 60- 80 cm (Fig. 5) and for siliquae on main shoot 53.1 per cent accessions had 40-50 siliquae on main shoot (Fig. 6). Twenty eight accessions had both long main shoot (> 80 cm) and high number of siliquae (> 50 siliquae) respectively. The coefficients of variation for siliqua length and seeds per siliqua was 11.0 and 9.7 per cent respectively. Siliqua length varied from 2.9 to 5.5 cm and 76.8 per cent accessions had 3.5-4.5 cm (Fig. 7). Seeds per siliqua ranged from 3.8 to 17.1 seeds. Maximum accessions (91.3%) had 11 to 15 seeds per siliqua (Fig. 8). Plant height and maturity are the two important varietal characters

Table 1. Mean, range and coefficient of variation (CV) for different characters in Indian mustard germplasm

Character	Mean	Range	S.D.	CV (%)
Days to maturity	139.1	131.0-149.0	2.8	2.0
Plant height (cm)	177.0	123.6-224.4	18.7	10.6
Primary branches/plant	5.2	2.8-11.8	1.0	19.3
Secondary branches/plant	8.0	3.0-29.0	5.3	67.0
Main shoot length (cm)	69.4	22.6-91.4	11.7	16.8
Siliquae on main shoot	42.2	23.4-63.0	6.7	15.9
Siliqua length (cm)	4.0	2.9-5.5	0.4	11.0
Seed/siliqua	12.6	3.8-17.1	1.2	9.7
1000-seed weight (g)	4.2	2.0-6.3	0.8	19.2
Oil content (%)	38.6	30.8-42.8	2.6	6.6
Seed yield/plant (g)	8.23	1.0-22.1	3.9	47.02

determining its suitability in a production system. Varieties with shorter height, early maturity and high yield are being preferred. Plant height in the present investigation ranged from 123.6 to 224.4 cm with mean value of 176.8 cm. This character, however, showed low variability. Most of the accessions (7.14%) had 161 to 200 cm height (Fig. 9). The present collection showed least variability (1.9%) for maturity. Majority of accessions (72.7%) took 136 to 140 days to mature (Fig. 10) while, maturity varied from 131 to 149 days. Only four accessions were of early maturity type (< 130 days). Oil content showed low magnitude of variability (6.6%) with mean and range 38.6 per cent and 30.8 to 42.8 per cent. Six accessions had oil content more than 42 per cent while, 66.2 per cent ranged from 38 to 42 per cent (Fig. 11). Similar results were reported earlier by Yadav *et. al.* (1997). The present collection proved to be an important gene pool for different traits and many accessions (Table 4) could be utilized for national hybridization programmes to improve seed yield and oil content

and suitable varieties could be developed for different production systems.

Correlation coefficients for eleven metric traits in mustard are presented in Table 2. Seed yield was positively and significantly correlated with all the characters except days to maturity (Khan and Gupta, 1998). However the positive correlations of seed yield were observed with siliquae on main shoot (0.465), secondary branches/plant (0.458), primary branches per plant (0.427), main shoot length (0.331) and plant height (0.271). Similar results have been reported by Reddy, (1991) and Kachroo *et al.* (1997). Therefore selection of high value for these characters will ultimately increase the seed yield. Tharsby, early maturing varieties are desired for escaping biotic and abiotic stresses. Siliqua length and seeds per siliqua have positive and significant correlation with yield and each other while, with rest of characters had non-significant correlation (Kachroo *et al.*, 1997). Seed weight and oil content have positive and significant association with seed yield and with each other. Whereas these have, negative but non-significant association with maturity, primary and secondary branches, main shoot length and siliqua length. Selection of plants with high oil content and bold seed will fetch higher price apart from high yield.

The contribution of these characters was further analyzed by computing their direct and indirect effects on seed yield and is presented in Table 3. Siliquae on main shoot, primary branches, and secondary branches had high direct positive effects whereas, 1000-seed weight, siliqua length and main shoot length had moderate direct effect on seed yield (Table 3). Similar results were reported by Rahman *et al.* (1982) and Khan *et al.* (1998). The direct effects of remaining characters were very low in magnitude. The characters showing high positive correlation with seed yield also had large positive direct effect and indirect effects via each other. The plant height had negative direct effect but correlation with seed yield is positive owing to high indirect effects through all other characters. Siliquae on main shoot showed the highest indirect effects on seed yield through plant height and main shoot length, whereas maturity showed negative indirect effects on seed yield through all the characters except plant height. The results of present investigation suggested in the selection programme the plant more with siliquae on main shoot, primary and

Table 2. Correlations among the different agro-morphological traits in Indian mustard germplasm

Character	Days to maturity	Plant height	Primary branches	Secondary branches	Main shoot length	Siliquae on main shoot	Siliqua length	Seeds/ siliqua	1000-seed weight	Oil content
Plant height (cm)	0.167**									
Primary branches/plant	–0.012	0.306**								
Secondary branches/plant	–0.006	0.171**	0.557**							
Main shoot length (cm)	–0.009	0.456**	0.134**	0.251**						
Siliquae on main shoot	0.081	0.523**	0.274**	0.306**	0.336**					
Siliqua length (cm)	–0.115	0.107	0.073	0.074	0.202**	–0.002				
Seeds/siliqua	0.049	0.029	0.121*	0.103	0.111	0.066	0.269**			
1000-seed weight (g)	–0.078	–0.031	–0.001	0.05	0.111	–0.039	0.161**	0.031		
Oil content (%)	–0.081	0.025	0.095	0.069	–0.001	0.116**	–0.015	0.122	0.347**	
Seed yield/plant (g)	0.046	0.271**	0.427**	00.458**	0.331**	0.465**	0.215**	0.134*	0.191**	0.124*

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

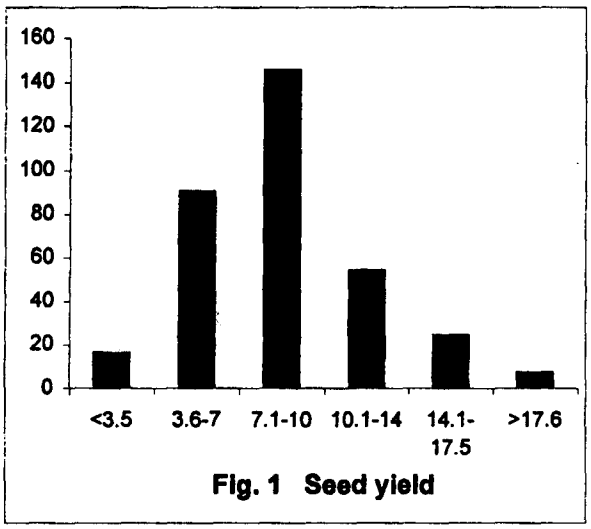

Fig. 1 Seed yield

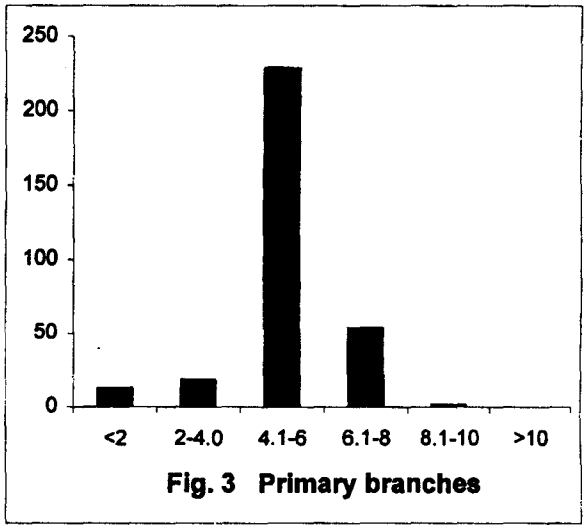

Fig. 3 Primary branches

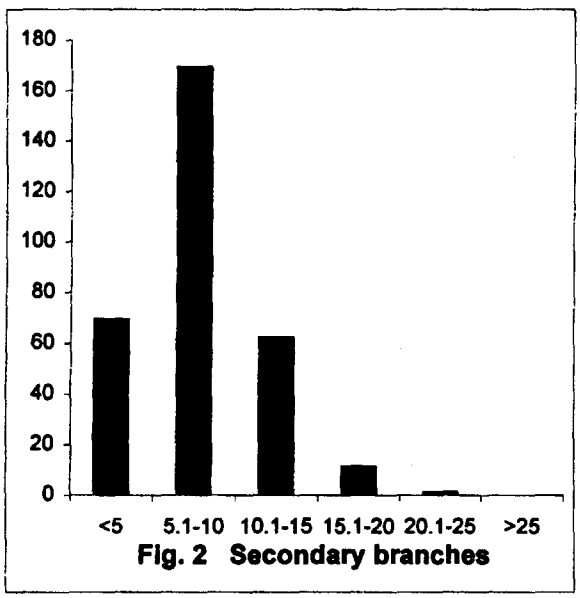

Fig. 2 Secondary branches

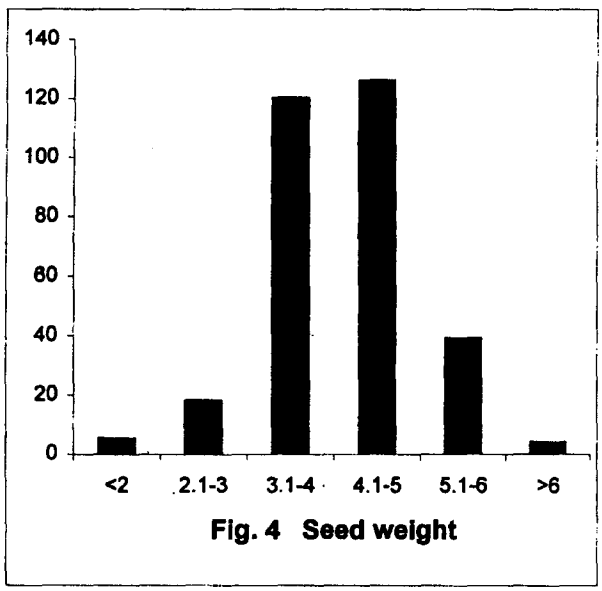

Fig. 4 Seed weight

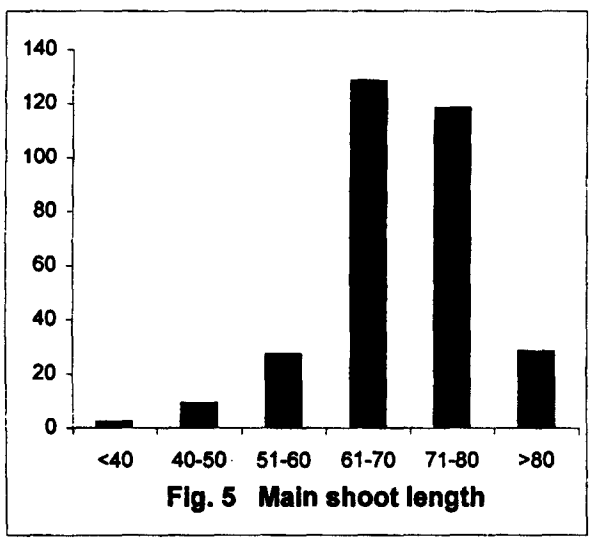

Fig. 5 Main shoot length

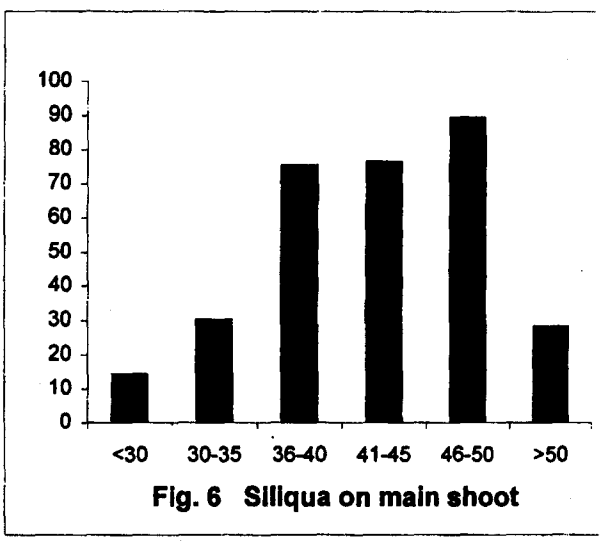

Fig. 6 Siliqua on main shoot

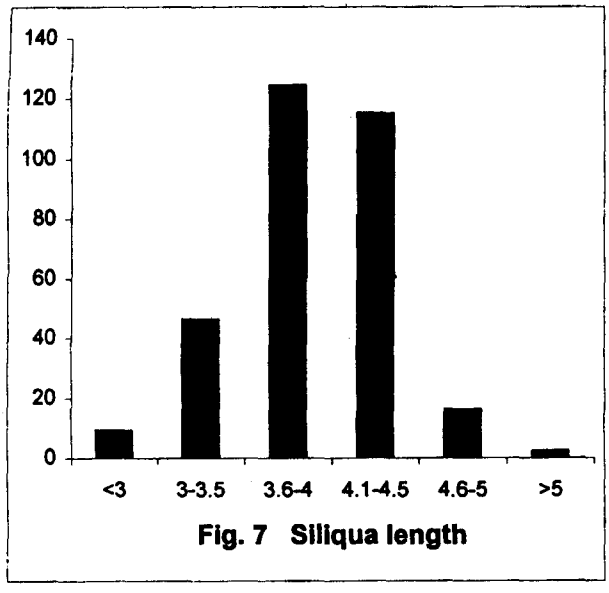

Fig. 7 Siliqua length

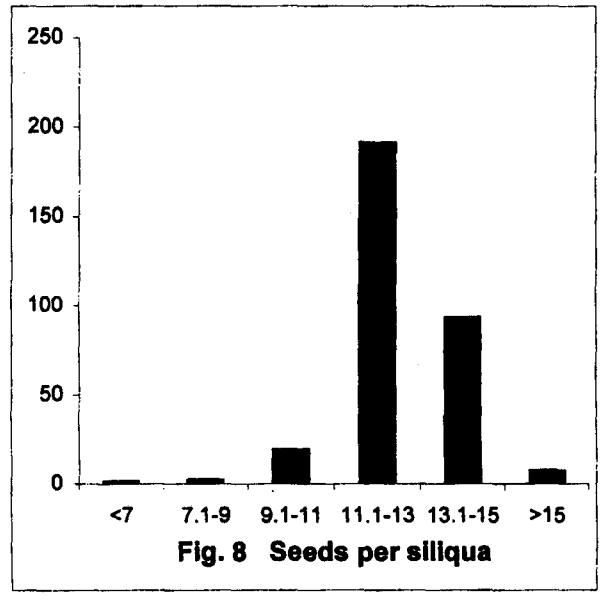

Fig. 8 Seeds per siliqua

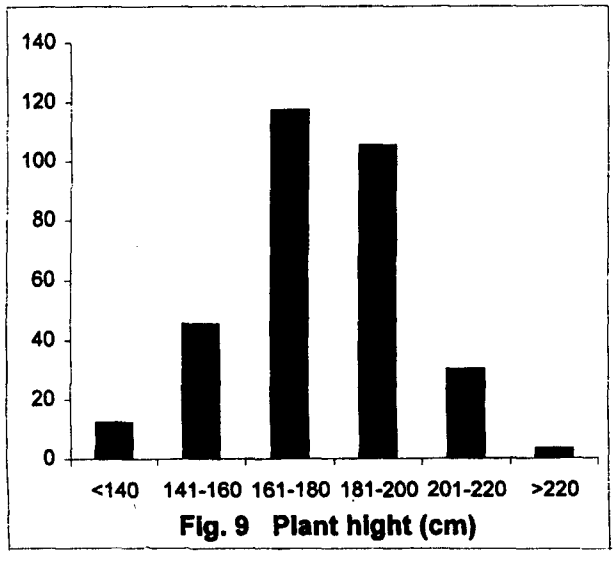

Fig. 9 Plant hight (cm)

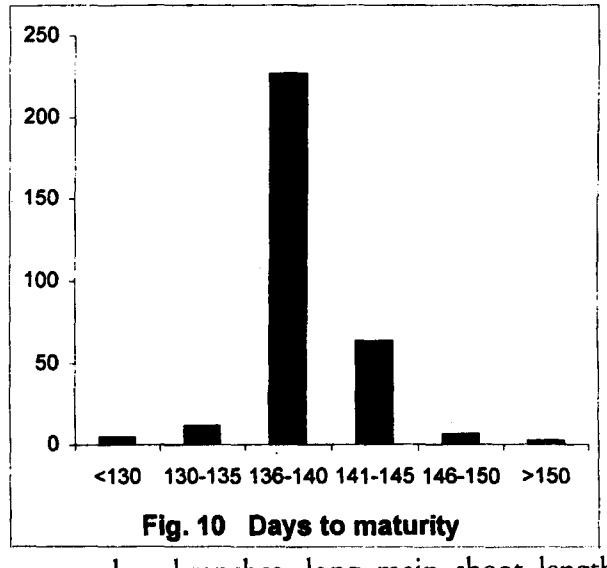

Fig. 10 Days to maturity

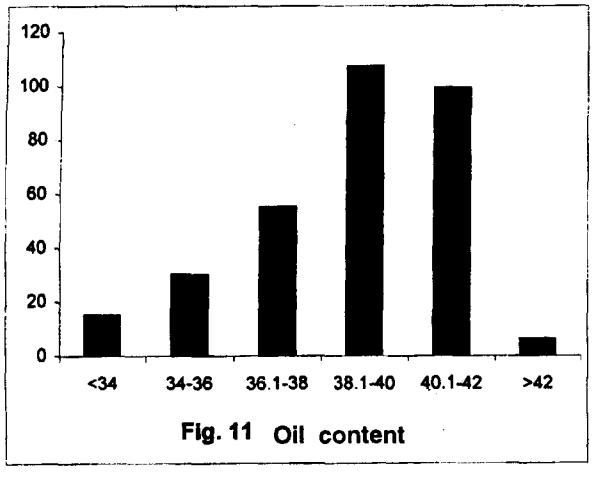

Fig. 11 Oil content

secondary branches, long main shoot length and siliqua length, medium plant height and bold seed should be selected for increasing the seed yield.

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Table 3. Direct and indirect effects of different agro-morphological traits on seed yield in Indian mustard germplasm

Character	Days to maturity	Plant height	Primary branches	Secondary branches	Main shoot length	Siliquae on main shoot	Siliqua length	Seeds/ siliqua	1000-seed weight	Oil content	Correlation with yield
Days to maturity	**0.067**	0.014	–0.003	–0.001	–0.001	0.028	–0.017	–0.001	–0.012	–0.001	0.046
Plant height (cm)	0.011	**–0.082**	0.068	0.032	0.058	0.173	0.016	0.001	–0.005	0.001	0.271**
Primary branches	–0.001	–0.025	**0.223**	0.105	0.017	0.094	0.011	0.002	–0.001	0.001	0.427**
Secondary branches	–0.001	–0.014	0.125	**0.189**	0.032	0.106	0.011	0.001	0.008	0.001	0.458**
Main shoot length (cm)	–0.001	–0.038	0.029	0.048	**0.127**	0.116	0.029	0.002	0.018	0.001	0.331**
Siliquae on main shoot	0.005	–0.042	0.061	0.058	0.043	**0.344**	–0.001	0.001	–0.006	0.002	0.465**
Siliqua length (cm)	–0.008	–0.009	0.016	0.014	0.026	–0.001	**0.147**	0.004	0.026	–0.001	0.215**
Seeds/siliqua	–0.003	–0.003	0.027	0.019	0.014	0.023	0.039	**0.014**	0.005	0.003	0.136*
1000-seed weight (g0	–0.005	0.003	–0.001	0.009	0.014	–0.013	0.024	0.001	**0.159**	0.002	0.191**
Oil content (%)	–0.005	–0.002	0.021	0.013	0.001	0.041	–0.002	0.002	0.056	**0.003**	0.124*

Residual effects = 0.5707; Figures in diagonals indicate direct effects; *Significant at 5 per cent level; **Significant at 1 per cent level

Table 4. Donors identified based on present studies for different characters in Indian mustard germplasm

Character		Donor
Days to maturity	< 132	NC-58365, RC 1069, CSR 465, RC51, RC 165
Plant height (cm)	< 125	RH-112, IB-1907, B-374, RW 338
Primary branches/plant	> 9	RH-112, RC-81, JMG-387, T 6342, JMG-429
Secondary branches/plant	> 20	CSR-724, PRG-907, RC-52, T 6342, CSR 717
Main shoot length (cm)	> 80	PRG 943, CSR-626, RC 426, CSR 420
Siliquae on main shoot	> 50	JMG-429, PR 8973, PRG-911, CSR- 873, RC-53
Siliqua length (cm)	> 4.5	JMG-429, PRG-911, CSR 873, RC-121
Seeds/siliqua	> 4.0	RC-150, PRG 922, RC-160, RC-84, JMG-423
1000-seed weight (g)	> 15	MDOC-43, PRG-901, RC-389, CSR 420, JMG 195
Oil content (%)	> 42	B-420, MHC-10, CSR-698, NC-59778

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EVALUATION OF INDIAN MUSTARD (*Brassica juncea* [L.] Czern & Coss.) GERMPLASM UNDER RAINFED CONDITION

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To identify suitable donors for different morpho-agronomic characters, 226 indigenous accessions of Indian mustard (*Brassica juncea* [L.] Czern & Coss.) were evaluated under rainfed agro-ecology. Appreciable range of variation was observed for all the characters except for days to maturity and oil content. Maximum variability was obtained for seed yield (CV 45.6 %) followed by secondary branches/plant (CV 28.8%) and harvest index (CV 26.9%). Seed yield was positively and significantly associated with all the characters studied except oil content, which was found to have positively significant correlation with days to maturity only. A number of useful accessions was identified for different agro-morphological characters and oil content. The accessions with high oil content and harvest index were also characterized.

Key words: Indian mustard, *Brassica juncea*, oilseeds, morpho-agronomic characters

Rapeseed-mustard group is the second important oilseed crop of India after groundnut. Indian mustard is the predominant crop occupying nearly 90 per cent of the total hectarage (7.0 m. ha). Seed and oil yields in Indian mustard is quite low as compared to other brassica species. It is therefore imperative to intensify efforts to improve seed and oil yield in this crop to fulfill ever-increasing demand of edible oil. Nearly 34 per cent of the hecterage of rapeseed mustard is still under rainfed agro-ecology and increase in productivity through breeding efforts in this crop has not been striking in rainfed areas. Consequently, characterization and evaluation of germplasm is necessary in order to search for potential donors (Yadav *et al.*, 1997). The envisaged investigation was therefore undertaken to characterize the genetic resources of Indian mustard maintained at this center to assess their potentiality as suitable donors for utilization in cultivar development programme for rainfed agro-ecology.

MATERIALS AND METHODS

Two hundred and twenty six germplasm lines of Indian mustard (*Brassica juncea* [L.] Czern & Coss.) were grown in augmented design during rabi 1997-98 under rainfed conditions at National Research Center on Rapeseed-Mustard, Bharatpur. Each line was grown in two-row plots of five meter length and plant and row distance were maintained at 10 x 30 cm., respectively. Standard agronomic and plant protection practices for rainfed agro-ecology were followed to raise a good and healthy crop. A basal dose of N : P @ 40 and 20 kg/ha was given just before seeding and the data were collected for days to maturity (row basis, plant height (cm), primary branches per plant, secondary branches per plant, main shoot length (cm), siliquae on main shoot, siliqua length (cm), seeds per siliqua, 1000-seed weight (g), harvest index (%), seed yield (g) and oil content (%) on individual plant basis on randomly selected five plants in each accession. The seed were counted by an electronic seed counter ("L" systems,

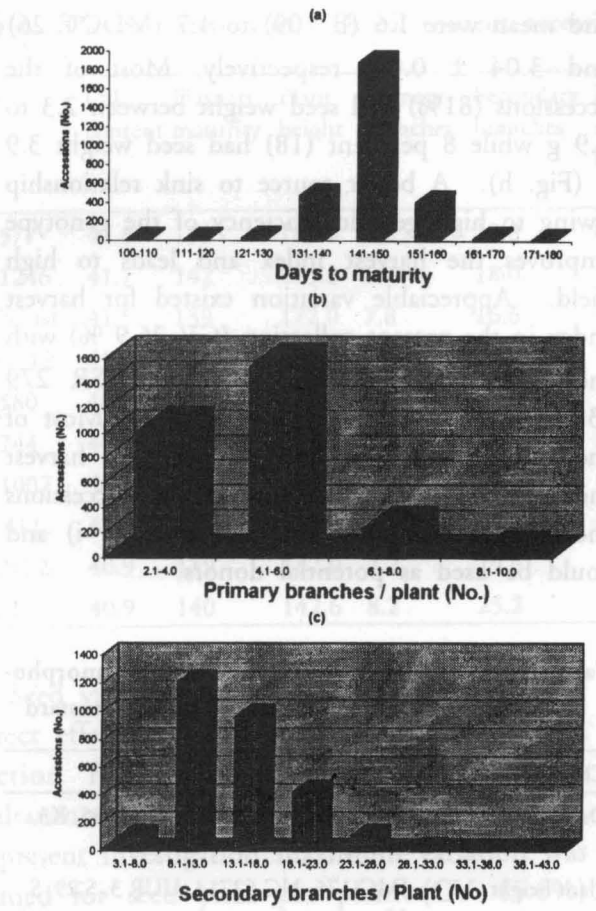
Old mill Co., USA) and the oil content was measured by Nuclear Magnetic Resonance (Oxford 5000). Range, mean, coefficient of variability and simple correlation coefficients were computed using standard statistical methods (Gomez & Gomez, 1984)

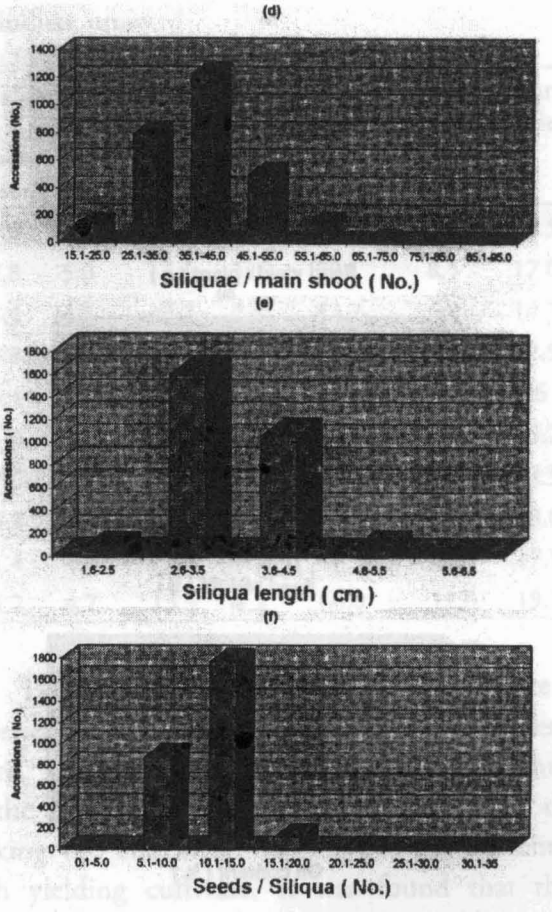
RESULTS AND DISCUSSIONS

The evaluated germplasm had considerable variability as indicated by coefficient of variability CV (Table 1) for all the characters studied except for days to maturity (CV 1.9%) followed by oil content (CV 3.7%) and plant height (CV 8.7%). Early maturity and dwarfness are desirable characters. Early maturity makes a variety suitable for multiple crop rotation. The range for days to maturity and plant height in the present collection was 131 (CSR 1054) to 142 days (JMG 423) and 141 (JMG 176) to 214.4 cm (CSR 1052) respectively. The earliest maturity group i.e. 130-135 days constituted 22.6 per cent of the accessions (Fig. a), whereas most of the accessions (69%) took 135 to 140 days to mature. The mean plant height for most of the accessions (81%) ranged between 160 to 200 cm, yet a few (28 accessions) had short height (160 cm). Only fifteen accessions were recorded to have a mean height of more than 2 m (Fig. b). The observations for mean number of primary branches ranged between 5 and 13 with CSR 741 having minimum and CSR 464 having maximum number of primary branches per plant. Similar results were reported earlier by Yadav *et al.*, 1997 in Indian mustard. The coefficient of variation being 19.2 per cent, the character showed moderate variation. Nineteen accessions had more than ten primary branches per plant (Fig. c). As evident from the CV number of secondary branches/plant showed high variability. The accessions, JMG 190 and JMG 200 flanked the range for this character with a mean value of 45.4 and 7.0 respectively. Approximately 89 per cent of accessions had number of secondary branches between 12-30 (Fig. d), whereas, 13 accessions had 30 secondary branches thus making a good bunch of potential donors for this trait. Correlation analysis also

Table 1: Performance of Indian mustard germplasm for various morpho-agronomic traits

Character	Range	Mean ± SEM	Coefficient of variation
Days to maturity	131.0. (RC 89) - 142.0 (CSR 1054)	137.6 ± 0.2	1.9
Plant height (cm)	141.0 (JMG 176) - 214.4 (CSR464)	178.3 ± 1.0	8.7
Primary branches/plant	5.0 (CSR 741) - 13.0 (CSR 464)	7.7 ± 0.1	19.2
Secondary branches/plant	7.0 (JMG 200) - 45.4 (JMG 190)	20.6 ± 0.4	28.8
Main shoot length (cm)	36.4 (CSR 435) - 81.6 (RH 7839)	58.0 ± 0.6	14.7
Siliquae/main shoot	18.0 (JMG 393) - 64.4 (NC 8258)	40.4 ± 0.5	19.4
Siliqua length (cm)	3.3 (RC 901) - 5.7 (CSR 920)	4.5 ± 0.04	12.3
Seeds/ siliqua	9.7 - (MDOC 30) - 18.4 (CSR 868)	12.8 ± 0.1	9.2
1000 - seed weight (g)	1.6 (B 1090) - 4.7 (MDOC 26)	3.0 ± 0.04	19.7
Harvest index	9.0 (JMG 190) - 38.6 (CSR 279)	16.1 ± 0.3	26.9
Seed yield/ plant (g)	2.5 (CSR 1070) - 32.1 (MDOC 21)	9.1 ± 0.3	45.6
Oil content (%)	34.8 (RW 873) - 41.8 (CSR 577)	38.7 ± 0.1	3.7

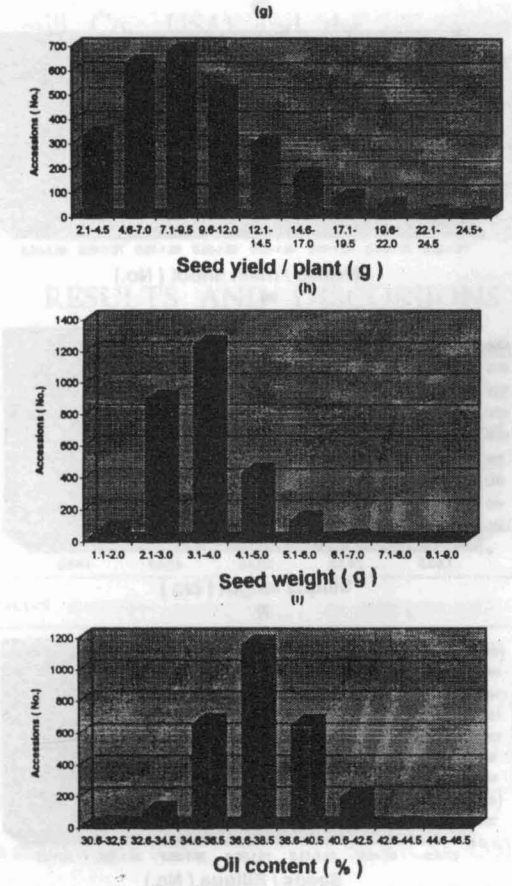




indicated a positive and significant association of primary and secondary branches per plant with seed yield (Table 2). Main shoot length exhibited moderate variation (CV 14.7%) and ranged between maximum and minimum value of 36.4 (CSR 435) to 81.6 cm (RH 7839). Out of the total, 173 (76.5 %) accessions had main shoot length between 50-70cm. Fifteen accessions registered main shoot length above 70 cm (Fig. e) and thus could be used in crossing programme to improve this character. As erdent by coefficient of variation, appreciable variability existed for number of siliquae on main shoot, the lowest and highest was recorded for JMG 393 (18) and NC 8258 (64.4), respectively. The frequency distribution (Fig. f) showed approximately 43 per cent of accessions deviated considerably from the mean. Siliqua length is an important character as longer siliqua accommodate higher number of seeds which in turn increase the yield as depicted by significant value of association between these characters (Table 2). Although the character exhibited moderate variation, yet 34 (14 %) accessions had more than 5 cm siliqua length (Fig. g).

Comparatively low variability existed for number of seeds per siliqua in the evaluated germplasm (CV 9.2%) and ranged from 9.7 (MDOC 30) to 18.4 (CSR 868) with a mean value of 12.8 + 0. 1. Ten accessions were found to have more than 15 seeds per siliqua and could be used in a hybridization to improve yield as this character had positive and significant association with seed yield (Table 2).

Increased seed weight augments the yield, furthermore, bold seeded varieties fetch higher price hence identification of suitable donors is



vital for cultivar development programme in Brassicas. Moderate variability was observed in the present collection (CV 19.7%). The range and mean were 1.6 (B 109) to 4.7 (MDOC 26) and 3.04 ± 0.04, respectively. Most of the accessions (81%) had seed weight between 2.3 to 3.9 g while 8 per cent (18) had seed weight 3.9 g (Fig. h). A better source to sink relationship owing to high genetic efficiency of the genotype improves the harvest index and leads to high yield. Appreciable variation existed for harvest index in the present collection (CV 26.9 %) with mean 16.1 ± 10.3. The accession, CSR 279 (38.6%) ahd the highest harvest index. Most of the accessions (95%) had 24 per cent harvest index under rainfed conditions, yet three accessions showed harvest index 32 per cent (Fig. i) and could be used as potential donors.

Table 2: Association of different characters with seed yield and oil content.

Characters	Seed yield	Oil content
Days to maturity	0.056	0.299**
Plant height	0.137	0.092
Primary branches/plant	0.207**	-0.015
Secondary branches/ plant	0.344**	-0.274**
Main shoot length	0.249**	-0. 159*
Siliquae on main shoot	0. 152*	-0.213**
Siliqua length	-0.009	0.117
Seeds/siliqua	0.193	-0.126
Seed weight	0.134	0.110
Harvest index	0.507**	-0.002
Seed yield	1.000	-0.184**

Table 3: Potential donors for various morpho-agronomic characters in Indian mustard

Characters	Accessions
Days to maturity	CSR 1054, NC 59787, JMG 385, K3, NC 6365
Plant height	JMG 176, NC 62713, UUR 3, S 29, S 35
Primary branches/plant	CSR 464, CSR 395, JMG 190, CSR 301, RC 80
Secondary branches/plant	JMG 190, B 145, MDOC 27, CSR 816, R-17-26
Main shoot length	RH 7839, IB 1705, JMG 400, UUR 3, CSR 498
Siliquae/main shoot	NC 8258, RC 290, CSR 743, STM 191, CSR 577
Siliqua length	CSR 920, JMG 193, CSR 377, CSR 607, CSR 313
Seeds/siliqua	CSR 868, PRG 942, RC 1023, CSR 313, PR 17
1000 - seed weight	MDOC 26, IB 1699, RC 413, RC 1124, CSR 691
Harvest index	CSR 279, RC-17-26, RC 817, CSR 154, MDOC 26
Seed yield	MDOC 21, MDOC3 ,CSR 305, CSR 1312, MDOC 13
Oil content	CSR 577, CSR 1246, MDOC 61, NC 58112, UUR 3

Table 4: Characterization of high oil content accessions of Indian mustard

Entry	Oil content	Days to maturity	Plant height	Primary branches	Secondary branches	Main shoot length	Siliquae on main shoot	Siliqua length	Seeds/ siliqua	1000-Seed weight	Biological yield/ plant	Seed yield/ plant	Harvest index
CSR 577	41.8	138	189.0	6.8	12.8	64.6	55.0	4.8	11.4	3.4	45.1	8.8	19.5
CSR 1246	41.7	142	175.0	7.4	18.0	55.0	27.8	5.0	14.1	3.0	50.1	8.5	17.0
MDOC 61	41.5	139	172.0	7.8	16.6	54.0	41.4	4.3	13.2	2.4	42.2	6.2	14.7
NC 58112	41.4	134	185.0	8.0	20.0	52.2	29.8	4.9	12.8	3.4	50.5	6.5	12.9
CSR 580	40.9	133	170.6	6.6	20.4	59.8	33.4	4.6	13.0	2.1	39.7	3.8	9.6
CSR 744	40.9	139	211.0	8.8	21.6	60.6	54.0	4.7	12.2	3.2	66.9	10.5	15.7
CSR 1007	40.9	136	205.4	7.4	21.0	61.8	37.6	5.2	13.2	2.4	29.6	3.7	12.5
JMG 411	40.9	137	171.2	7.2	14.8	55.0	44.8	4.2	12.6	2.8	38.6	5.0	13.0
MDOC 2	40.9	139	182.0	7.2	19.6	48.8	31.4	4.3	12.4	3.0	47.3	8.1	17.1
UUR 3	40.9	140	142.6	8.2	25.2	78.4	44.2	4.7	13.5	4.2	66.0	12.6	19.1

Seed yield is the end product of direct and indirect effects of yield associated attributes and selection for high yield accompanies with simultaneous improvement of related traits. In the present investigation maximum variation was obtained for seed yield per plant (CV 45.6%) with accessions ranging from 2.5 (CSR 1070) to 32.1 g yield (MDOC 21). Only two accessions yielded 24.9 per plant (Fig. 11). These results are in agreement with the results of Yadav *et al.*, (1997) in Indian mustard.

The oil content, has high significance as varieties with greater oil content are preferred more. This objective gains rather more weightage in the face of edible oil deficits being faced thus making the endeavour to improve oil content of high yielding cuftivars. It was found that there existed little variation for oil content in the germplasm (CV 3.7%) with overall mean 38.71 0.1%. Thirty-eight accessions had oil content 40%. Maximum oil content was observed in the line CSR 577 (41.8%). The association of oil

Table 5: Characteristics of promising Indian mustard strains having high harvest index

Strain	Plant height (Cm)	Primary branches /plant	Secondary branches/ plant	Main shoot length (cm)	Siliquae on main shoot	Siliqua length (cm)	Seeds/ siliqua	1000-Seed weight (g)	Oil content (%)	Seed yield/ plant(g)	Dry matter/ plant (g)	Harvest index (%)
CSR 279	193.2	7.6	23.4	60.8	43.4	4.2	12.9	2.5	38.7	8.8	22.8	38.7
R 17-26	174.6	10.8	34.6	54.2	50.8	4.6	12.4	2.3	38.6	10.6	28.8	36.7
CSR 817	204.2	10.8	32.2	56.4	34.6	4.5	14.0	3.0	40.5	17.3	48.3	35.9
CSR 154	177.6	9.0	23.2	58.0	42.0	3.4	12.3	2.7	39.5	16.4	53.4	30.6
MDOC 26	166.2	7.2	22.0	62.2	48.0	4.4	15.0	4.7	36.2	14.4	51.6	27.9
CSR 1227	177.0	10.4	30.6	42.0	30.0	5.1	15.0	2.3	38.8	12.8	47.3	27.2
MDOC 21	180.8	7.0	22.6	62.6	45.6	4.0	10.7	2.5	38.2	32.1	122.0	26.3
CSR 968	201.8	8.8	23.6	60.0	38.0	4.9	15.0	3.8	36.2	12.6	48.2	26.1
CSR 960	186.0	7.2	17.4	44.0	32.8	5.0	13.7	3.0	39.8	12.5	49.9	25.1

content was positive and significant, only with days to maturity but in fact further studies are advocated as there can be a shift in the direction of correlation due to impact of environment on the character. Ten high oil yielding accessions with their agro-morphological traits have been listed in the Table 3.

It can be concluded that the present collection proved to be a good source of genetic variability, which could be harnessed to develop improved high yielding genotypes for rainfed agro-ecology. Potential donors for different morpho-agronomic traits have been identified (Table 3). The accessions having more than 25 per cent harvest index were also characterized (Table 5).

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Short Communication

CHROMOSOME NUMBER IN *Piper* spp.*

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Cytological studies in nine *Piper* spp. were conducted to find out the chromosome number of these species. The procedure for mitotic studies in *Piper* spp. was standardized. Chromosome number of 36, 52, 32, 32, 24, 25, 32, 52, 52 and 32 was observed in *P. argyrophyllum, P. attennuatum, P. bababudani, P. betle, P. chaba, P. colubrinum, P. longum, P. nigrum* (Panniyur-1), *P. nigrum* (wild) and *P. pseudonigrum* respectively. Except for the South American species, *P. colubrinum*, all the species studied possessed chromosomes in multiples of four, suggesting a basic number of four for the Indian *Piper*.

Key words : *Piper* spp., cytology, chromosome number

The genus *Piper* is the largest in the family Piperaceae comprising over 3000 species. The species of the genus are distributed mainly in South America, Malaysia, Indonesia and India. In India, the genus has a disjunct distribution concentrated mainly in the Eastern Himalayas and in the Western Ghats. Many economically important species such as *P. nigrum* (black pepper), *P. betle* (betel vine), *P. longum* (thippali), *P. chaba* (chaba thippali) etc. are included in the genus. Of these species, *P. nigrum*, black pepper is the most important spice crop of Kerala and an important foreign exchange earner. Despite the great economic importance and the wide distribution of a large number of species and varieties in *Piper*, cytological studies in the genus *Piper* is still in its infancy and the available reports are highly controversial. This may be due to the large number of extremely small chromosomes in *Piper* species. Under these circumstances, cytological studies in nine *Piper* species were undertaken with the objective of finding out the chromosome number of these species.

Materials included nine species of *Piper* maintained in the germplasm collection of the Department of Plantation Crops and Spices, College of Horticulture, Vellanikkara. The list of species are given in Table 1.

Table 1. *Piper* spp. included in the study

Sl. No.	Name of spp.	Acc. No.
1.	*P. argyrophyllum* Miq.	P-48
2.	*P. attenuatum* Buch. Ham.	P-80
3.	*P. bababudani* Rahiman	P-89
4.	*P. betle* L (var. Kasoori)	P-87
5.	*P. chaba* Hunter	P-86
6.	*P. colubrinum* Lamk.	P-85
7.	*P. longum* L	P-92
8.	*P. nigrum* L (Panniyur-1)	P-33
9.	*P. nigrum* L (wild)	Pn-134
10.	*P. psuedonigrum* Velayudhan and Amalraj	P-45

To find out the somatic chromosome number of different *Piper* spp., mitotic studies were carried out using root tip squash method. The roots were

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collected between 11.15 a.m. and 12.15 pm. and pre-treated in 8-hydroxyquinoline for two to three hours at 4°C. The pre-treated roots were fixed in Carnoy's A/Carnoy's B for one or two days. The material was then hydrolysed in 1N hydrochloric acid in a water bath maintained at a temperature of 60°C for 15 minutes. After that the roots were stained in 0.5 per cent aceto orcein for 45 minutes. After staining, the root tips were taken from the stain, squashed and slides were prepared.

Somatic chromosome number of nine different *Piper* spp. studied are given in Table 2.

Table 2. Somatic chromosome number in *Piper* spp.

Sl. No.	Species	Chromosome number (2 n)
1.	*P. argyrophyllum*	36
2.	*P. attenuatum*	52
3.	*P. bababudani*	32
4.	*P. betle*	32
5.	*P. chaba*	24
6.	*P. colubrinum*	26
7.	*P. longum*	32
8.	*P. nigrum*	52
9.	*P. pseudonigrum*	32

Chromosome number of *P. argyrophyllum* was reported as 2n=36 and 39 (Samuel and Bavappa, 1981) and 2n=52 (Rahiman and Nair, 1986 and IISR, unpublished). The results of the present investigation agree with the result obtained by Samuel and Bavappa (1981) as 2n=36. Somatic chromosome number of *P. attenuatum* had been reported differently by different workers, 2n=26 and 39 (Samuel and Bavappa, 1981), 2n=36 (Bai and Subramanian, 1985), 2n=104 (IISR, unpublished). However, chromosome number of 2n=52 was also reported by various workers like Jose and Sharma (1983 and 1984), Rahiman and Nair (1986) and IISR (unpublished). The result of the present study is in agreement with their results. Chromosome number of *P. bababudani* was observed to be 2n=32. This was contradictory to the report of Rahiman (1981) as 2n=52. Somatic chromosome number of *P. betle* was also varyingly reported by different workers as 2n=78 (Mathew, 1958), 2n=64 (Sharma and Bhattacharya, 1959; Dasgupta and Datta, 1976) etc. The result of the present study is in agreement with the earlier findings of Johnson (1910) and Janakiammal (1945) who reported the 2n number as 32.

Chromosome number of *P. chaba* was reported as 2n=104 by Jose and Sharma (1984). Janakiammal (1945) observed the chromosome number as 2n=24 and the result of the present study is in confirmation with the latter findings. In *P. colubrunim*, there is no published report on chromosome number. However, there was one unpublished report from IISR where the 2n number was reported as 26 and the result of the present study do agree with their findings. In *P. longum*, chromosome number was reported varyingly by different workers as 2n=52 (Mathew, 1958; Jose and Sharma, 1983 and 1984; Rahiman and Nair, 1986), 2n=48 (Dasgupta and Dutta, 1976) etc. In the current study, chromosome number was observed as 2n=32 and this is a new count in *P. longum*, not reported by earlier workers.

Somatic chromosome number of *P. nigrum* has been reported differently by various workers in the past. 2n=128 (Janakiammal, 1945), 2n=48 (Sharma and Bhattacharya, 1959), 2n=36 and 60 (Dasgupta and Datta, 1976) and 2n=104 (Jose and Sharma, 1984) were the numbers thus reported. However, most of the workers agreed with the number 2n=52 (Mathew, 1958; Mathew, 1972; Samuel and Bavappa, 1981; Jose and Sharma, 1983 and 1984; Rahiman and Nair, 1986 and Nair *et al.*, 1993). The results of the present study is in agreement with the majority's view that in cultivated *P. nigrum*, 2n number is 52.

Two diploid chromosome numbers have been reported in wild accessions of *P. nigrum* by Mathew (1958 and 1972). They were 2n=52 and 104, suggesting a role of polyploidy in the evolution of *piper*. The accessions used in the current study showed 2n number as 52 which is a number earlier reported by Mathew in wild *P. nigrum*.

Lack of uniformity in the reports of chromosome number by different workers indicate the existence of many cytotypes in *P. nigrum* and other species of *Piper* as suggested by Ravindran and Babu (1994). Occurrence of different cytotypes in *P. nigrum* and other species of the genus suggested a probable role of polyploidy in the evolution of species of the genus. These cytotypes are being maintained in the population by predominant vegetative propagation. In the present study, chromosome numbers of 2n=24, 26, 32, 36 and 52 have been observed in different *Piper* spp. Apart from the South American species, all other species studied possessed chromosome numbers which were multiples of four suggesting a basic chromosome number of four for Indian *Piper*. However, more detailed and exhaustive studies are required before arriving at a definite conclusion.

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Short Communication

SORGHUM GERMPLASM FROM THAILAND SHOWING RESISTANCE TO SUGARCANE APHID, *Melanaphis sacchari* Zehntner

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Three accessions in Sorghum imported from Thailand have shown resistance to yellow sugarcane aphid (*Melanaphis sacchari*). Accessions EC-434431&434432 appeared to be immune whereas EC-434430 was highly resistant to aphid infestations and sooty mould formation.

Key words : Sorghum germplasm, resistance, sugarcane aphid, *Melanaphis sacchari*

Sorghum is one of the mandate crops of the International Crops Research Institute for the Semi Arid Tropics (ICRISAT), Patancheru, AP, India. Sorghum germplasm is regularly exchanged between ICRISAT and several sorghum growing countries in Africa, America, Asia, and Europe. The ICRISAT gene bank through National Bureau of Plant Genetic Resources (NBPGR) imports the sorghum germplasm after necessary quarantine processing. The germplasm, after processing in the laboratory, is transferred to the post- entry quarantine isolation area (PEQIA) to ensure that only insect and disease free germplasm enters into India and the ICRISAT gene bank.

Recently, nine accessions of sorghum germplasm imported from Indonesia, Thailand and China were sown in the PEQIA. At maturity, three entries from Thailand viz., EC-434430, EC-434431 and EC-434432 sown in the middle three blocks between the entries from Indonesia and China were found to be totally free from infestation by the yellow sugarcane aphid, *Melanaphis sacchari* Zehntner and the sooty mould (*Capnodium* sp.) The honeydew secreted by aphids favours the development of sooty mould, which hinders the photosynthesis by enveloping the green leaves leading to reduction in fodder quality and grain yield. The thick black sooty mould had completely covered the leaves of the other six entries from china (EC-434433, EC-434434, and EC- 434435) and Indonesia (EC-434436, EC-434437 and EC-434438). The affected plants appeared to be burnt up in contrast to the unaffected plants of three entries from Thailand.

Aphid populations on the susceptible entries covered the panicles and the tender shoots. Observations wre recorded on Number of plants affected by sooty mould and the aphids (Table 1). Of the three entries from Thailand showing resistance to the yellow sugarcane aphid EC-434431 and EC-434432 appeared to be immune as the plants remained completely free from aphid infestation and sooty mould formation. The third entry from Thailand EC-434430 was found to be highly resistant, in which only 4% plants were infested by the aphid. The rest six

Table 1. Reaction of the sorghum germplasm accessions to the yellow sugarcane aphid, *Melanaphis scchari* (post-Entry Quarantine Isolation Area, ICRISAT center, 1998 rainy season)

Germplasm accession (Local name)	Origin	Infestation (%)	Remarks
EC-434430 (U-Thank 1)	Thailand	3.95	Highly resistant
EC-434431 (Suphan Buri #1)	Thailand	Nil	Immune
EC-434432 (Suphan Buri 60)	Thailand	Nil	Immune
EC-434433 (LS-1)	China	100	Highly susceptible
EC-434434 (LS-2)	China	100	Highly susceptible
EC-434435 (LS-3)	China	100	Highly susceptible
EC-434436 (Mandau)	Indonesia	91.86	Susceptible
EC-434437 (UPCS-S1)	Indonesia	97.06	Highly susceptible
EC-434438 (Keris)	Indonesia	100	Highly susceptible

entries from China and Indonesia were susceptible to highly susceptible with aphid infestation ranging from 91.9 to 100 per cent.

Literature search indicated that except for a few reports, there is not much of screening of the germplasm to identify the sources of resistance and their utilization in resistance breeding programmes. Scientists in Japan at the National Agricultural Experiment Station, Fukuyama, Hiroshima and Research Institute for Bioresources. Okayama University, Kurashiki, have carried out considerable work on aphid resistance. Tsumuki *et al.*, (1995) reported that although leaf surface wax was similar among all varieties, the total sugar content and the free amino acid concentrations were slightly more in the aphid-resistant varieties than in the susceptible ones. Hagio (1992) classified six varieties as highly resistant, and he reported that the resistance in two varieties (PE 954 177, and Senkinshiro) may be conditioned by a dominant gene. Mote and Shahane (1994) reported that the varieties with greater height, greater distance between 2 leaves, smaller leaf angle and presence of waxy lamina were less susceptible to the aphid. Development of aphid was more pronounced on varieties with high nitrogen, sugar and total chlorophyll contents (IS 105, IS2217, IS1063, and IS553). They reported that varieties ICSCTV9, BTP28, IS1640, ICSV148, and SPV504, with higher contents of phosphorus, potassium and polyphenols were less preferred by the aphids.

The three sorghum accessions from Thailand showed a nearly immune reaction to the aphid *Melanphis sacchari.* These lines can be used in sorghum improvement to increase the production and productivity of this crop in the semi-arid tropics. The immune reactions to aphid infestation need to be studied further to understand the contributing factors to resistance to this insect.

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Short Communication

MULTIPLE DISEASE RESISTANCE IN INDIAN MAIZE HYBRIDS AND COMPOSITS

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Two hundred fifty hybrids and composites in maize were tested for resistance to bacterial stalk rot, brown stripe downy mildew maydis leaf blight. It was observed that hybrids KH 150, X-1174 MV, PRO 312, PRO 316, JH 3189, MMH 69, EH 230792, X-1123G and composite Navjot, Prabhat, L118 and Deccan 107 were identified as multiple resistant lines which may be directly used for cultivation in disease prone areas.

Key words : Maize, *Zea mays*, resistance, bacterial stalk rot, Maydis leafblight, brown stripe downy mildew

Maize is third important cereal crop in India after rice and wheat. During 1997-98, maize was grown in an area of 6.3 million hectares with production of 10.8 m. tonnes and productivity of 1,722 kg/ha. Predominantly maize crop in India is grown during *kharif* season. Diseases cause a significant reduction in grain yield (Sharma *et al.*, 1993). Though the diseases can be managed with chemicals and fungicides, but cultivation of resistant varieties is an eco-friendly, cost effective and practically feasible method. The present paper embodies information on identification of some Indian hybrids and composites resistant to bacterial stalk rot (*Erwinia chrysanthemum* pv. *zea*), *Maydis* leaf blight (*Dreschslera cochlicobolus*) and brown stripe downy mildew (*Scleropathora rayssiae* pv. *zeae*), the widely prevalent diseases in northern parts of the country.

The material comprised 250 hybrid and composite stocks of Advanced Evaluation Trials(1^{st} and 2^{nd} year) received from Directorate of Maize Research, New Delhi. The stocks were planted during *kharif* 1995 at experimental farm of RRS Dhaulakuan, following recommended agronomic practices. Artificial epiphytotic conditions for bacterial stalk rot were created by inoculating about 75-100 plants per entry with 48h old cell suspension of *E. chrysanthemi* pv. *zeae* at pretasseling stage using hypodermic syringe method (Anonymous, 1983). The field was sufficiently sick with inoculum of brown stripe downy mildew (*Scleropthora rayssiae* pv. *zeae*). Additionally, in an effort to avoid disease escape, 30 days old plants were whorl inoculated in the evening hours. The Maydis leaf blight observations were based on natural infection. The data for *Erwinia* stalk rot were recorded on percent wilted plants, 20 days after inoculation, whereas the data for brown stripe downy mildew and Maydis leaf blight were recorded on 1-5 and 0-5 scale, respectively (Annonymous. 1983). A part of seed of each entry was retained and was evaluated during the subsequent *kharif* season (1996) to confirm their reaction to the diseases.

The hybrid and composite stocks showing resistance against *Erwinia* stalk rot brown stripe

Table 1. Maize (*Zea mays* L.) stocks resistant to *Erwinia* stalk rot, brown stripe downy mildew and *Maydis* leaf blight

Erwinia stalk rot (*E. chrysanthemi* pv. *zeae*)	
Free resistant (0- > 10%)	Modertately resistant (10-..20%)
JH1345, JH1354, JH1558, JH1386, JH1413, JH3125, JH3181, JH3189	AH54, JH1385, JH1387, JH3180, JH3221, JH3222, JH3482, KH5052, Deccan 107, NAVJOT, SC92026
Brown stripe downy mildew (*Scelerophthora rayssiae* var. *zeae*)	
Free/resistant (1->2)	Moderately resistant (2-> 2.5)
AH34, AH739, AH742, BH 1041, BH3034, BH3037, L 110, L122, A15, D 742, EV.92, EH3022, EH 50836, EH203792, F733, FH 3040, FH 3046, FH 3047, FH 3050, HKH 943, JH 1345, JH1353, JH 1354, JH 1385, JH 1386, JH 1387, JH 3188, JH3188, JH 3125, JH3193, JH 3221, JH 3226, JH 3459, JH 3469, JH3495, KH510, KH3151, KH 93451, MMH69, MMH81, MMH 82, MMH579, MMH830, MMH82, Navjot, PMZ 115, PRO310, PRO314, PRO317, SURYA X-1123, X-1123G, X-1174WV, 3054W, AH 742, AH 60, BIO 9684(Y), BH 3034, EM 3027, EH 22, JC 3224, JH 1368, JH 1458, JH 1345, JH 1353, JH 1368, JH 1385, JH 1386, JH 1387, JH 3037, JH 3047 JH 3181, JH 3221, JH 3222, JH 3224, JH 3226, JH 3461, JH 3482, JH 3500, JK 1493, JK 3193, KH 5002, H510, KH 93451, MMH 308, MMH 830, PRO 317, PRO 310, Parbhat, SC 92026, SSF 53042, X-1123G	AH776, AH60, L-118, L-113903, Exp. Comp. 9102, Exp. comp. 85134, Exp. Comp. 8551, EH 50824, EH 50534, EHF 1151, E H 22, FH 3036, HKH 950, HKH 947, HKH 941, JH 1368, JH 458, JH 1413, JH 3136, JH 3180, JH 3181, JH 3189, JC3218, JH 3222, JH 3425, JH 3500, JC 3224, JH 3037, JK 194, JH 3047, KH 5009, KH 5052, KH 5005, IMH 333, MMH 501, MMH 4324, PRO 316, PMZ 202, PRO 312 R 21, R 44, SSF 92387, SSF 93448, AH 54, AH 714, AH 739, AH 776, BIO 9561 (Y) BIO 9626(Y), BIO 9718, BH 3037, L 110, L113, Comp. A-15, D-742, D 903, De, Exp. Comp. 9120, EH 2037, EH 50836, EV 92, F-733, FH 3028, FH 3036, FH 3040, FH 3046, HKH 943, HKH 950, JH 1354, JH 1413, JH 3125, JH 3136, JH 3180, JH 3188, JH 3189, JH 3425, JH 3459, JH3469, JH 3495, JH 4593, KH5009, KH 5052, KH 93151, MMH 4324, MDR Synthetic, MMH 69, MMH 81, MMH 82, Navjot PMZ 115, PRO 312, R, 21, R 44, SSF 93448, Y 1124 WW, SSF 92387 (w).

downy mildew and Maydis leaf blight during the year 1995 and 1996 are given in table 1. Two hybrid JH 1386 and JH 3226 were free from brown stripe downy mildew and none of the stocks was free from *Erwinia* stalk rot and *Maydis* leaf blight. Cultivars JH 1345, JH 1354, JH 1386, JH 1413, JH 1558, JH 3125, JH 3181, JH 3184 and JH 3189 with less than 10% stalk rot incidence were resistant, and 9 hybrid with 10-20% disease incidence were moderately resistant to *Erwinia* stalk rot. Fifty one entries were resistant (disease reaction < 2) and 38 entries were moderately resistant (disease reaction 2-3) to brown stripe downy mildew. Thirty five stock with 1-2 disease reaction, were resistant and 59 stocks, with diseases reaction 2.1 < 3, were moderately resistant to *maydis* leaf blight. It has been observed that frequency of entries resistant to *Erwinia* stalk rot was more in stocks of full season maturity. In case of *maydis* leaf blight and brown stripe downy mildew resistance was more frequent in early maturing entries. Sources of resistance among inbreds, hybrids and composites have been identified against *Erwinia* stalk rot (Anonymous, 1983, Ebron *et al.*, 1987), *maydis* leaf blight (Anonymous, 1983); Khan *et al.*, 1992; Liu *et al.*, 1990; Sharma and Payak, 1990) and brown stripe downy mildew (Anonymous, 1983; Bains *et al.*, 1989).

It has been observed that hybrids JH 1345, JH 1354, JH 1387, JH 3125, JH 3180, JH 3181, JH 3221, JH 3222, KH 5052 and SC 92026 showed multiple resistance against all the three diseases. Hybrid JH 3482 and JH 1386 showed combined resistance against *Erwinia* stalk rot and *maydis* leaf blight, and *Erwinia* stalk rot

and brown stripe downy mildew, respectively. Stocks AH 742, AH 60, MMH 830, KH 5009, SSF 92387, AH 776, BIO 9718 (W), PRO 312, MMH 4324, HKH 950, JH 3459, JH 3469, JH 3495 Parbhat, MMH 69, D 903, HKH 943, PRo 310, FH 3046, FH 3050, FH3036, L122, BH 3034, KH 93151, EH 203792 X 1123a, A 15, KH 93451, JK 3193, MMH 81, MMH 82, AH 732, SSF 93448, L 113, EH 50534, R 21 and R 44 were resistant to *Maydis* leaf blight and brown stripe downy mildew. Sources with multiple resistance have been reported against Maydis leaf blight and brown stripe downy mildew (Day *et al.*, 1993) *Turcicum* leaf blight, Maydis leaf blight and brown spot (Kaiser and Pardhan, 1990). Probably it is the first report on identification of hybrids or composites with combined resistance against *Erwinia* stalk rot, Maydis leaf blight and brown stripe downy mildew.

Interestingly, hybrids KH 510, X-1174 WV, PRO 312, PRO 316, JH 3189, MMH 69, EH 230792, X-1123G and composites, Navjot, Parbhat, L-118 and Deccan 107 are identified varieties, which may be directly recommended for cultivation in diseases prone areas.

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Short Communication

COLLECTING RICE GERMPLASM FROM PARTS OF TELANGANA REGION OF ANDHRA PRADESH, INDIA

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This paper communicates collection of 109 landraces of rice from Telangana region of Andhra Pradesh. The germplasm varied in grain type, husk colour, grain colour and in maturity period. Considerable variation was also observed in panicle structure, glume and awn colour, kernel colour, 1000 seed weight, lengthm width and thickness of grain.

Key words: Rice, collection, germplasm, Telangana region

Rice is the principal crop of Andhra Pradesh cultivated in all the seven agro-climatic regions, in more than 75 farming situations, under varied physiographic, climatic and soil conditions. Rice is being grown in three distinct seasons viz., *Kharif* (May/June to November/December), *Rabi* (December to March/April) and Summer (April/May to July/August) and is rotated with pulses, oilseeds, millets and vegetables. Majority of the areas surveyed in the northern Telangana zone, the rice based cropping system followed was single crop rice, rice-rice, dry paddy, rice-groundnut etc.

Rice is being cultivated since time immemorial in this region of the state. Several local cultivars are still available in this region inspite of the introduction of improved cultivars. Based on our observations in several explorations undertaken, it has been found that the local cultivars/landraces of rice are confined to tribal pockets/villages in the interior places which are well adapted to the local conditions and stresses. In order to collect and conserve the available endemic genetic diversity in rice, an exploration was undertaken during November-December, 1997 in the districts of Nizamabad, Karimnagar, Warangal and Khammam of Telangana region. In this region an exploration was undertaken in 1994 in the Adilabad district for sampling of rice germplasm which resulted in the collection of over 109 accessions (Pandravada *et al.*, 1996) and the variability in grain morphological characters described (Sivaraj and Pandravada, 1996).

Farmer's field was taken as an unit area and random samples of the population and biased sample of elite material were collected. Germplasm samples were also collected from threshing yards and farm stores. The IRRI descriptors for rice, *Oryza sativa* L. (IRRI, 1980) was used as a guideline for studying the variability in the collected germplasm. The survey resulted in the collection of 100 germplasm accessions of rice (*Oryza sativa*) including one accession of *oryza nivara*. Some of the characteristics of important germplasm accessions collected are given in Table 1.

Table 1. Characteristics of some of the collected rice germplasm

Name of the local cultivar/landrace	IC. No.	Days to Maturity	Grain type	Husk colour	Grain colour	Others
Bobbiligantlu	211222	140	Medium slender	Brown	Red	
Bundamavadlu	211231	90-100	Medium bold	Brown	White	Rainfed
Chalkabuchchivadlu	211237	130	Long slender	Straw	White	Rainfed
Chalkavadlu	211250	90-100	Medium bold	Straw	Red	Rainfed
Cherukulutchchalu	211211 211215	70-125	Medium slender	Yellow	White	Rainfed crop
Chinnasindhubayalu	211210	175	Medium slender	Yellow	White	Rainfed crop
Chittimuchchalu	211248 211249	90-100	Medium slender	Brownish yellow	White	Rainfed
Chittimutyalu	211206	130	Fine	Straw	White	Scented
Dubbabairagi	211172	105	Long slender	Yellow	Red	
Duppitokalu	211212 211209	95	Medium bold	Yellow	White/ green	Rainfed
Dusavadlu	211207	180	Medium bold	Black	Red	Wild type
Erramallelu	211193	136	Long slender	Straw	White	
Erramasoori	211170	125	Medium slender	Straw	White	
Erravadlu	211158 211141	120	Medium slender	Brown Red	Rainfed	
Gandharivadlu	211173	120	Medium slender	Yellow	Red	
Godavari Iskalu	211176 211203	150	Medium slender	Yellow	White	
Gorankamukkulu	211225 211223	120-130	Medium slender	Black	White	Rainfed drought resistant
Karrebudamalu	211224	90	Medium bold	Black	Red	Rainfed
Karevadlu	211229	90	Medium slender	Black	White	Rainfed
Kattakichchidi	211238	150	Fine	Yellow	White	Rainfed
Kunkumbanthulu	211205	120	Medium slender	Brown	Red	Rainfed
Mettasannalu	211253	90	Long slender	Yellow	White	Rainfed
Motikka	211244	120	Short bold	Yellow	White	Rainfed
Nallavodlu	211169	90-100	Medium bold	Black	Red	Rainfed
Orugallu	211186	150	Lond bold	Straw	White	Rainfed
Peddamasuri	211179	150	Medium bold	Straw	Green	Susceptible to blast
Peddavadlu	211246	180	Bold	Yellow	Red	Rainfed
Ramabanalu	211252	180	Bold	Yellow	Red	Rainfed
Richchalu	211235	180	Bold	Yellow	White	Rainfed
Rottisingaralu	211296	140	Long bold	Straw	White	Rainfed
Sindhubayalu	211240	150	Medium slender	Yellow	White	Rainfed
Sudivanja	211242	90	Medium bold	Yellow	White	Rainfed
Surilu	211251	150	Long slender	Yellow	White	Rainfed
Tharkavadlu	211157	105	Long slender	Yellow	White	Rainfed
Vulliguththulu	211236	130	Medium bold	Yellow	White	Rainfed

The duration of the collected rice germplasm falls under early, medium and late groups varying from 90 to 180 days of maturity. Majority of them are grown as a rainfed and a few under semi- irrigated/irrigated conditions also. Germplasm of collected rice germplasm can be classified into medium tall and tall groups up to 175 cm in plant height. Considerable variation was also observed in panicle structure, grain morphological characters viz., glume and awn colour (black/brown/gold/straw), shape of grain (slender/medium/bold), kernel colour (red/white/green), 1000-seed weight, length, width and thickness of grain (Table 2). Such type of variability in landraces of rice during genepool sampling were encountered earlier by many rice workers from various parts of India (Chandel *et al.*, 1989; Richharia, 1979; Ray *et al.*, 1985).

Table 2. Diversity in grain morphology and weight

Character	Range	Mean	C.V.%
Grain length (mm)	5.6-11.5	8.2. 11.7	
Grain width (mm)	2.2-3.3	3.0	73.3
Grain thickness (mm)	1.5-2.3	2.0	80.0
1000-seed weight (g)	9.0-30.0	20.7	25.0

The germplasm of rice collected from this region is being conserved in the National Gene Bank at National Bureau of Plant Genetic Resources, New Delhi, India

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Short Communication

EVALUATION OF OKRA GENOTYPES FOR YELLOW VEIN MOSAIC RESISTANCE

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One hundred fifty seven germplasm lines of okra including some wild related species were evaluated for resistance against yellow vein mosaic disease under natural epiphytotic conditions. Three accessions of *A. tetraphyllus*, three accessions of *A. ficulneus* and one accession each of *A. manihot* ssp *manihot*, *Hibiscus panduraeformis* and *H. vitifolius* were observed to be completely free from the disease. Most of the accessions of *A. esculentus* and all the five accessions of *A. tuberculatus* were highly susceptible to the yellow vein mosaic disease

Key words : *Abelmoschus* sp., *Hibiscus* sp., yellow vein mosaic

Okra (*Abelmoschus esculentus*) is an important vegetable crop of India. Amongst various diseases affecting the crop, yellow vein mosaic (YVM) is the most serious one. YVM is caused by virus (YVMV) and transmitted by insect vector white fly (*Bemisia tabaci* Gen.). The control of disease is very difficult and only viable alternative is to develop resistant cultivars. In this study, we have evaluated 157 germplasm accessions of okra, including some of wild relatives, against YVM disease under natural epiphytotic conditions in field to identify the resistant genotypes.

In all 131 accessions of *A. esculentus*, 11 accessions of *A. tetraphyllus*, 4 accessions of *A. moschatus*, 5 accessions of *A. tuberculatus*, 4 accessions of *A. ficulneus* and 1 accession each of *A. manihot*, *H. panduraeformis* and *H. vitifolius* were evaluated for YVM infection under field conditions in the *Kharif* season of 1998. Seeds of cultivated as well as wild types were sown at a spacing of 60 × 45 cm. Observations on the disease incidence were recorded at regular interval after one month of sowing. The accessions were classified in different categories viz., immune, resistant, moderately resistant, susceptible and highly susceptible, on the basis of disease incidence after Memane *et al.* (1986), as shown in Table 1.

The disease incidence in different accessions is presented in Table 2. Most of the accessions of *A. esculentus* were highly susceptible to YVM disease. Only two accessions showed disease incidence of less than ten per cent whereas 113 accessions were highly susceptible with disease incidence of more than 50 per cent. Among the wild species *H. panduraeformis*, *H. vitifolius* and *A. manihot* ssp *manihot* were observed to be completely free from the disease whereas *A. tuberculatus* was found to be highly susceptible. Three accessions of *A. tetraphyllus* were completely free from the disease and only one accession was highly susceptible. Three accessions of *A. ficulneus*

Table 1. Classification of okra genotypes on the basis of disease incidence

Incidence (%)	Reaction category	No. of accessions							
		A. esculentus	*A. tetraphyllus*	*A. moschatus*	*A. tuberculatus*	*A. ficulneus*	*A. manihot* ssp *manihot*	*H. panduraef ormis*	*H. vitifolius*
0.00	Immune/free (I)	-	3	-	-	3	1	1	1
0.1-10.0	Resistant (R)	2	5	-	-	1	-	-	-
10.1-25.0	Moderately resistant (MR)	6	2	2	-	-	-	-	-
25.1-50.0	Susceptible (S)	9	-	-	-	-	-	-	-
50.1 & above	Highly susceptible (HS)	113	1	2	5	-	-	-	-
Total		130	11	4	5	5	1	1	1

Table 2. Reaction of okra genotypes to yellow vein mosaic virus

Name of species	Accession number	Average disease incidence	Reaction
Abelmoschus tetraphyllus	IC-90530	0.0	I
	IC-140977	10.0	R
	IC-140997	0.0	I
	IC-141003	20.0	MR
	IC-141015	10.0	R
	IC-141037	2.0	R
	IC-141038	95.0	HS
	IC-141041	2.0	R
	IC-141046	20.0	MR
	Ac-552	2.0	R
	NIC-53	0.0	O
Abelmoschus moschatus	EC-316073	100.0	HS
	EC-316077	90.0	HS
	IC-141058	20.0	MR
	IC-141055	20.0	MR
Abelmoschus tuberculatus	IC-90328	100.0	HS
	IC-90340	100.0	HS
	IC-90379	100.0	HS
	IC-90398	100.0	HS
	IC-90378	100.0	HS
Abelmoschus ficulneus	IC-90420	0.0	I
	IC-90464	0.0	I
	IC-90491	0.0	I
	IC-90986	5.0	R
Abelmoschus manihot ssp *manihot*	Ac-218	0.0	I
Abelmoschus panduraeformis	214	0.0	I
Abelmoschus vitifolius	217	0.0	I
Abelmoschus esculentus	IC 45831	88.9	HS
	IC 90169	100	HS
	IC 90150	100	HS
	IC 90176	100	HS
	IC 90212	100	HS
	IC 90263	33.3	S
	IC 90298	100	HS
	IC 117005	55.6	HS
	IC 117011	100	HS
	IC 117012	100	HS
	IC 117018	83.3	HS
	IC 117020	100	HS
	IC 117034	100	HS
	IC 117078	100	HS
	IC 117095	50.0	S
	IC 117212	8.3	R
	IC 117216	6.7	HS
	IC 117218	85.0	HS
	IC 117238	100	HS
	IC 117323	100	HS
	IC 117329	50.0	S
	IC 128036	9.1	R

IC 128064	100	HS
IC 329353	100	HS
IC 329355	100	HS
IC 329369	94.1	HS
IC 329370	50.0	S
IC 329375	28.6	S
IC 329411	100	HS
IC 305616	16.7	MR
IC 305617	100	HS
IC 305618	66.7	HS
IC 305620	100	HS
IC 305623	100	HS
IC 305626	100	HS
IC 305628	16.7	MR
IC 305651	100	HS
EC 329369	100	HS
EC 329370	66.7	HS
EC 329375	25.0	MR
EC 329384	100	HS
EC 329411	100	HS
EC 329415	100	HS
IC 90177	16.7	MR
IC 90184	100	HS
IC 90185	25.0	MR
IC 90198	100	HS
IC 90201	100	HS
IC 90227	100	HS
IC 90230	100	HS
IC 90262	100	HS
IC 90263	100	HS
IC 90264	100	HS
IC 90265	100	HS
IC 90266	100	HS
IC 99734	88.9	HS
IC 99741	100	HS
IC 111350	100	HS
IC 111424	100	HS
IC 111438	100	HS
IC 111459	100	HS
IC 111472	100	HS
IC 111490	100	HS
IC 111497	28.6	S
IC 111503	37.5	S
IC 111508	100	HS
IC 111509	100	HS
IC 111533	66.7	HS
IC 111545	50.0	S
IC 112485	100	HS
IC 128071	100	HS
IC 128145	25.0	MR
IC 128147	50.0	S
IC 43279	100	HS
IC 50755	100	HS
IC 69113	100	HS
IC 69248	100	HS
IC 69257	100	HS
IC 69263	100	HS
IC 69272	100	HS
IC 69286	100	HS
IC 69303	100	HS
IC 85583	100	HS
IC 85584	100	HS
IC 72081	100	HS
IC 72082	100	HS
IC 85588	100	HS
Col. V4307	100	HS
IC 113904	100	HS
Col. V4380	100	HS
Col. V4395	100	HS
Col. V4447	100	HS
IC 14093	100	HS
IC 128035	100	HS
IC 128076	100	HS
IC 128093	100	HS
IC 128900	100	HS
IC 128122	100	HS
EC 329402	75.0	HS
EC 329411	100	HS
EC 305619	100	HS
EC 305698	100	HS
EC 305716	100	HS
EC 306742	100	HS
Col. VB9101	100	HS
Col. VB9104	100	HS
Col. VB9105	100	HS
EC 169367	100	HS
IC 85536	100	HS
Col. V 4549	100	HS

	Col. V 4968	100	HS
	Col. A 646	100	HS
	Col. V/89/0-125	100	HS
	Col. V/90/0-8	100	HS
	IC 111324	100	HS
	Col. V/90/0-81	100	HS
	Col. V/90/0-170	100	HS
	IC 111466	100	HS
	NIC 3226-A	100	HS
	NIC 3227	100	HS
	NIC 3257	100	HS
	NIC 3311	100	HS
	NIC 3331	100	HS
	NIC 3345	100	HS
	EC 305746	100	HS
	EC 140902	100	HS
	EC 140907	100	HS
	NIC 13948	100	HS
	IC 140929	100	HS
	IC 140931	100	HS

were found to be completely free from the disease whereas *A. moschatus* showed moderate resistance to high susceptibility in different accessions.

The present study shows that there is hardly any resistance in *A. esculentus* against YVMV. However, some accessions of wild species showed resistance against the disease. Earlier studies also indicated that there is no source of resistance to YVMV in cultivated okra through some related wild species are resistant to the disease (Arumugam *et al.*, 1975; Thakur, 1976; Arumugam and Muthukrishnan, 1978, Memane *et al.*, 1986). The resistant genotypes identified in the present study can be utilised for breeding resistant varieties.

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Short Communication

ESTIMATION OF LEAF AREA IN CERTAIN GRAPE CULTIVARS

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The present communication aimed at calculation of leaf area constant of six cultivars and correlation between leaf area, leaf length and width. Leaf constant value of these cultivars will be helpful to determine the actual leaf area for biometric studies.

Key words : Grape, leaf area, leaf length, leaf width, leaf area constant

The importance of leaf area in plant vigour, productivity in quantity and quality is immense as the leaves are prime organs for synthesis of carbohydrates and other organic substances. Manivel and Weaver (1974) have suggested biometric correlation between leaf area and length, width of leaf and petiole length in 'Grenache' cv. of grape and Arora and Chanana (1975) has studied 10 other cultivars i.e., Anab-e-Shahi, Banquabad, Beauty Seedless, Cardinal, Fosters seedling, Gold, Himrod, Kishmish Charni, Perlette and Thompson Seedless to test feasibility of biometric correlation between leaf area and length, width of leaf and petiole length and Gill and Brar (1984) has calculated leaf area constant as 0.8 in Perlette and 0.87 in Delight cultivars of grape. The present study is aimed at calculation of leaf area constant of six other cultivars and correlation between leaf area, leaf length and width.

Twenty five leaves with their petioles were plucked at random and actual leaf area was determined by leaf area meter (LICOR 3600). Leaf length and leaf width of respective leaves were also recorded. Correlation between leaf length, leaf width and leaf area were calculated. Leaf length and width (at the widest point) were measured with the help of a Digital caliper (CD-6^{11} Mitutayo). The estimated leaf area was obtained by multiplying length and width of the leaves. Values of the leaf constant was obtained as the ratio of actual area to estimated leaf area.

Relationship between leaf length and leaf area

The correlation existed between leaf area and leaf length indicated that leaf area is a function of leaf length in all the cultivars under study (Table 1). Significant correlation between leaf length and leaf area was also observed by Manivel and weaver (1974) and Arora and Chanana (1975).

Relationship between leaf width and leaf area

Similar to leaf length, leaf width also showed significant correlation with leaf area in all the cultivars under study, which shows that leaf area is also a function of leaf width (Table 2). Therefore, leaf width may also be used as one of the criterion for determining the leaf area. Present findings are also in a close conformity of the observations of Manivel and Weaver (1974) and Arora and Chanana (1975).

The leaf area constant values obtained for different cultivars were given in Table 1. The actual leaf area can be calculated by multiplying the length and width (at the widest point) with

Table 1. Leaf area constant values of six grape cultivars

Cultivar	Leaf length cm	r	Leaf width cm	r	Estimated leaf area sq. cm	Actual leaf area sq. cm	Leaf constant
Arka Soma	9.796	0.5660	12.988	0.6262	127.23	101.275	0.796
Arka Majestic	9.544	0.9020	12.116	0.9378	115.64	93.55	0.809
Tas-e-ganesh	9.176	0.7367	10.608	0.8778	97.34	66.09	0.679
Angur Kalan	7.020	0.6000	8.905	0.4600	62.52	52.45	0.839
Convent Large Black	6.936	0.8079	9.000	0.7860	62.429	58.56	0.938
Azabella	8.079	0.079	9.380	0.7728	75.79	62.22	0.821

*r correlation coefficient

the constant of respective cultivars as it is useful for estimating the leaf area without removing them from the plant and the constant can be used at any stage of crop (Gill and Brar, 1984). Direct measurement require detachment of the leaves and are therefore unsuitable for biometric studies requiring continuous observation of the same leaf till its maturity and full growth or when the number of leaves is too small to permit detachment. (Mohan Kumaran *et al*, 1964).

Correlations obtained between leaf length, leaf width and leaf area of Arka Soma, Arka Majestic, Tas-e-Ganesh, Angur Kalan, Convent Large Black, Azabella, indicated that leaf area was a function of leaf length and leaf width in dependently in all cultivars. Hence, for the determination of leaf area leaf length or leaf width, can be usefully employed. The leaf constant values of these cultivars will be helpful to determine the actual leaf area for biometric studies.

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Short Communication

Galium aparine L. (RUBIACEAE) — A NEW RECORD FOR NORTHERN PLAINS OF INDIA

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Galium aparine L. is a weed of wastelands and roadsides mainly in the northern cooler climates. It has been reported from the foothills of India, but this is a first report from the plains of northern India. This species comes up in the post-winter period in the plains, but has been recorded before the winter season in the hills. It is a species of the Eurasian region; record of this species from the plains of India assumes significance as it has naturalised over extensive areas and is one of the important invasive weeds of cereals and canola in Canada, USA, Australia and New Zealand.

Key words: *Galium aparine*, weed, northern plains of India

Galium was one of the larger genera of family Rubiaceae (over 600 species reported), represented in India by over 22 species (Bamber, 1916; Chowdhery and Wadhwa, 1984; Hooker, 1882). The species available in India were largely confined to hilly tracts (1700-4500 m). Few species such as *G. setaceum* and *G. tenuisissimum* were reported from the plains. Species were available over a wide range of habitats- *G. verum* and *G. acutum* from stony areas, *G. javanicum* and *G. asperuloides* in grassy areas and meadows, and the latter as also *G. tricorne* in cultivated areas (Duthie, 1903; Polunin and Stainton, 1984). Species were mostly reported in the summer and pre-winter period (June to September); others such as *G. elegans* were found throughout the hilly regions of northern parts of India and in all seasons except in winter (May-November).

The state of Delhi, characterised by severe summer during May-June, appeared to be beyond the area suitable for occurrence of *Galium* spp. In this area, family Rubiaceae was represented by species of *Oldenlandia* and *Borreria* appearing in the post-monsoon period (August-December; Maheshwari, 1963). Detection of *Galium* during March-April, which was identified as *G. aparine* was therefore significant in the spread of the species and assessing its probable weediness.

Characteristics of *Galium aparine* in Delhi state

During a survey of weeds of the roadside areas of Delhi, two populations were located in southwest Delhi and identified as *G. aparine* L. This constituted a new record for the state of Delhi and the upper gangetic plains (Duthie, 1903; Maheshwari, 1963). The characteristics of *G. aparine* populations in relation to its variation and distribution were worked out.

Charateristics of plants - *Habit*: Annual, erect to straggling plants, and variable in size (0.5-46 cm tall). *Stem*: Quadrangular with retrorsely hooked spines along the edges, nodes/ stem variable (5-16), nodes pubescent. *Leaves*: lanceolate-linear (upto 0.75 cm), borne in whorls

of 4-6 at the nodes. *Inflorescence*: 1-3 flowers per cyme. *Flowers*: Greenish white, small, calyx teeth missing, and with tetramerous corolla and stamens (alternate with petals). *Fruits*: Rounded, mostly in pairs and densely covered by tuberculate and hooked hairs, dark brown to black at maturity. Populations were fairly dense (nearly 30 plants/ sq. m.). Flowering and fruiting was recorded in March- April, prior to the summer season.

G. aparine was identifiable by its finely toothed leaves and retrorse spines on the edges of its squared stem making them 'stick' to adjoining plants. The fruit was composed of two rounded nuts, joined together and covered with hooked tuberculate hairs. The plants were present as moderately large populations, small plants occurring alone on bare patches of land, and straggly plants co-occurring with other weedy species of the area such as *Cannabis sativa*, *Phalaris minor*, *Malva verticellata* and seedlings of *Leucaena leucocephala*. Despite wide variations in size of plants, nodes/stem, leaves and seeds produced per plant, related to differences in habitat conditions, size of fruits was more or less similar in both tall and short plants.

This species was also reported to be variable (Table 1), in keeping with its wide distribution over a range of altitudes in temperate Himalaya, and extending from Kashmir to Sikkim in India and north west Asia, in Europe and north Africa. However, only part of the variation reported in floristic literature was recorded in these populations. Furthermore, lower values for vegetative characters were noted, namely leaves per node and seed size (Table 1), whereas reproductive values, given by seeds per node, were high. These trends of higher reproductive growth and lower vegetative growth could be indicative of weedy nature of these populations.

Table 1. Variation in Galium aparine L.

Character	Characteristics reported in literature*	Characteristics recorded in Delhi collections
Habit	Trailing,rambling or climbing	Short and erect (0.5-4 cm) or tall and straggling (upto 46 cm); 5-6 nodes/stem on short plants and 9-16 nodes/ stem for taller plants.
Nodes	Tomentose or sometimes almost glabrous	Tomentose
Leaves	Variable in size (1.3-3.9-5.0 x 0.3-0.8 cm) and leaves in a whorl (4-8); linear or narrowly oblanceolate	0.9-1.5 x 0. 1 cm; 4-6 leaves per whorl
Inflore-scence	Peduncles longer or shorter than leaves; 1-3 flowered, rarely 1 flowered	Mostly peduncles longer than leaves; 2-3 flowered. Peduncles 1/node in smaller plants and 2-3/node in taller plants
Flower	Calyx tube ovoid or round	Round
Fruit	2.8-4 mm (or smaller); Covered with hooked tuberculate hairs, rarely smooth (var. intermedium)	1.5-2.0 mm; no smooth-surfaced forms noted. Seed potential output/ plant (flowers/peduncle x peduncles/node x nodes/ plant) ranging from 10-18 for small plants; 36-144 for taller plants

*Literature records: Babu, 1977; Bamber, 1916; Hooker, 1882; Moore, 1975

Assessment of weediness of *Galium aparine*

Galium aparine was representative of the temperate element of family Rubiaceae in the northern plains. *G. aperifolium* and *G. tricorne* were already represented in the foothills (Babu, 1977; Duthie, 1903). Family Rubiaceae was hence represented by both temperate and tropical plants in the northern plains, a trend already recorded in other families and noted to be typical for the northern plains of India (Maheshwari, 1963).

Several species of rubiaceous genera such as *Borreria* and *Galium* were found on the noxious weed lists of USA, Canada and Australia (USDA,

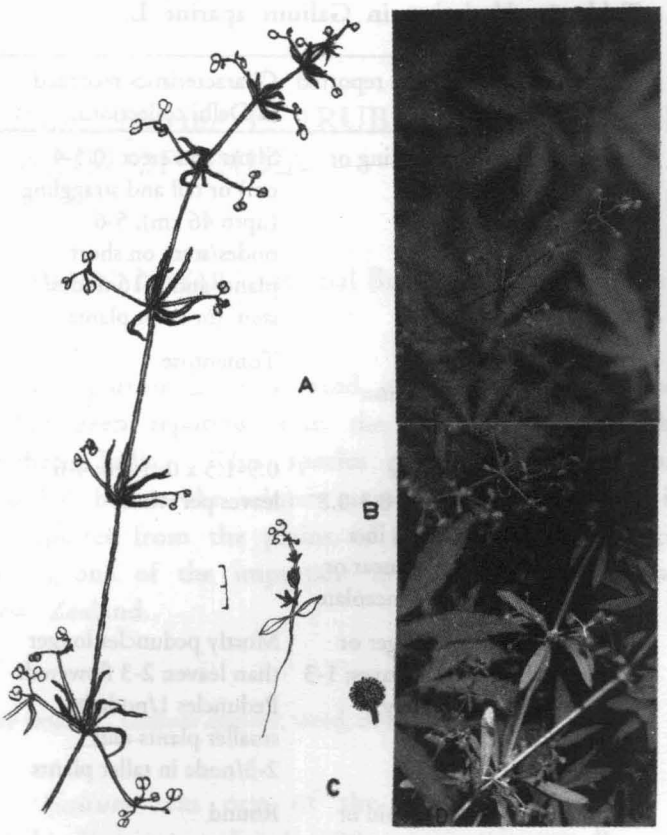

Fig. 1. Galium aparine L. (a) Tall plants co-occurring with other weeds (× 1.), (b) Small plants of barren areas (× 1), (c) Fruit with hooked hairs (× 4.3), (d) Plant with maturing fruits, (e) Plant with flowers and developing fruits

2001; Weeds Australia, 1998). *Galium* aparine and other closely similar species such as *G. spurium* were listed as potential threats to emerging large-scale *Brassica* (canola) producing countries. 'Stickiness' of the plants making it difficult to remove them, similarity in seed size to *Brassica* seeds, their germination in autumn making it difficult to eradicate it at the seedling stage using pesticides, persistence of seeds upto three years in the soil contributed to their success as weeds. Moreover, the *G. aparine* complex of Euroasian origin were reported to attain weedy traits in parts of Europe (Moore, 1975). Therefore, the Indian region too could be a potential region for expression of weediness of the species, considering its adaptability to wide range of habitats, changing agricultural practices, and similarities in location and rainfall to the area of occurrence of weedy forms of *Galium* aparine.

To conclude, in the Indian plains, probably because of a short 'spring' period, *Galium aparine* and related species did not attain the significance of major weeds, unlike in the USA, Canada and Australia. A check on inadvertent introduction of more weedy strains into the Indian region would be an important precaution, especially its inclusion in the noxious weed list of India (Moolchand *et al.*, 1999).

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Short Communication

VARIABILITY IN MILLING AND COOKING QUALITY OF TRADITIONAL RICES FROM KORAPUT DISTRICT OF ORISSA, INDIA

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Twenty-five traditional rice genotypes were assessed to identify suitable lines having good milling and cooking qualities. On the basis of high percentage of polished rice (> 70%), head rice recovery (> 60%) and good cooking quality, five cultivars, two from short bold group (Malsundri and Rottadhan) two from long bold group (Gadakatha and Ratanchud) and one from slender group (Dubraj) were selected.

Key words : Rice, traditional varieties, milling, head rice, cooking quality

Marketability and profitability in rice business solely depend on its good milling and cooking qualities. Higher the total as well as whole rice recovery during milling more better will be the margin of profit. Therefore, rice breeders all over the world are in search of donors having good milling and cooking qualities along with yield attributes. The present study aims at identifying promising accessions for good milling and cooking qualities.

Twenty-five traditional rice cultivars collected from different parts of undivided Koraput district of Orissa were used for the present study. The area is considered as secondary centre of diversity for rice (Ramiah and Ghose, 1951). A systematic survey of the area known as Jeypore Botanical Survey yielded many valuable germplasm for utilisation as donors in breeding programmes. (Govindaswamy and Krishna Murty, 1959). For the purpose of identifying promising types having desirable attributes for cooking and milling characteristics, a set of twenty-five collected earlier from Koraput district were grown under similar conditions at Base Centre Farm during *Kharif* 1994. After harvesting and threshing, the samples were cleaned and then dried in the sun up to a moisture level of about 14% (W.B).

The shelling, polishing and head rice recovery percents were determined for 100 g samples in duplicate using laboratory milling machines of Satake, Japan make (Bal, 1974). The kernel length and breadth were determined by means of dial micrometer for ten milled kernels and then their average values were recorded (Govindaswamy and Ghosh, 1969). Standard method of cooking quality (Beachel and Stansel, 1963), expansion of volume and water uptake (Azeez and Shafi, 1966) and the alkali value was determined following the method of Little *et al.*. (1958).

A variety is commercially acceptable only when its total polished Rice (PR) as well as head rice recovery (HRR) during milling is maximum. From the present study, it was observed (Table 1) that the SB varieties yielded 62.5-72.2 per

Table 1. Milling and cooking quality of traditional rices of Koraput district, Orissa

Sl. No.	IC No.	Variety	BR %	HC%	PR%	HRR %	KL (nm)	KW (mm)	L/B	Shape	1000 grain wt. (g)	Kernel colour	Abdominal white	Alkali value	Kernel length after cooking	Elongation ratio	Water uptake	Volume expansion ratio
1	137542	Malsundri	78.42	21.58	72.20	61.55	4.25	2.50	1.70	SB	23.1	Red	Occ. P	3.0,2.0	7.26	1.71	295	37
2	137536	Chatianaki	78.12	21.82	71.87	36.29	4.40	2.00	2.20	SB	23.2	Red	Absent	3.0,2.0	7.56	1.72	220	4.0
3	137553	Bodidhan	68.68	31.32	62.51	21.44	4.95	2.20	2.25	SB	15.0	White	Absent	4.0,3.0	8.56	1.73	235	3.7
4	214897	Rottadhan	74.60	25.40	70.14	62.48	5.00	3.00	1.66	SB	24.5	White	Absent	4.0,3.0	8.75	1.75	220	3.7
5	265345	Mirladhan	75.08	24.92	68.74	33.42	5.35	2.25	2.37	SB	20.0	White	Absent	3.0,2.0	9.41	1.79	320	4.0
6	199329	Padadhan	73.38	26.62	67.54	56.42	5.38	2.42	2.22	SB	25.0	White	Absent	3.0,2.0	9.57	1.78	285	3.7
7	145635	Kendulkatti	76.70	23.30	69.04	37.30	5.60	2.90	1.93	SB	27.5	R+W	Absent	3.0,2.0	10.08	1.80	215	3.7
8	145636	Padmavati	76.46	23.54	68.70	51.10	5.65	2.30	2.45	SB	22.5	White	Absent	3.0,2.0	9.54	1.69	195	3.7
9	137532	Mundadhan	74.71	25.29	64.60	39.35	5.70	3.00	1.90	SB	22.5	Red	Absent	3.0,2.0	10.14	1.78	245	4.0
10	137540	Dhobakhudi	75.30	24.70	69.22	40.76	5.95	2.60	2.28	SB	24.5	White	Absent	3.0,2.0	9.52	1.60	195	3.7
11	145631	Sonakathi	75.10	24.90	68.10	45.50	6.00	2.65	2.26	LB	22.5	R+W	Absent	4.0,3.0	10.32	1.72	255	3.7
12	137538	Kharandi	72.80	27.20	64.04	35.64	6.00	2.70	2.22	LB	27.0	White	Occ.P	3.0,2.0	10.20	1.70	255	4.0
13	145814	Sebakdhan	74.50	25.50	68.12	51.57	6.04	2.75	2.20	LB	28.5	White	Absent	4.0,3.0	9.96	1.65	220	3.7
14	145640	Lokuti Munj	74.00	26.00	66.60	54.80	6.05	2.10	2.88	LB	18.0	White	Absent	3.0,2.0	10.28	1.70	205	4.0
15	135629	Muandhan	72.16	27.84	70.84	61.88	6.15	2.40	2.56	LB	24.0	White	Absent	4.0,3.0	10.70	1.74	280	3.7
16	145812	Gadakatha	76.22	23.78	70.84	61.88	6.15	2.40	2.56	LB	24.0	White	Absent	4.0,3.0	10.57	1.72	280	3.7
17	145634	Japanidhan	75.24	24.76	66.30	37.00	6.20	2.40	2.38	LB	28.0	Red	Absent	4.0,3.0	10.35	1.67	210	4.0
18	145639	Ratan chudi	84.53	15.42	79.26	62.43	6.20	2.60	2.58	LB	22.4	White	Absent	4.0,3.0	10.23	1.65	190	3.7
19	137531	Malgoindi	75.94	24.06	67.06	40.00	6.25	2.40	2.08	LB	31.0	Red	Absent	4.0,3.0	10.37	1.66	210	3.7
20	145628	Mohiphlidha	75.37	24.63	68.12	56.75	6.40	3.00	2.56	LB	25.0	Red	Absent	3.0,2.0	11.13	1.74	245	3.7
21	145638	Mahipal	77.06	22.94	67.70	27.52	6.42	2.50	2.56	LB	26.2	Red	Absent	3.0,2.0	10.20	1.59	190	3.7
22	137534	Karandi	74.10	25.90	64.48	37.04	6.45	2.80	2.30	LB	27.5	White	Absent	3.0,2.0	11.15	1.73	260	3.7
23	145632	Dhruvaraj	79.13	20.87	74.16	61.83	5.90	2.00	2.95	MS	18.2	White	ABsent	3.0,2.0	11.44	1.94	270	3.7
24	145811	Lachidhan	75.00	25.00	60.84	48.20	6.00	2.00	3.00	LS	21.0	White	Absent	4.0,2.0	10.20	1.70	255	4.0
25	145633	Machhakanta	75.50	24.50	70.10	20.58	6.25	2.00	3.12	LS	22.0	White	Absent	3.0,2.0	10.68	1.71	230	3.7

cent polished rice, whereas the long bold and slender groups produced 60.6-79.26 per cent and 66.84-74.16 per cent. The mean values of plished rice for the above three groups of rice varieties are 68.45, 67.60 and 70.37 per cent respectively. The head rice recovery of SB group was observed to be in the range of 33.42-62.48 per cent, whereas the LB and slender groups produced 23.44-62.43 per cent and 20.58-61.83 per cent. The mean values of HRR for the above three groups of rice varieties are 44.01, 44.46 and 43.53 per cent respectively.

There was little variation in the mean values of PR and HRR among the three groups of rice varieties. However, in each groups, variability could be noticed among different varieties in respect of PR and HRR. High coefficient of variation was observed among medium slender varieties (48.26%) followed by short bold (29.90%) and long bold (29.35%). This suggests that there exists a great scope to select varieties with best combinations of PR and HRR (%) which can be used as donor in the breeding programme. The findings on husk content (HC) and 1000 grain weight in the present study did not reflect any specific effect on either PR or HRR (%).

The cooking and kernel characteristics indicated that kernel characteristics are either red or white or both in some cases. Abdominal white absent in 23 varieties and present only in two varieties. Variation was also observed with respect to alkali value (2.0-4.0), elongation ratio (1.70-1.94), water uptake (1.90-3.20) and volume expansion (3.7-4.0) These characteristics are also important from consumers preference point of view. In the present study, these quality characters did not vary much among the genotypes and remained within the permissible limits.

The results of the present investigation revealed that five cultivars, two from the SB group (Malsundri and Rottadhan), two from the LB group (Gadakatha and Ratanchudi) and one from the slender group (Druvaj) exhibited high percentage of PR (> 70%) and HRR (> 60%) along with good cooking quality. Therefore, these five traditional rice cultivars could be used by the breeders as donors for breeding varieties with an aim to achieve higher milling and head rice recovery along with good cooking quality.

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BOOK REVIEWS

Phogat, B.S. and G.D. Sharma. 2000. Underutilized Food Crops: Their Uses Adaptation and Production Technology. All India Coordinated Research Project on Under-utilized crops, National Bureau of Plant Genetic Resources, New Delhi. 58 p.

This bulletin provides a well-synthesized information on about 15 underutilized food crops; their cultivation, production and uses are briefly discussed. The crops dealt with are- pseudocereals such as grain amaranth, buckwheat; minor cereals like jobs tears; food legumes such as faba bean, adzuki bean and winged bean; oilseeds like *Simarouba glauca* and *Perilla frutescens*; vegetables like *Momordica* spp., and *Citrullus lanatus*. It is hoped that this publication will be very useful to all those interested in research related to under-utilized crops.

Srivastava, Umesh., R.L. Sapra and G.D. Sharma. 2000. Evaluation studies in world germplasm of tomato (*Lycopersicum esculentum* Mill.) and Developing Core Set. National Bureau of Plant genetic Resources, New Delhi. 212p.

The NBPGR over the years, has assembled 2900 germplasm accessions including wild species from diverse agro-climatic zones of the world (from 47 countries). This publication is based on characterization and evaluation of these accessions using 41 descriptors. One of the major issue that Gene Bank managers (curators) face is the need to increase the accessibility of their collection to a large group of users. Developing procedure for reducing the size of a collection to a manageable and accessible level is becoming one of the most important issues in the management and utilization of large germplasm collections. Concept of developing core germplasm set as a minimal, yet diverse set, representing the diversity of the germplasm collection has attracted wide attention in recent years. Developing a core set for efficient management of germplasm helps in maintaining comparatively fewer accessions rather than entire set of accessions. Principal Component Analysis (PCA) strategy was used to estimate the inertia and the corresponding relative contribution (RC) of each accession. Fourteen principal components with eigen values over 1 and explaining a total of 65 per cent variation were selected for computing the inertia and relative contribution of each accession. An improved method based on RC score and requiring low number of accessions to be sampled, is suggested for establishing the core set. For tomato core, an optimum sample size of 140 was estimated on the basis of pooled diversity A sample of 140 accessions (nearly 7 per cent of the base collection of 2021 germplasm lines) was finally selected for the final core (of 2021 tomato germplasm lines). The methodology adopted in selecting accessions is efficient and can be safely used, even when the passport information is partially available or unavailable. Retrieval of useful information for specific characters is also given. It is hoped that this publication will be very useful to botanists, tomato breeders, Gene Bank managers, curators and students alike in selecting germplasm material of their choice and use them in tomato improvement programme.

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