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Crop Improvement in Guava: An Overview

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Guava is a major fruit crop of India and popularly known as 'apple of the tropics' since it is consumed as a fresh fruit or processed into a variety of products. Efforts have been made over the past few decades to widen its genetic base by creating new variability and utilizing it for the selection of elite variety or hybrids for commercial cultivation. Attempts are still on to improve upon the existing commercial cultivars through selection of germplasm and combining the desirable traits of various genotypes through hybridization. A variety with in-built resistance to the biotic and abiotic resistance besides high yielding capacity of good quality fruit is lacking in guava. The DNA marker assisted selection has the potential to introduce and deploy favourable gene combinations for disease control along with the other agronomically important traits. The available information covering different aspects of crop improvement of guava has been reviewed.

Key words: Breeding, Crop Improvement, Genetic Diversity, Germplasm Management, Guava, Marker-Assisted Selection, Molecular Markers, *Psidium guajava* Linn

The common guava (*Psidium guajava* Linn) is mainly self pollinated, but cross pollination is also common resulting in a greater variation in the seedling population. Seed propagation, therefore, has created considerable variability from which promising genotypes were selected in different agro-climatic regions of the country (Pathak and Ojha, 1993). A proper understanding and management of variation present within the natural and other cultivated varieties as well as in the wild relatives of guava is very essential in the establishment of an efficient programme aimed at its crop improvement. The description and nomenclature of the present day guava varieties are greatly confusing and the genetic uniformity in the crop is undesirable because it tends to make the crop more vulnerable to epidemics. Hence from the germplasm maintenance and breeding point of view, the identification of duplicate accessions in different cultivar names and its elimination from the germplasm collections is yet another important task. The promising guava cultivars which are deficient in one or more traits can be improved by crossing such cultivars between the lines which possess the desired trait. A conventional breeding programme thus involves crossing the whole genome followed by selection of superior recombinants from several segregation products. Such a procedure is laborious and time consuming involving several crosses, many generations and careful phenotypic selection. Also tight linkage of desired loci with an undesired loci may make it difficult to achieve the desired objective. With the advent of DNA marker technology, several types of DNA markers and molecular breeding strategies are now available to plant breeders and geneticists helping them to overcome many of the problems faced during conventional plant breeding. The present effort outlines the history of the crop and to review the present status of guava crop improvement programmes conducted at various centres with special emphasis on the novel technologies which could be implemented in its breeding programme.

Origin and Distribution

The guava is believed to have originated in tropical America, from Mexico to Peru (Hayes, 1953), where it still occurs in the wild and forms extensive thickets. It is common throughout all warm areas of tropical America and in the West Indies (Purseglove, 1968) and was domesticated 2000 years ago (Cobley, 1976). Guava was adapted as a crop in the warmer parts of Africa and Asia including India during early 17th century soon after it was introduced by Spanish and Portuguese colonizers (Hayes, 1953; Menzel, 1985; Singh, 1985).

The common guava, *Psidium guajava* Linn, is widely distributed throughout the world and is grown mainly for its fruits in many tropical and subtropical countries. It grows in a wide range of environments from sea level up to an altitude of 1500 m (Singh, 1985) throughout Asia, South Africa, America and Australia. It exceeds the other fruit crops in productivity, adaptability and in the total vitamin content of fruits. Guava is an important fruit crop in India and stands fourth in area and production after mango, banana and citrus (Anonymous, 1985). In India, the most important guava growing states are Uttar Pradesh (UP), Bihar, Madhya Pradesh and Maharashtra.

Allahabad (UP) has the reputation of growing the best quality of guava fruits in the world (Mitra and Bose, 1990). It is cultivated on a commercial scale in many countries and India leads the world in guava production (Adsule and Kadam, 1995). The other major producers of guava are Mexico, Pakistan, Colombia, Egypt, South Africa, Venezuela, Dominican Republic, Puerto Rico, Jamaica, Kenya, Australia and Hawaii.

The Plant and its Importance

The guavas belong to the genus *Psidium* (family – Myrtaceae) which comprises approximately 153 species of trees and shrubs and about 20 species have edible fruits (Hayes, 1953; Iyer and Subramanyan, 1987; Yadav, 1990). Out of these, the common guava *Psidium guajava* is commercially and economically utilized so far. The plant is a shallow rooted shrub or a small tree up to 33 feet with spreading branches close to the ground with an attractive 'bony' appearance of the trunk. Young twigs are quadrangular and downy with opposite decussate with short-petioled leaves. The flowers are characteristic by a prominent tuft of around 250 abundantly incurred white stamens of various size. The guava trees produce a large number of fruits which vary between genotypes in colour, size, flavour and has a characteristic musky odour. The guava fruit is a rich source of vitamin C – contains four to five times higher than in citrus fruits; vitamin A, vitamin B_2 (riboflavin), thiamin, niacin and minerals like calcium, phosphorus and iron. The fruit pulp is a commercial source of pectin and oil from its seeds. Ripe guavas are eaten out of hand and are processed into innumerable products. Guava shells, concentrated pulp, paste, jelly, jam, juice powder and confectionaries are a few among them. The guava fruits are often referred as 'apple of the tropics' (Rangacharlu, 1954; Menzel, 1985). The wood is valued for engravings, useful as tool handles and in making implements. The leaves, bark and immature fruits are rich in tannin and are used for dyeing. The roots, bark, leaves and immature fruits can be used in local medicine.

Related Species of Common Guava

The important cultivated species related to common guava are Brazilian guava or Guisaro (*Psidium guinese* Sw); Cattley guava or Strawberry Guava (*P. cattleanum* Sibne), Costa Rican guava (*P. friedrichsthalianum* Ndz), Para guava (*P. acutangulaum* DC), *P. littorale, P. longipes, P. montanum, P. microphyllum, P. sartorianum, P. quidanense* and the other genus *Myrcaria floribunda* Berg, the Rumberry or guavaberry (Mortan, 1987).

Species like *Psidium araca, P. cattleianum, P. corecium, P. cujavillus, P. cumini, P. friedrichsthalianum, P. guinese, P. molle, P. quidanense* and phillipine guava are reported to be tolerant or resistant to the wilt disease (Edward and Shankar 1964; OmPrakash and Mishra, 1993; Rawal, 1993).

Genetic Diversity among Cultivars

Genetic variation and its assessment in the existing germplasm of guava is an essential component to its improvement. Plant breeders need the sources of genetic diversity to draw upon when required, to breed for better nutritive value, adaptability and resistance for biotic and abiotic stresses. Among the cultivated genotypes of common guava, extensive genetic diversity exists in different countries (Teaotia, 1967; Pandey, 1968; Purseglove, 1968). Diversity exists in tree size, flowering and fruiting characteristics, yield, qualitative fruit characters like size, shape, skin colour, texture and colour of flesh, flavour, aroma, ascorbic acid content of fruit, pulp to seed ratio, seed characteristics, post-harvest characteristics and susceptibility to pests and diseases (Mortan, 1987). A list of germplasm collections of different agroclimatic regions of the world is given in Table 1.

The germplasm evaluation studies have successfully identified some promising genotypes which have economic potential in early flowering and maturity, yield, qualitative fruit characteristics, post harvest and fruit processing characteristics and tolerance or resistance to biotic stresses (Pathak and Ojha, 1993; Subramanyan and Iyer, 1993).

Genetics and Breeding

The cultivated guava is a diploid species (basic chromosome number is 11; 2n =22) with a high bearing capacity. However, it has a disadvantage of high seed content. A natural as well as an artificial triploid species 2n = 3x = 33 produces seedless fruits but they are almost shy bearers (Kumar and Ranade, 1952; Sharma and Majumdar, 1957; Raman *et al.* 1969, 1971). Naithani and Srivastava (1966) reported natural autotetraploids in the genus. Ramkumar (1973) induced tetraploidy in Allahabad Safeda variety by treating shoot tip with 0.1 % aqueous solution of colchicine. Ploidy levels higher than this are not reported in guava. Studies on the inheritance pattern of important traits in guava have indicated that the flesh colour of fruits and the seed size are linked characters; Red pulp colour is dominant

Table 1. Local and introduced cultivars, selections, breeding lines and hybrids of guava grown in different agro climatic regions of the world

Country & Cultivar	Pulp colour	Country & Cultivar	Pulp colour	Country & Cultivar	Pulp colour	Country & Cultivar	Pulp colour	Country & Cultivar	Pulp colour
Bangladesh		**Florida (Contd)**		**India (Contd)**		**India (Contd)**		**India (Contd)**	
Deshipeyara	n.a.	Red Indian	R	Allahabad-Safada	W	Hybrid 1	W	Wickramasekara	R
Kazipeyara	n.a.	Red land	W			Hybrid 16-1	W	WhiteSupreme-xRuby	W
Sarupakatti	n.a.	Ruby	R	Allababad-Surkha	W	Hybrid 45	n.a.		
Mukundhupuri	n.a.	Supreme	W		n.	Hybrid 53	n.a.	**Malaysia**	
Brazil		**France**		Am Sophri	n.a.	Hybrid 84	n.a.	Gu 4	n.a.
Brune Branca	n.a.	Acid Speer	PY	Anakapalle	R	Hybrid 105	n.a.	Gu 5	n.a.
IAC – 4	n.a.	Beaumont	P	Aneuploid-82	n.a.	Hybrid 161	n.a.	Gu 7	n.a.
IMC	n.a.	Elisabeth	P	Apple Colour	n.a.	Indonesian-Seedless	n.a.	HongKong Pink	n.a.
PB	n.a.	Large White	W	Arka Amulya	n.a.			Jambu Biji	n.a.
PV	n.a.	Patricia	PO	Arka Mridula	W	Kafroe	R	**Miami**	
Rica	n.a.	Pink Indian	R	AS 1	n.a.	Karela	W	Miami Red	R
TL	n.a.	Red Hybrid	R	AS 2	n.a.	Kohir Safada	W	Miami White	W
California		RedxSupreme-xRuby	DP	AS 3	n.a.	Kothrud	R	**New South Wales**	
Detwiler	n.a.			Banarasi	R	Lalit	n.a.	GA 11-56	n.a.
Hart	PY	RedxSupreme-XRubyxWhite	CW	Banarasi-Surkha	W	Lal Seiba	R	1050	n.a.
Red Indian	R					Lucknow-24	n.a.	**Puerto Rico**	
Rolfs	P	Stone	DP	Bangalore	W	Lucknow-42	W	Corozal Mixta	n.a.
Turnbull	n.a.	Supreme	P	Bariampur	n.a.	Lucknow-46	n.a.	Corriente	n.a.
Webber	PY	SupremexRuby	W	Beaumont G35	P	Lucknow-49	W	Seedling 57-6-79	n.a.
White Indian	W	**Hawaii**		Behat Coconut	W	Madhuri-am	n.a.	**Queensland**	
Coloumbia		Allahabad-Safada	W	BHR – 3	n.a.	Mirzapuri	W	GA9-39-R1T2	n.a.
Agrio	n.a.			BHR – 5	n.a.	M25988	n.a.	GA11-56R1T1	n.a.
D-13	n.a.	Apple	n.a.	Chakaiya	n.a.	Nagpur Seedless	n.a.	GA11-56R5T2	n.a.
D-14	n.a.	Beaumont	P	China Surkha	R	Nasik	W	GA11-564T1	n.a.
Puerto Rico	n.a.	Burma	n.a.	Chittidar	W	Navalur	n.a.	GA11-56T3	n.a.
Red	n.a.	HongKong Pink	P	CHN	n.a.	Oakey Pink	n.a.	GA11-56T7	n.a.
Rojo Africano	n.a.	HongKongWhite	W	Dharbar	W	Patillo	n.a.	**South Africa**	
Trujillo 2	n.a.	Indonesian-seedless	W	Dharidar	n.a.	Portugal	n.a.	Dimple	n.a.
White	n.a.			Dharwar	W	Redfleshed	R	Fan Retief	n.a.
Cuba		Indonesian-White	W	Dholka	R	Rewa 72	n.a.	Frank Malherbe	n.a.
Belic L-97	n.a.			EthridgeSelection	n.a.	Safeda	W	Fredene	n.a.
Belic L-207	n.a.	Ka Hua Kula	DP	FloridaSeedling	n.a.	Safrior Payere	n.a.	Fredericka	n.a.
EEA 18-40	n.a.	Lucknow-49	W	FS 1	n.a.	Sangam	n.a.	Jonelle	n.a.
Egypt		No. 6362	n.a.	FS 2	n.a.	SeedlessTriploid	W	Weiheim	n.a.
Bassateen-Edfina	W	No. 6363	W	Gwalior 27	n.a.	Seedless-Triploid Poona	W	**Taiwan**	
		No.7198	DP	Habshi	W			Chung Shangpa	n.a.
Bassateen-El-sabahia	n.a.	No.7199	n.a.	Hapi	R	Sindh	W	Laiapa	n.a.
Florida		**India**		Harijha	n.a.	Smooth Green	W	Peipa	n.a.
Blitch	LP	ABD 3	n.a.	Hasijaka	R	Super Acid	R	**Trinidad**	
Patillo	P	AC 10	n.a.	HybridRed-Supreme	R	Tathen White	n.a.	Cayenne	n.a.
		Allahabad	W			Verdie	n.a.		

Source: Mortan (1987)
W – White, CW – Creamy White, PY – Pale Yellow, L – Light Pink, P – Pink, PO – Pinkish Orange (Salmon fleshed), DP – Deep Pink, R – Red, n.a. – information not available.

to white which are governed monogenically and bold seeds are found to be dominant over soft seeds and are also governed monogenically (Subramanyan and Iyer, 1982). The systematic breeding work done for the crop improvement in guava was reviewed by Subramanyan and Iyer (1993).

In India, guava improvement programme was initiated during 1907 at Ganesh Khind Fruit Experimental Station, Pune (Phadnis, 1970) with objectives to develop dwarf, as well as high yielding, good post harvest characteristics in fruits and to evolve resistant lines to biotic and abiotic stresses. As a result, many varieties and hybrids of agronomic and commercial importance have been evolved through selection and hybridization. Most of the popular varieties existing today are developed from selections from the seedling progenies of open pollinated seeds. Out of 600 seedlings selected from the different regions of the country, Lucknow 49 was identified (Cheema and Deshmukh, 1927) as a promising strain evolved from the open pollinated seedlings of Allahabad Safeda. This strain had distinguishing characters like spreading growth habit, large globose fruits with white flesh, high TSS content, sugar:acid ratio and yield (Cheema *et al.* 1954). After successful field trials at Saharanpur (Singh, 1953) and Kodur (Rangacharulu, 1954) the variety is now renamed as Sardar and recommended for large-scale commercial cultivation. The work initiated by Singh (1953) at Horticultural Research Station, Saharanpur led to the evolution of superior selection known as S-1 which had good fruit shape, less number of seeds, sweet taste and high yield (Singh, 1959).

A large germplasm of guava was established and evaluated for morphological features, fruit quality and yield at Central Institute of Horticulture for Northern Plains, Lucknow where after the evaluation of 20 varieties, Lucknow-49 was found to be the best (Chadha *et al.* 1981). In Karnataka, 16 high performing seedlings were selected from a variety named after a village *viz.*, Navalur which was hardy, drought tolerant and canker resistant (Hulamani *et al.* 1981). Similarly, three superior strains viz., ABD 3, BHR 3 and BHR 5 were identified from twelve strains collected from Aurangabad and Bhir Districts of Maharashtra (Thonte and Chakrawar, 1981). At Narendra Dev University of Agriculture and Technology, Faizabad, three seedlings of Allahabad Safeda (AS_1, AS_2 and AS_3) and two seedlings of Faizabad Selection (FS_1 and FS_2) were found to be promising out of 23 strains evaluated with respect to the fruit quality and yield (Pathak and Dwivedi, 1988). Apart from this, surveys conducted in Gujarat and Rajasthan also resulted in the identification of few outstanding trees of desirable attributes (Anonymous, 1988). Similarly from Indian Institute of Horticulture, Bangalore, two varieties *viz.*, Arka Mridula (Selection 8) and Arka Amulya were released (Iyer and Subramanyan, 1988) from open pollinated seedlings of Allahabad Safeda. They are heavy yielders, dwarf plant type, fruits white fleshed with high sugar and TSS content, soft seeded and with good keeping quality. Allahabad Surkha, a red skinned guava variety was obtained by chance selection of Allahabad Safeda.

Crop improvement programme in guava through hybridization was initiated at Indian Agricultural Research Institute(IARI), New Delhi, Andhra Pradesh Agricultural University Station at Sangareddy and at Indian Institute of Horticultural Research, Bangalore. The seeded diploid variety of Allahabad Safeda was crossed with a seedless triploid at IARI, New Delhi and a series of aneuploids were produced (Majumder and Mukherjee, 1972 a, b; Mukherjee, 1977) with dwarf tree growth habit, normal shape and size of fruits with few seeds. Nijar (1977) suggested that aneuploidy breeding may be profitable in fruit trees where high seed content of fruits is a defect. Crosses were made and a tetrasomic species namely, Aneuploid-82 was developed with normal size and shape of fruit, few seeds and with tremendous scope to be utilized as root stock. The hybrids Safed Jam and Kohir Safed were released from A.P. University Station, Sangareddy (Mitra and Bose, 1985) and Hybrid-1 and Hybrid 16-1 were released from IIHR, Bangalore (Subramanyan and Iyer, 1988). At Rajendra Agricultural University, Sabour, F_1 hybrid seedlings were raised from crosses between Chittidar x Apple Colour, Chittidar x Sardar, Chittidar x Redflesh, Chittidar x Allahabad Safeda; Sardar x Allahabad Safeda, Sardar x Chittidar; Apple Colour x Sardar; Allahabad Safeda x Apple Colour, Allahabad Safeda x Sardar (Singh and Hoda, 1988). Ghosh *et al.* (1998) mentioned the characteristics of a few more promising guava hybrids *viz.*, Hybrid-45, 53, 58, 84, 105 and 161 at IIHR., Bangalore. A brief breeding and selection programme was initiated at Institute for Tropical and Subtropical Crops, South Africa to develop a wilt resistant cultivar along with other desirable characters suitable for processing, canning and fresh market (Preez and Du-Preez, 1996). At Taiwan

Agricultural Research Institute, Kohsinag, Wan-WuChang *et al.* (1999) have selected the crosses between R4 x Pepia and R1 x Pepia resistant against *Myxosporium* wilt in guava.

Attempts were made through grafting in guava with major objective of developing root stocks with resistance to guava wilt. The wild *Psidium* species can be utilized as root stocks for regulation of vigour, bearing, fruit quality and resistance to pest and diseases (Mitra and Bose, 1990). The Chinese guava (*Psidium friedrichsthalianum*) is a compatible root stock and has been reported to be resistant to wilt disease. Its dwarfing effect would be used in commercial plantings (Edward and Shankar, 1964). Allahabad Safeda trees grafted on *P. pumilum* had a dwarfing influence and on *P. cujavillis* produced the largest trees but non uniform and rough skinned fruits. Fruits from trees of Florida seedling stock had the highest total acidity (Teaotia and Phogat, 1970). Singh *et al.* (1976) observed that fruits of Allahabad Safeda contained higher sugar content on *P. pumilum* while higher ascorbic acid content was recorded in those grafted on *P. cujavillis*. In the attempts made for the interspecific hybridization in guava with a major objective of developing root stocks for wilt resistance, it was observed that *P. guajava* and *P. chinensis* are crossable. Similarly *P. chinensis* when used as female parent with *P. molle*, the cross was compatible where as the cross between *P. guajava* as female parent and *P. molle* was incompatible (Subramanyan and Iyer, 1982). However cross incompatibility exists between several cultivars of superior traits. Seth (1960) reported varietal cross incompatibility since neither fruit nor seed set was obtained when crosses were made between Behat Coconut and Lucknow 49; S-1 and Behat Coconut; Behat Coconut and Apple Colour; and Apple Colour and S-1.

Biotechnology Applications in Crop Improvement

The advent of plant molecular biology techniques related to DNA based markers provide powerful and reliable tools for a variety of purposes including variation within the crop germplasm, tagging of genes for agronomically important traits and genome mapping. A variety of molecular markers have been developed for these purposes. Some of the DNA markers currently in use are RFLPs, RAPDs, SCARs, DAF, Minisatellites, Microsatellites or SSRs, ISSRs, AFLPs, S-SAPs, REMAP and IRAPs. The role of DNA markers in crop improvement has been reviewed by many authors (Joshi *et al.* 1999; Kumar, 1999; Thomas and Raman, 2000).

The molecular markers are specially advantageous for improving agronomic traits in perennial fruit crops that are otherwise time consuming and difficult to tag the genes conferring resistance to pathogens, insects, nematodes, tolerance to abiotic stresses, quality parameters and quantitative traits. By using Marker Assisted Selection (MAS), the breeder could select molecular markers that are tightly linked to resistant genes for identifying resistant genotypes. Unfortunately, information on these aspects assisted by molecular marker aided studies is lacking in guava. Hence the task of developing molecular marker based genetic map is challenging and important in the crop improvement of guava.

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Plant Genetic Resources Management of Horticultural Crops in Eastern India

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The eastern part of India is endowed with rich gene pool of major horticultural crops. Plant genetic resources activities were carried out by Horticultural and Agro-Forestry Research Programme (HARP), Ranchi. Consequenty, a total of 2001 germplasm including fruits (569), vegetables (1125) and ornamental plants (207) have been augmented, characterised, evaluated and judiciously utilised in the breeding programmes to develop varieties of different crops. As a result, Swarna Roopa in litchi; Swarna Shree, Swarna Mani, Swarna Shyamali and Swarna Pratibha in brinjal; Swarna Poorna, Swarna Ageti and Swarna Sheetal in cucumber, Swarna Rekha and Swarna Alaukik in parwal; Swarna manjari and Swarna Uphar in ridge gourd; Swarna Lata in French bean (pole type); Swarna Priya in French bean (bush type) and Swarna Lalima (determinate) and Swarna Naveen (indeterminate) in tomato have been released by Central/Institute Veriety Release Committee. A total of 18 lines in different vegetable crops including brinjal (6), tomato (5), sponge gourd (2), dolichos bean (3), garden pea (1) and vegetable cowpea (1) have been developed and are being tested under AICVIP at various locations spread over the country. In addition, elite lines in litchi (CHES-2) and jackfruit (CHES-1 & CHES-2) have also been developed and are in the pipeline for release.

Key words : Brinjal, Cucumber, Dolichos Bean, Garden Pea, Germplasm, Parwal, PGR, Ridge Gourd, Sponge Gourd, Tomato, Varietal Improvement, Vegetable Cowpea

Plant genetic resources are the basic raw materials required for developing new varieties in crop improvement programmes. The eastern region of India is endowed with most ideal climatic condition and vast geographical area for cultivation of a number of horticultural crops. The sexual method of propagation have resulted in generation of rich genetic variability in horticultural crops which need to be conserved and utilised in crop improvement programmes. Several factors such as population pressure, deforestation, changing cropping pattern and introduction of new varieties/hybrids contribute for considerable amount of genetic erosion in this region. Hence, collection, characterisation, evaluation, documentation, conservation and judicious utilisation of plant genetic resources of horticultural crops in crop improvement have attracted the attention of scientists and policy makers at national and international level. In this regard, the Horticulture and Agro-Forestry Research Programme (HARP), Ranchi is entrusted with the responsibility of management of plant genetic resources of horticultural crops in eastern India.

Materials and Methods

Efforts were made for augmentation of germplasm of fruits, vegetables and ornamental crops through exploration in different parts of the country and collection from Agricultrual Institutions/Universities and introduction from exotic sources through National Bureau of Plant Genetic Resources. Consequently, a total of 2001 germplasm inlcuding mango (248), guava (48), aonla (10), sapota (12), custard apple (25), bael (10), lime (2), lemon(1), litchi (51), pomegranate (8), jackfruit (111), peach (5), pear (1), tamarind (30) and jamun (7) in fruits; brinjal (280), French bean bush type (150), French bean pole type (131), tomato (202), peas (175), dolichos bean (30), vegetable soybean (12), winged bean (9), pointed gourd (65), sponge gourd (30), cucumber (80), ridge gourd (35), cowpea (20), lima bean (1), velvet bean (1), pumpkin (2), sword bean (1) and bitter gourd (1) in vegetables; rose (150), chrysanthemum (12), gladiolus (15), Hibiscus (6), croton (8), bougainvillea (8) and dahlia (8) in ornamental plants were augmented. These germplasm lines were characterised, evaluated for a set of descriptors developed by this Station for each crop. Promising lines for various traits in different horticultural crops were identified for direct utilisation and use in breeding programme. Systematic breeding was also undertaken to develop suitable varieties resistant to biotic stresses and having quality traits. This has resulted in development of 16 varieties in different fruit and vegetable crops which have already been released by Central Variety Release Committee/Institute Variety Release Committee and have been discussed in the text. Additionally, a total of 18 lines have also been developed in vegetables and 3 in fruit crops which are being tested at different locations spread all over the country. Among these, a number of lines have been

Table 1. Important horticultural crops developed at HARP, Ranchi

Crop	Botanical name	Name of Variety	Pedigree	Important Characters	Yield Potential	Area and Period Recommended for Cultivation
Litchi	*Litchi chinensis*	Swarna Roopa	Developed through clonal selection from seedling population	High yielder, fruits borne in cluster (25-30), cracking resistant, mid season maturing (May end) with attrative deep pink skin colour having high TSS (19°B), sugar (12.5 g/100 g), edible portion (75%) and less acidity (0.39%).	70-80 kg/tree	Released by Institute Varietal Release Committee during 1995 and recommended for all the litchi growing states namely Bihar, Jharkhand, Uttaranchal, West Bengal, etc.
		Elite line CHES-2	Developed through clonal selection from seedling population	Regular bearer; fruits borne at the periphery as well as inside the canopy, crimson red in colour with high TSS (25° brix) and low acidity (0.37%) having high pulp (aril) content (75%).	70-80 kg/tree	Suitable for cultivation in Jharkhand, Bihar and other litchi growing states.
Jackfruit	*Artocarpus heterophyllus*	Elite line CHES-1	Developed through clonal selection from seedling population	A table purpose variety; fruits oblong, weighing 15-20 kg, with high percentage of flakes and small seed, high TSS and low acidity.	700-750 kg/tree	Suitable for cultivation in Jharkhand, eastern Uttar Pradesh, Bihar, Orissa, West Bengal and North eastern states.
		Elite line CHES-2	Developed through clonal selection from seedling population	A vegetable type; fruits round, weighing about 4-5 kg, with dark green surface colour; flakes-compactly arranged, less fibrous containing small seeds with very high thin seed coat having very good cooking quality.	300-400 kg/tree	Suitable for cultivation in Jharkhand, Bihar, eastern Uttar Pradesh, West Bengal and parts of North eastern states
Brinjal	*Solanum melongena*	Swarna Shree	Developed through pure line selection from local land races of Ranchi district.	Fruits cream coloured, round, soft and highly suitable for 'Bharta' preparation; moderately resistant to bacterial wilt; foliage light green in colour.	550-600 q/ha	Released by Insitute Variety Release Committee during 1995 and recommended for the growers of Jharkhand, Bihar (Maurya, 1999), Orissa, Uttar Pradesh, Andhra Pradesh, Madhya Pradesh, Harayana, Delhi, Punjab, Gujarat, Maharashtra, Kerala and Karnataka.
		Swarna Mani	Developed by crossing elite germplasm lines CH-26 and CH-82 followed by pedigree selection and back cross method of breeding.	Fruits round and attrative, shiny purple in colour; moderately resistant to bacterial wilt.	600-650 q/ha	Identified for release by AICVIP Workshop during 1999 and recommended for cultivation in Jharkhand, Bihar, Uttar Pradesh, Uttaranchal and Punjab (Anon., 2000).
		Swarna Shyamli	Developed through pure line selection from the local germplasm of Irba village of Ranchi district.	Resistant to bacterial wilt; fruits medium sized (250 g), less seeded, round; the cooked flesh very sweet in taste.	500 q/ ha	Released by the Institute Variety Release Committee during 2001 and recommended for cultivation round the year in Jharkhand, Bihar and adjoining areas where bacterial wilt is a serious problem in brinjal cultivation.
		Swarna Pratibha	Developed through pure line selection from the local germplasm line collected from Simdega area of Jharkhand.	Resistant to bacterial wilt; fruits long, (average weight 200 g), shiny purple in colour, having good cooking quality.	500 q/ ha	Released by the Institute Variety Release Committee during 2001 and recommended for cultivation round the year in Jharkhand, Bihar and adjoining areas where bacterial wilt is a serious problem in brinjal cultivation.

Contd.

Contd.

Crop	Botanical name	Name of Variety	Pedigree	Important Characters	Yield Potential	Area and Period Recommended for Cultivation
		Elite line CHGR-1	Developed through hybridisation and back crossing utilising the germplasm lines CH-249 (bacterial wilt resistant) and Arka Sirish (susceptible).	Fruits round, green with non spiny calyx.	450-500 q/ha	Suitable for cultivation round the year in Jharkhand, Bihar and adjoining areas where bacterial wilt is a serious problem in brinjal cultivation.
		CHGR-2	Developed through hybridisation and back crossing utilising CH-249 and Arka Sirish.	Fruits round, striped green with spiny calyx.	450-500 q/ha	Suitable for cultivation round the year in Jharkhand, Bihar and adjoining areas where bacterial wilt is a serious problem in brinjal cultivation.
		CHBR-2	Developed through crossing between germplasm lines Ch-82 and Ch-4 and followed by selection in segregating generations.	Fruits round, shiny purple in colour and preferred by consumers.	600 q/ha	Suitable for cultivation round the year in Jharkhand, Bihar and adjoining areas where bacterial wilt is a serious problem in brinjal cultivation.
		CHBR-3	Developed through back cross breeding method utilising the germplasm lines Ch-82 and Ch-4.	Fruits round, shiny purple in colour.	600 q/ha	Suitable for cultivation round the year in Jharkhand, Bihar and adjoining areas where bacterial wilt is a serious problem in brinjal cultivation.
		CHRBH-1	This hybrid is the cross between Ch-26 and Ch-27.	Fruits round, shiny purple in colour.	700 q/ha	Suitable for cultivation round the year in Jharkhand, Bihar and adjoining areas where bacterial wilt is a serious problem in brinjal cultivation.
		CHRBH-2	This hybrid is the cross between Ch-26 and Swarna Shree.	Fruits round, purple in colour.	750-800 q/ha	Suitable for cultivation round the year in Jharkhand, Bihar and adjoining areas where bacterial wilt is a serious problem in brinjal cultivation.
Cucumber	*Cucumis sativus*	Swarna Poorna	Developed through pure line selection from indigenous land races collected from Bhubaneswar district of Orissa.	Fruits medium sized, light green in colour having no placental hollowness; tolerant to powdery mildew.	300-350 q/ha	Released by the Institute Variety Release Committee during 1995 and recommended for cultivation in Jharkhand, Bihar, Orissa, Uttar Pradesh and Madhya Pradesh; also identified for release in Sub-humid Sutlej Ganga alluvial plain by AICRP (VC) Group Meeting during 2002.
		Swarna Ageti	Developed through mutation breeding and selection pressure exercised in M5 generation for individual plant with high yield and disease resistance.	Fruits medium sized, green in colour having no placental hollowness; tolerant to powdery mildew.	300-325 q/ha.	Released by the Institute Variety Release Committee during 1999 and recommended for cultivation in Jharkhand, Bihar, Uttar Pradesh, Andhra Pradesh, Delhi and Himachal Pradesh; also identified for release in Sub humid Sutlej-Ganga alluvial plain by AICRP (VC) Group Meeting during 2001.
		Swarna Sheetal	Developed by crossing the elite germplasm lines Hot Season and Long Green	Fruits medium sized, greenish white without any placental hollowness; early maturing and	250-300 q/ha	Released by the Institute Variety Release Committee during 1999 and recommended for cultivation

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Crop	Botanical name	Name of Variety	Pedigree	Important Characters	Yield Potential	Area and Period Recommended for Cultivation
			follwed by pedigree and recurrent selection.	tolerant to powdery mildew.		in Jharkhand, Bihar, Uttar Pradesh, Maharashtra, Delhi, Andhra Pradesh, Himachal Pradesh and Kerala.
Ridge gourd	*Luffa acutangula*	Swarna Manjari	Developed by crossing the germplasm lines CH-15 and CH-4 followed by selection in segregating generations.	Fruits medium-long, highly ridged, green, fibreless, soft; tolerant to powdery mildew.	180-200 q/ha.	Released by the Institute Variety Release Committee during 1999 and recommended for cultivation in Jharkhand, Bihar,Orissa, Tamil Nadu, Maharashtra and Andhra Pradesh; also identified for release in Sub humid Sutlej-Ganga alluvial plain by AICRP (VC) Group Meeting during 2001.
		Swarna Uphar	Developed through hybridisation between CH-5 (Jaipuri-a Rajasthan collection and CH-3 (a local collection from Andhra Pradesh) followed by pedigree selection in segregating generation.	Fruits medium sized (200 g), low ridged and fibreless at edible stage; suitable for growing during summer and rainy season.	200-300 q/ha.	Released by the Institute Variety Release Committee during 2001 and recommended for cultivation in Jharkhand, Bihar and adjoining areas.
Parwal	*Trichosanthes diocia*	Swarna Rekha	Developed through clonal selection from germplasm of Champaran district of Bihar.	Fruits elongated, striped green and soft seeded.	150-200 q/ha.	Released by the Institute Variety Release Committee during 1995 and recommended for cultivation in Jharkhand, Bihar, Orissa, West Bengal and parts of Eastern Uttar Pradesh.
		Swarna Alaukik	Developed through clonal selection from germplasm collected from Bhagalpur district of Bihar.	Fruits elongated having long shelf life; suitable for sweet preparation.	200-250 q/ha.	Released by the Institute Variety Release Committee during 1995 and recommended for cultivation in Jharkhand, Bihar, Orissa, West Bengal and parts of Eastern Uttar Pradesh.
French bean (Bush type)	*Phaseolus vulagris*	Swarna Priya	Developed through pure line selection from the NBPGR germplasm line EC-76402.	Plant growth vigorous; pods fleshy, flat green having good cooking quality; maroon coloured dried bold seeds are highly suitable for Rajma preparation.	120-140 q/ha.	Identified for release at 19th AICVIP workshop during 2001 for the regions of Sikkim, Meghalaya, Manipur, Nagaland, Mizorum, Tripura, Arunachal Pradesh, Western Madhya Pradesh, Maharashtra and Andaman and Nicobar islands (Anon.,2001 b).
French bean (Pole type)	*Phaseohlus vulgaris*	Swarna Lata	Developed through pure line selection from NBPGR germplasm line EC-94498.	Pods fleshy, round and stringless having good cooking quality and preferred by local consumers.	120-140 q/ha.	Identified for release at 19th AICVIP workshop during 2001 for Jammu Kashmir, Himachal Pradesh and hills of Uttar Pradesh (Anon.,2001 b).
Tomato	*Lycopersicon esculentum*	Swarna Lalima	Determinate variety developed through pure line selection from NBPGR germplam line EC-339074.	Resistant to bacterial wilt and bears deep red, round fruits (125 g) having TSS 4° brix.	500-550 q/ha.	Released by the Institute Variety Release Committee during 2001 and recommended for cultivation round the year in Jharkhand, Bihar and adjoining, areas where bacterial wilt is a serious problem in tomato cultivation.

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Crop	Botanical name	Name of Variety	Pedigree	Important Characters	Yield Potential	Area and Period Recommended for Cultivation
		Swarna Naveen	Indeterminate variety developed through pure line selection from NBPGR germplam line EC-386019.	Resistant to bacterial wilt; fruits medium sized, oblong, deep red (60 g) having TSS (5° brix) and longer shelf life.	600 q/ha.	Released by the Institute Variety Release Committee during 2001 and recommended for cultivation round the year in Jharkhand, Bihar and adjoining, areas where bacterial wilt is a serious problem in tomato cultivation.
		Elite line CHRT-4	Determinate fresh market variety developed through selection in segregating generation of an Australian hybrid variety.	Fruits very firm, round, rich in red colour pigment lycopene; having high pulp content;suitable for long distance transportation.	450-500 q/ha.	Suitable for cultivation during autumn-winter season in Jharkhand, Bihar and adjoining areas.
		CHTH-1	Determine fresh market hybrid is the cross between the germplasm lines Ch-3 and CHRT-4.	Fruits deep red coloured, round, firm with very high pulp content; highly suitable for transportation to distant markets.	700-800 q/ha.	Indentified for release at 20th AICRP (VC) Group Meeting during 2002 for Punjab, Tarai region of U.P, Bihar and Jharkhand.
		Elite line CHDT-1	Determinate variety developed through pure line selection from exotic germplasm.	Fruits red, round with pointed tip at blossom end; suitable for fresh market use.	600-700 q/ha.	Suitable for cultivation in Jharkhand, Bihar and adjoining states.
		Elite line CHDT-2	Determinate variety developed through pure line selection from exotic germplasm.	Fruits bigger sized, pear shaped, deep red coloured on ripening having high TSS and pulp content; suitable for processing purpose; better than the old processing variety Roma.	700-750 q/ha.	Suitable for cultivation in Jharkhand, Bihar and adjoining states.
		Elite line CHIDT-1	Indeterminate variety developed through pure line selection from exotic germplasm.	Fruits oval shaped, medium sized, red coloured; duration of harvest is more.	650-700 q/ha.	Suitable for cultivation in Jharkhand, Bihar and adjoining states.
Sponge Gourd	*Luffa cylindrica*	CHSG-1	Developed through pure line selection from locally collected germplasm.	Fruits medium round and whitish green in colour.	200-250 q/ha.	Suitable for cultivation in Jharkhand, Bihar and adjoining states.
		CHSG-2	Developed through pure line selection from locally collected germplasm.	Fruits medium long, dark green in colour and soft at edible stage.	250-300 q/ha.	Suitable for cultivation in Jharkhand, Bihar and adjoining states.
Dolichos bean	*Lablab purpureus*	Elite line CHDB-15	Photoinsensitive variety developed through selection from locally collected germplasm.	Pods bold, flat and green coloured suitable for off-season cultivation during summer and rainy season.	140-180 q/ha.	Suitable for cultivation in Jharkhand, Bihar and adjoining states.
		Elite line CHDB-1	Photosensitive variety developed through pure line selection from locally collected germplasm.	Pods flat, green fleshy in clusters in long inflorescence profusely; suitable for growing during autumn-winter season.	250-300 q/ha.	Suitable for cultivation in Jharkhand, Bihar and adjoining states.
		Elite line CHDB-2	Photosensitive variety developed through pure line selection from locally collected germplasm.	Pods bold, flat, fleshy green having light violet margins in long inflorescence profusely; suitable for growing during autumn-winter season.	250-300 q/ha.	Suitable for cultivation in Jharkhand, Bihar and adjoining states.

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Crop	Botanical name	Name of Variety	Pedigree	Important Characters	Yield Potential	Area and Period Recommended for Cultivation
Garden pea	*Pisum sativum*	Elite line CHPMR-1	Mid season variety developed through pure line selection from germplasm collected from IIHR, Bangalore.	Pods and seeds dark green in colour with high shelling percentage (more than 50 per cent); highly resistant to powdery mildew.	120-140 q/ha.	Suitable for cultivation in Jharkhand, Bihar and adjoining states.
Vegetable Cowpea	*Vigna unguiculata*	Elite line CHCP-1	Developed through pure line selection from locally collected germplasm.	Pole type in growth habit; pods straight, long (30 cm), smooth, fleshy and whitish green in colour.	300-350 q/ha.	Suitable for cultivation in Jharkhand, Bihar and adjoining states.

found to be very promising at different testing centres (Anon., 2001 a).

Results and Discussion

A total of 16 varieties including Swarna Roopa in litchi; Swarna Mani, Swarna Shree, Swarna Shyamli and Swarna Pratibha in brinjal; Swarna Poorna, Swarna Ageti and Swarna Sheetal in cucumber; Swarna Manjari and Swarna Uphar in ridge gourd; Swarna Rekha and Swarna Alaukik in parwal; Swarna Priya in bush bean, Swarana Lata in pole bean and Swarna Lalima and Swarna Naveen in tomato have been developed through selection, hybridisation and mutation breeding. In addition, 3 elite lines in fruits and 18 in vegetable crops have also been evolved which are being evaluated under AICRP (vegetables and fruits) spread all over the country and the same have been discussed in Table 1 (Rai *et al.*, 1997 a & b; Rai *et al.*, 1998 and Rai, 2001).

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Evaluation of Genetic Resources of Groundnut

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Two hundred seventy Spanish bunch groundnut genotypes were assessed for pod yield against six different elite varieties viz. AK-12-24, JL-24, TAG-24, OG-52-1, Girnar-1 and ICGS-11 in Augmented Design under paddy fallow during *rabi*, 1999-2000. There was no significant difference among blocks and as well as checks. The variety TAG-24, among the checks registered highest mean pod yield/plant, Seven test entries viz. ICGS-387, 1931, 2499, 3317, 3336, 3345 and 6474 showed higher pod yield/plant against best check variety, TAG-24.

Key words: Genetic Resources, Germplasm, Groundnut

Groundnut is one of the most important crops grown in India for edible oilseed production. It is grown over an area of 8.6 million hectares with a production of about 8.2 million tonnes. Efforts have been made to evaluate, characterize, preserve and catalouge the genetic resources of groundnut. Improvement of seed and oil yield in this crop to meet the increasing demand is foremost. Hence, there is a need to intensify efforts to search for appropriate donors for utilization in the location specific breeding programme. In the present paper attempts have been made to evaluate the genetic resources of groundnut maintained at this centre to assess their potential use in cultivar development programme for rice based groundnut cropping system.

Materials and Methods

Two hundred and seventy accessions of groundnut along with six check varieties were evaluated in Augmented Design during *rabi* 1999-2000 at Out-reach centre of National Research Centre for Groundnut, Bhubaneswar. The accessions were grown in three rows of 5 m bed with plant to plant and row to row spacing of 10 x5 cm., respectively. NPK were applied @ 20:40:40 at the time of sowing. Standard agronomic practices were followed and plant protection measures were adopted as and when required. Observations were recorded on 5 competitive randomly selected plants for pod yield/ plant at harvest. Data was analysed according to Agrawal and Sapra (1995). Two hundred and seventy test entries were equally distributed to six blocks containing 45 entries per block. Six different checks namely AK-12-24, JL-24, TAG-24, OG-52-1, Girnar-1 and ICGS-11 were randomly distributed in each block. Thus, total plots/block were 51 (45 test entries and 6 check entries). Total number of plots in six blocks were three hundred and six.

Results and Discussion

Mean pod yield/plant of six different checks over the block and ANOVA have been given in Table 1 and 2, respectively. No significant difference was observed among the blocks and as well as checks (Table 2). Since, there is no block effect on the test entries, observed value of a test entries will be the actual performance of a particular genotype. Observed pod yield/plant of 270 test entry and different standard errors have been shown in Table 3 and 4, respectively. TAG-24 registered highest mean pod yield/plant (12.0) among the checks and standard error between check mean and variety yield is 2.36. Since, there is no block effect highest check mean value (12.0) along with standard error (2.36) has been opted here as criteria for selecting better performing genotypes on the basis of observed pod yield/plant without considering their block. Seven genotypes (Table 5) out yielded than best check mean value.

Table 1. Mean pod yield/plant (gm) of six check varieties over blocks

Sl. No.	Checks	Mean pod yield/plant (gm).
1.	Ak-12-24	8.9
2.	JL-24	10.0
3.	TAG-24	12.0
4.	OG-52-01	11.3
5.	Girnar-01	10.9
6.	ICGS-II	10.8

Table 2. ANOVA for check varieties

Source	d f	MSS	F value
Block	5	5.95	1.44
Checks	5	6.67	1.61
Error	25	4.12	
Total	35	4.75	

Table 3. Observed pod yield/plant (gm) of 270 test entries in six different blocks

Block1		Block2		Block3		Block4		Block5		Block6	
ICG No.	Yield	ICG No.	Yield	ICG No.	Yield	ICG No.	Yield	ICG No.	Yield	ICG No.	Yield
45	8.8	1517	10.0	3317	16.8	4069	6.4	4893	12.0	6679	3.0
183	10.0	1537	10.0	3327	10.0	4071	10.0	6027	10.8	6710	6.8
317	9.6	1538	6.8	3336	21.2	4075	8.4	6028	7.0	6769	8.2
372	6.0	1571	6.4	3345	15.0	4078	9.4	6030	8.9	6823	8.0
387	14.5	1572	7.8	3354	10.0	40.83	10.6	6035	8.8	6906	8.0
1064	10.4	1750	7.8	3369	4.4	4084	13.0	6038	10.4	3242	8.0
1102	11.6	1834	10.0	3388	12.4	4102	9.2	6042	8.1	3272	8.0
1103	13.6	1826	6.0	3383	7.2	4091	10.0	6040	7.2	3264	8.4
1135	11.6	1834	10.0	3388	12.4	4102	9.2	6042	8.1	3272	8.0
1204	8.0	1837	8.8	3409	12.8	4104	4.0	6058	7.0	3273	9.0
1212	9.2	1839	6.8	3438	11.6	4107	9.2	6069	10.0	3287	6.0
1214	11.2	1856	12.0	3463	10.0	4112	7.4	6104	10.8	3298	5.2
1215	8.0	1859	11.0	3469	12.0	4114	6.0	6105	8.0	3630	5.6
1235	12.4	1873	9.6	3491	6.4	4117	7.6	6166	5.6	3653	5.6
1259	11.9	1880	9.6	3495	8.4	4118	12.0	6168	11.2	3660	7.6
1315	11.2	2220	11.6	3500	4.8	4518	7.0	6172	6.8	7018	8.4
1330	10.2	2221	8.0	3537	8.0	4549	6.0	6174	9.0	7022	12.0
1331	10.0	2395	6.8	3555	12.0	4551	12.0	6176	7.0	7029	6.6
1338	9.2	2499	16.4	3569	7.6	4563	6.0	6177	5.6	7036	9.2
1347	10.0	3028	10.8	3572	8.1	4565	6.4	6178	4.4	7037	10.6
1353	10.4	3098	9.6	3575	12.0	4570	5.6	6117	9.6	7041	10.4
1354	10.8	3100	5.6	3606	12.4	4571	4.8	6238	4.8	7044	11.6
1355	12.0	3106	6.4	3613	11.0	4588	6.0	6270	8.0	11618	7.0
1358	10.0	3158	10.4	3616	12.0	4593	6.0	1917	12.0	11645	8.0
1361	9.6	2028	6.4	3617	9.6	4594	13.6	1922	9.8	11663	6.4
1365	9.2	2038	5.2	3618	10.8	4600	6.8	1923	8.8	11684	4.8
1391	8.0	2055	12.8	3621	4.0	4603	7.0	1930	7.2	11748	7.6
1404	10.8	2061	9.0	3622	6.0	4604	8.0	1931	14.5	11749	8.8
1407	12.0	2067	9.2	3625	6.0	4606	6.0	1967	10.8	11948	8.0
1424	12.0	2077	8.0	3527	8.0	4607	8.0	1982	7.6	11953	8.0
1912	8.8	2080	10.0	3723	10.0	4612	9.6	6320	10.4	12115	5.2
1916	12.0	2081	9.0	3727	7.6	4626	10.6	6362	10.8	12121	5.0
1449	6.0	2087	9.2	3740	10.4	4635	3.6	6380	9.0	12126	8.4
1451	9.6	2089	7.0	3746	9.6	4636	7.2	6473	8.4	12305	5.0
1480	10.8	2099	10.0	3575	8.4	4637	6.4	6474	14.5	12312	4.0
1487	10.6	2107	7.6	3762	16.0	4642	4.4	6486	5.2	2044	3.6
1489	9.2	2119	12.0	3765	10.4	4660	8.8	6503	10.0	2412	6.6
1491	11.2	2132	5.2	3772	12.8	4661	6.0	6508	10.8	6497	4.0
1496	8.4	2152	5.0	3773	12.0	4574	11.0	6573	8.0	6499	6.0
1507	6.8	2176	7.0	3774	6.8	4686	6.0	6595	5.0	6529	4.0
1509	4.0	2179	5.0	3785	9.0	4690	3.6	6617	9.2	6658	3.0
1510	2.	2193	10.8	3823	10.0	4691	5.2	6625	9.0	1427	12.2
1511	8.0	2194	6.0	4038	10.8	4702	6.6	6630	6.0	1437	11.6
1512	7.0	2196	10.0	4043	6.0	4708	9.2	6676	8.0	2674	9.0
1513	8.0	2210	10.4	4044	8.0	4710	6.4	6677	8.0	3698	6.4

Table 4. Standard error for different components

Sl. No.	Components	S.E. Value
1	Between two check means	1.17
2	Between variety yield and check mean	2.36
3	Between yield of two varieties	2.87

Table 5. Promising genotypes against best check

Sl. No.	Genotypes	Observed Pod Yield/Plant
1	ICGS-387	14.5
2	ICGS-1931	14.5
3	ICGS-2499	16.4
4	ICGS-3317	16.8
5	ICGS-3336	21.2
6	ICGS-3345	15.0
7	ICGS-6474	14.5
8	TAG-24 ± S.E. (Best check)	12.0 ± 2.36

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Genetic Diversity and Variability in Exotic Winter and Facultative Wheat Germplasm under Semi-Arid Condition

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Magnitude and nature of genetic divergence was assessed in 69 exotic winter and facultative wheat germplasm using non-hierarchical Euclidean cluster analysis for different traits. The accessions were grouped into eight clusters. Cluster V was most divergent as well as early flowering. Cluster I was the best for yield while Cluster VII for test weight. Cluster II and VII were highly diverse from each other while Cluster VI and VIII were closely related. Geographical diversity did not relate to genetic diversity.

Key word: Cluster analysis, Facultative wheat, Genetic divergence, *Triticum aestivum*, Wheat, Winter wheat

Wheat (*Triticum aestivum* L. em. Thell.) is the most important winter cereal crop of India. During 1999-2000, India produced 75.2 mt of wheat and ranked as second largest producer in the world. North western hills of India constitute about 4.2 per cent of wheat area and 2.4 per cent of the total production of India (Jag Shoran *et. al.*, 1995). Around 82 per cent area in this part of the country is under rainfed conditions and productivity of wheat is around 16 q/ha, which is quite low as compared to the national average of 27 q/ha. However, the cool climate and comparatively longer crop season in hills are congenial to harvest high yields with suitable genotype and matching agro-technology. The climatic conditions of North-Western Himalayas of India are ideally suited for growing the winter and facultative wheat, which otherwise cannot be grown in plains owing to their specific vernalization requirement. Winter and facultative group of wheat are considered to possess genes for may desirable attributes and high yield and efforts are on to harness these through hybridisation.

The more diverse the parents within over all limits of fitness, the greater are the chances of obtaining higher amounts of heterotic expression in F1's and broad spectrum of variability in segregating generations. Mahalnobis D^2 statistics has been used for identifying diverse parents for hybridization in spring wheat (Bhatt 1970, Singhal and Upadhyaya 1977, Jatasra and Paroda 1978 and Garg and Gautam 1997) and in winter wheat (Jag Shoran and Tandon 1995 and Kant *et. al.*, 1999). Multivariate analysis based on Mahalnobis D^2 statistics and canonical analysis has the limitations for classifying huge germplasm collections (Arunachalam 1981). However, non-hierarchical Euclidean cluster analysis suggested by Beale (1969) and Sparks (1973) is capable of overcoming the limitations of Mahalnobis D^2 statistics. Utility of this analysis for choosing parents for generating good segregants, though enormous, yet has received very little attention. The present study was undertaken to study the nature and extent of genetic variability and divergence in the 69 germplasm lines under semi-arid conditions and to identify donors for different characters, for their use in developing genotypes which can suit well under rainfed conditions.

Materials and Methods

Sixty six winter and facultative wheat germplasm lines and six checks viz., Bez, Seri, BLL, GRK, ATAY 85 and VL 616 were selected for genetic divergence studies. All winter and facultative wheat lines were of exotic origin and were selected from International nurseries supplied by CIMMYT, Mexico. Total sixty nine germplasm lines including checks were evaluated under semi-arid, low fertility ($N:P_2O_5:K_2O$:: 60:30:0 kg/ha) conditions at Vivekananda Parvatiya Krishi Anusandhan Sansthan (VPKAS) Experimental Farm, Hawalbagh, Almora, India (29^0 36'N and 79^0 30'E and 1250 m) during winter season of (*rabi*) 1997-98.

The experiment was conducted in an augmented block design with 2 replications of checks. The plot size comprised two rows, 3 m long, with inter-and intra-row spacing 0.3 and 0.1 m respectively. The crop received 30 kg/ha N and 30 kg/ha P_2O_5 as basal dose and 30 kg/ha N as top dressing after first irrigation. In additional to a total 414.6 mm rainfall the crop received, one supplemental irrigation (50 mm) was provided. The crop was not protected against leaf rust (*Ustilago nuda tritic*) and powdery mildew (*Erysphi tritici*) as the disease appeared in traces.

Observations were recorded on four quantitative characters namely days to 50 per cent heading, plant height (cm), grain yield (g/plot) and test weight (g). Five competitive plants were randomly selected for recording observation on plant height. Rest of the observations were recorded on plot basis. Genetic divergence was studied using Non-Hierarchical Euclidean cluster analysis (Beale, 1969 and Spark, 1973). The SPAR1 package developed by Indian Agricultural Statistical Research Institute (IASRI), New Delhi, was used for classifying the genotypes.

Results and Discussion

The range of various characters exhibited wide differences (Table 1) in the winter and facultative wheat germplasm, which indicates ample scope for genetic manipulation. Further variability can be incorporated in other characters

Table 1. Range, mean, check mean and coefficient of variation for different in winter and facultative wheat germplasm

Character	Days to 50% flowering	Plant height (cm)	Grain yield (g/plot)	Test weight (g)
Mean	154.30	115.64	699.71	35.93
Range	116-190	90-150	410-1200	25.1-46.5
Best check mean	122	98	880	46.5
CV	10.42%	10.51%	22.16%	12.85%

by hybridization among distant accessions. A number of research workers (Griffing and Lindstrom, 1954; Moll *et al.*, 1962; Arunachalam, 1981) have emphasized classificatory procedures for identifying distant genotypes which can be used as donor parents. Non-Hierarchical Euclidean analysis has been found quite useful for estimating the genetic divergence utilizing unreplicated data in larrge germplasm collection. In this method all the variables are converted to single inde of similarity in the form of principal component. The eigen vectors, roots and associated variances have been given in (Table 2). The maximum variation of 52.73 per cent was explained by first latent vector followed by second vector (25.30%). Thus around 78% of variation was explained by first two vectors and rest by other two.

Non-Hierarchical Euclidean analysis proved useful

Table 2. Eigen root vector, eigen roots and associated variances for various components in winter and facultative wheat germplasm

	Eigen root vector			
Characters	1	2	3	4
Days to 50% heading	0.619	-0.0091	-0.540	-0.563
Plant height (cm)	0.149	0.988	0.032	-0.027
Grain yield (g/plot)	-0.058	0.051	-0.755	0.651
Test weight (g)	0.769	-0.114	0.371	0.508
Eigen roots	2.109	1.001	0.606	0.284
% variation	52.73	25.03	15.14	7.10

for estimating the genetic divergence in 69 winter and facultative wheat genotypes, which were grouped in to 8 different non-overlapping clusters (Table 3). The grouping indicated considerable amount of genetic diversity in the germplasm. The appropriate cluster arrangement as determined by F test revealed that the 8 clusters were most suited. Genotypes from 9 different origins were accommodated in the same cluster (III, VI and VII) and thus indicated their close affinity. On the other hand, genotypes developed from the same area were distributed to different clusters. These results indicate that geographical diversity may not necessarily be related to genetic diversity. These findings are in general agreement with the results obtained by Murty and Arunachalam (1966), Bhatt (1970) and Tewari (1970) in different crops. Cluster I is the smallest containing only four accessions which had highest values for grain yield (1045 g/plot). Cluster VIII consisted maximum number of accessions (17) and had highest value for days to 50 per cent heading (168.18). Cluster II contained 8 accessions, which had lowest values for plant height (100 cm), grain yield (566.25 g/plot) and test weight (30.45 g). Cluster V and VII both consisted of 6 accessions each which had lowest value for days to 50% heading (126.67) and highest value for test (43.21 g) respectively. Cluster III consisted of 7 accessions, which had highest value for plant height (137.86). All clusters have exotic strains suggesting wide spectrum of genetic diversity among the germplasm.

The average inter- and intra-cluster distance are presented in Table 4, which provide an index of genetic diversity among and within the cluster. The generalized

Table 3. Characters mean in different clusters in facultative and winter wheat germplasm

Characters	I(4)	II(8)	III(7)	IV(11)	V(6)	VI(10)	VII(6)	VIII(17)
Days to 50% heading	133.00	166.62	153.57	149.45	128.67	164.20	133.00	168.18
Plant height (cm)	111.25	100.00	137.86	114.09	102.17	115.00	125.00	117.71
Grain yield (g/plot)	1045.00	566.25	785.00	811.82	768.33	573.00	827.50	603.53
Test weight (g)	37.60	30.45	35.87	36.22	41.47	38.57	43.21	31.88

Figures in parenthesis indicate the number of accessions

Table 4. Average inter-cluster and intra-cluster distance D. values among 9 clusters in winter and facultative wheat germplasm

	1	2	3	4	5	6	7	8
1	0.921							
2	4.111	1.049						
3	3.290	3.561	1.039					
4	1.858	2.534	2.051	0.982				
5	2.125	3.564	3.544	2.001	1.164			
6	3.629	2.150	2.296	1.865	2.825	0.841		
7	2.180	4.346	2.399	2.047	1.974	2.858	0.976	
8	3.836	1.516	2.221	2.033	3.621	1.580	3.649	0.959

intra-cluster distance value ranged from 0.841 (Cluster VI) to 1.164 (Cluster V). Therefore, broadly it can be concluded that relatively less genetic divergence exists in Cluster VI while individuals in Cluster V were genetically more divergent. Maximum inter-cluster distance (4.346) were found between Clusters II and VII suggesting wide diversity between the groups. The crosses between the genotypes from these clusters may give putative transgressive segregants. In contrast minimum distance occurred between Clusters VI and VIII (1.500) indicating close relationship. The genetic diversity among the parents to be included in crop hybridization programme has been greatly emphasized, therefore the inter-cluster distance must be taken into consideration while selecting the parents. The situation also reflected the relative divergence of clusters which allows a convenient selection of group of genotypes for any hybridization progrmme, facilitating better exploitation of germplasm resources. Thus intercrossing between the genotypes of Cluster II and VII may be helpful in developing heterotic combinations to drive desirable recombinants.

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Table 5. Minimum and maximum values for various traits in winter and facultative wheat germplasm

Character	Minimum			Maximum		
	Name	Value	Group	Name	Value	Group
Days to 50% heading	494J6.11/TRAP//1/BOW	116	V	UT 1545.80/ID 13.1 MLT	190	VIII
Plant height (cm)	TAST/SPRW/IT 176.73/7/SOTY/SUT/LER/4/2*/RFN/ 3/FR//KAD/GB/5/TMP 64 BLL/F7223/3/TLLA/2*FR/KAD11	90	II	SA 1684/*MOLOPO61	150	III
	KC 5550 B/GRATSIYAB		V			
Grain yield (g/plot)	MAYA 74/ON//1160/147/3/BB/GLL/4/CHAT /5/ID 13.1/MLT	410	II	MANCH/ITX71A374.4/TAXYI A 10.39, VI/3/74/CB 462/TRAPPER//VONA	1200	I
Test weight (g)	TX71A1039.V 1*3/ANI/1 SDY/OK 78047/3/CTY	25.1	II	SERI	46.5	II

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Strategies for Developing Core Collections of Safflower (*Carthamus tinctorius* L.) Germplasm – Part III. Obtaining Diversity Groups Based on an Information Measure

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Evaluation and passport data collected from a germplasm collection of 3250 safflower (*Carthamus tinctorius* L.) accessions were used to obtain diversity groups based on three different methods. In the first method, 30 diversity groups were obtained by using multivariate cluster analysis followed by further classification into geographical origin and plant types as proposed by Suresh and Balakrishnan (2001). In the second method 13 diversity groups were obtained based on the geographical origin of the accessions. In the third method, the evaluation data were used to compute an information measure (designated as the Length of Encoded Attribute Values or Length of Encoded Attribute Values (LEAV) of the accessions) and this measure was used to divide the whole collection into fourteen diversity groups. Estimates of phenotypic diversity of core samples of size ranging from 5% to 20% of the whole collection were obtained through stratified random sampling from each set of diversity groups obtained by these three methods. The sampling variance of the pooled Shannon Diversity Index (SDI) of 28 descriptors was compared among the three methods of grouping of the accessions. It was found that grouping of the accessions based on the proposed information measure (LEAV) resulted in the least sampling variance. The LEAV index was also used to obtain core samples of required size by ranking the accessions as per the magnitude of this index. It compared better than the core samples obtained through the Principal Component Score method proposed by Noirot et al (1996) in terms of diversity of several qualitative descriptors.

Key words: Core Sample, Information Measure, Safflower, Shannon Diversity Index, Stratified Sampling

One of the important aspects of obtaining a core sample from a large germplasm collection concerns with the sampling strategies that could help in selecting accessions that reproduce the variation for several characters in the whole collection to the maximum possible extent. The sampling strategies are mainly concerned with grouping of accessions into homogenous groups or clusters and selecting sub samples from each group to obtain a pooled core sample. The grouping approaches described could be hierarchical (Hintum, 1995; Peeters and Martenelli, 1989) or non-hierarchical cluster analysis methods using quantitative or a mixture of both quantitative and qualitative descriptors (Spagnoletti Zeuli and Qualset, 1993; Mahajan *et al.* 1996; Harch *et al.* 1996; Bisht *et al.* 1998). Grouping of the accessions based on their geographical origin had also been suggested by several of the authors. The most common method is stratified random sampling to obtain core sample of desired size. Several strategies had also been suggested for deciding appropriate sampling fraction from each group or strata. These methods included proportional allocation, log frequency allocation, square root frequency proportion allocation etc. (Brown 1989, Spagnoletti Zeuli & Qualset, 1993; Mahajan *et al.* 1999; Balakrishnan and Suresh, 2000). Noirot *et al.* (1996) suggested that the accessions could be ranked on the basis of their relative contribution to the overall variance and a desired proportion of top ranked accessions could be selected from each group to constitute the core sample.

In Part I of the present investigation (Suresh and Balakrishnan, 2001), the mean and variance of the pooled Shannon Diversity Index (SDI) were compared by drawing core samples from 30 diversity groups obtained from a large germplasm collection of 3250 safflower accessions. In this approach, multivariate cluster analysis was used to group the accessions into 6 major clusters based on 18 morphological and 10 agronomic characters. These major clusters were further divided into 30 diversity groups based on the geographical origin and plant type of the accessions. Simple random sampling and stratified random sampling with 5 methods of group allocation in the core samples were used to compare the diversity of the core sample with that of the whole collection. In the present investigation two more schemes of grouping of the accessions have been considered. They are (i) grouping according to geographical origin of the accessions and (ii) grouping based on an information measure that quantifies how far each accession deviated from the average density of the whole collection with respect to the set of descriptors. The usefulness of this

measure designated as the Length of Encoded Attribute Values (LEAV index in short) computed for each accession in the germplasm collection was also studied in obtaining core samples by selecting desired percentages of the top ranked accessions on this index.

Materials and Methods

Details on the source data, the list of descriptors and the number of accessions from different geographical regions have been described in Part I of this investigation by Suresh and Balakrishnan (2001). The procedures for obtaining 30 diversity groups (of 3250 accessions) based on multivariate cluster analysis followed by further sub-division into geographical regions and plant types were also described. In the present investigation the grouping of the accessions based on the geographical origin of the accessions was also considered. There were 13 such groups. One more method, grouping the accessions based on an information measure was also considered and the details are explained in the following sections.

LEAV Index:

For each multi-state or qualitative descriptor '*d*' the probability of occurrence of a descriptor state '*m*' of the attribute in the whole collection was evaluated as:

$$p[m,d] = n[m,d] / n[d], \quad ...(1)$$

n[m,d] denoting the number of accessions having attribute state *m* of the descriptor *d*; and n[d], the number of accessions having any known value of the attribute *d*. Based on information theory concepts, the length of the information code that can optimally indicate the possession of descriptor state *m* of attribute *d* is computed as

$$c[m,d] = -\log_e p[m,d] = -\log_e \{n[m,d]/\{n[d]\} \quad ...(2)$$

For each continuous attribute d assumed to be normally distributed with mean *m* and standard deviation *s*, the length of the information code that can optimally indicate the possession of a value *x* by the attribute is given by (Wallace and Boulton, 1968):

$$c[d] = g + (x - \mu)^2/(2\sigma^2) \quad ...(3)$$

Where a distribution normalizing constant *g* is estimated by

$$g = \log_e (\sigma/(K^* \varepsilon)) \quad ...(4)$$

and $K = 1/\sqrt{2\Pi}$. It is assumed that a measurement *x*[d] of the attribute *d* of an accession s is quoted to a least count of ε, i.e. to an accuracy of $\pm\varepsilon$ and that the probability of getting such a measurement form the distribution (μ, σ) is approximately

$$(K^* \varepsilon/\sigma)^* \exp(-(x-\mu)^2/ 2\sigma^2)$$

Each attribute value possessed by an entry in the collection can be regarded as a message about that entry. We consider the length of a message that can convey the description of all *N* accessions as is contained in the N x D attribute values. The optimum method of encoding this message is to use a Shannon-Fano code (Oliver, 1952), where the length of the message required is minus the logarithm of the probability of obtaining the given set of accessions. Assuming that the set of *N* accessions in the whole collection is a random sample from a very large genetic resource, this probability is the product of the probabilities of obtaining each individual accession. Therefore, for each accession *s* in the collection, a message length F[s] that is required to optimally encode all the d attributes of s using the joint density distribution of the whole collection, is then computed using the formula (Wallace and Boulton, 1968):

$$F[s] = \Sigma_{dis}\, c[x[d,s],d] + \Sigma_{Cont} \{g[d] + (x[d,s] - \mu[d])^2/2\sigma[d]^2\} \quad ....(5)$$

where Σ_{dis} means summing over all discrete or qualitative attributes; Σ_{Cont} means summing over all continuous descriptors; x[d,s] indicates any descriptor state *m* of a qualitative attribute *d* possessed by the accession and it indicates the numerical value if *d* is a qualitative attribute. The message length that corresponds to each descriptor (discrete or continuous) can be obtained by substituting appropriate values from (2) and (3) and hence the total message length that corresponds to each of the accessions with a given set of attribute values can be computed from (5). This value is a numerical quantity measured in natural logarithm (or nits in short). When the accessions could be properly grouped based on this value, groups with larger average message length of the accessions would be far removed from the centroid of the whole collection than groups with smaller average message length. In other words, this quantity (LEAV) can be used as an index to quantify the dispersal of each accession from the centroid of the whole collection. For computing the values of LEAV, four descriptors *viz.*, days to 50% elongation, days to primary branch initiation, days to first flowering and days to 50% flowering were omitted as they were directly correlated with 'days to physiological maturity'. One more descriptor *viz.*, 'plant spread' was also omitted, which was closely associated with 'plant growth habit'. Thus 23 descriptors were used for computing the LEAV index. In the present investigation, as the quantitative descriptors were not

normally distributed, they were categorized into class-intervals and these classes were treated as the descriptor states as in the case of a discrete descriptor. Hence the second part on the right-hand side of (5) was not used.

Grouping of the Accessions Based on LEAV

By ordering the computed LEAV for the entries, an optimum strategy for stratification of the accessions was arrived at by dividing the accessions into L strata by finding the stratum boundaries $x_1, x_2,.....x_{(L-1)}$ (subject to the condition $x_0 < x_1 < x_2 < ..... x_L$ where x_0 = min (x) and x_L=Max(x)) such that the pooled variance of LEAV evaluated through the stratification was minimized. Since LEAV could be treated as a continuous variable, the stratum boundaries were fixed by using the Dalenius formula (Jarque, 1981):

$$x_{(h)} = \frac{1}{2}\left\{\left[\int_{x(h-1)}^{x(h)} x.f(x)dx \Big/ \int_{x(h-1)}^{x(h)} f(x)dx\right] + \left[\int_{x(h)}^{x(h+1)} x.f(x)dx \Big/ \int_{x(h)}^{x(h+1)} f(x)\ dx\right]\right\} \quad ...6$$

The values of x_h were computed in an iterative way. Since the optimum number of strata (L) was unknown initially, the process was initiated by dividing the whole distribution into 2 groups and the stratum boundary x, was first fixed. Subsequently, these two groups were further sub-divided in an orderly fashion, obtaining the stratum boundaries in each stage. For the computation purpose, the whole set of LEAV values was arranged in the form of a frequency table with a class-interval of 0.5 to get a continuous distribution. A computer program was developed to interactively divide each larger group into sub-groups. At each stage of partition (which is user defined), the ordered stratum boundaries, the variance of each stratum and the pooled variance computed after the most recent partitioning were made available by the program. Using the program, a larger group was sub-divided if the partition resulted in two sub-groups with much smaller variance than the parent group and/ or if there was an appreciable reduction in the overall pooled variance after the partition. Any partition that did not result in appreciable variance reduction was cancelled and an alternative partition was decided. Using this program the optimum number of strata and the stratum boundaries could be fixed very easily. There were two values that were discontinuous towards the tail of the distribution and they were excluded at the data-input stage. These two accessions were allocated to the last stratum after obtaining the groups.

Diversity Index

The diversity index was computed using the Shannon formula and for computing the diversity index for the numerical descriptors they were converted into appropriate class intervals and each class interval was treated as a descriptor state. The population Shannon Diversity Index (SDI) for each descriptor was computed using the formula : $SDI_i = -\Sigma_j P_{ij} * \log_e (P_{ij})$. A pooled diversity index SDI across all the 28 descriptors was then computed by adding the SDI values for the individual descriptors. Similarly in case of computing the pooled diversity index for a core sample of a given size, the same formula was used by replacing the population proportion P_{ij} with the sample proportion p_{ij} for a given descriptor state.

Estimation of Mean and Variance of the Pooled SDI through Sampling

For obtaining core samples, 4 different sizes were considered. They were approximately fixed at 5, 10, 15, and 20% of the whole collection and were respectively 150, 330, 480, and 660. For drawing samples from each of the diversity groups, stratified random samples were considered. The group sizes in the core sample were fixed according to five different methods and they were explained in Part I of this investigation (Suresh and Balakrishnan, 2001). To estimate the expected value and sampling variance of the pooled SDI, 100 independent random samples of a given size were drawn without replacement from the given data set. It was also ensured that the number of accessions from each group was fixed as per the method of allocation. The sample pooled SDI was computed in each case and also the mean and variance of the pooled SDI was computed over the 100 samples. This procedure was repeated with regard to each of the three methods of grouping the accessions.

Purposive Selection of Core Samples

Apart from obtaining the core samples using the method of random sampling, purposive selection to obtain a higher diversity level in the core sample was also attempted. For this two procedures were followed. In the first method, the principal component scores of the individual accessions were evaluated based on 10 quantitative descriptors. The accessions' contribution to overall variance or generalized sum of squares (GSS)

was evaluated and the top ranking accessions for a desired core sample size were selected (Noirot *et al.* 1996). In the second method, the accessions were ranked in the descending order of their LEAV and the top ranking accessions for a desired core sample size were selected. The SDI values for the individual descriptors in these core samples were evaluated and they were compared using a t-test (Hutcheson, 1970). In addition, a coefficient of similarity proposed by Harch *et al.* (1996) was computed for all possible pairs of accessions in the core samples obtained by these two methods. The relative frequency of pairs of accessions with different degrees of similarity was computed. This frequency pattern was used to assess which of the two methods resulted in core samples with lesser number of probable duplicates.

Results and Discussion

The values of LEAV for the individual accessions in the whole collection were computed. The frequency distribution of LEAV was divided into 78 class intervals with the width of a class interval of 0.5 nits. The stratum boundaries were decided based on Dalenius formula (equ. 6) using the computer program developed for the purpose. This resulted in 14 diversity groups. Also the pooled SDI and the mean LEAV were computed for each group. The relationship between the mean LEAV and pooled SDI is presented graphically in Fig. 1. It is seen from Fig. 1 that the relationship between mean LEAV and the pooled SDI for the groups is nearly linear in case of grouping of the accessions based on the LEAV index. Only in the last few groups, there was same reduction in the pooled SDI. This could be due to reduced group sizes and quite different distribution patterns in relation to the centroid of the whole collection, but resulting in SDI values that were nearer to those of the groups with lesser mean LEAV index. It was quite possible that two different distribution patterns of the descriptor states could still yield SDI values that were nearly equal. In the case of grouping of the accessions according to geographical origin, the relationship between mean LEAV and the pooled SDI for the groups was low and it was intermediate in the case of grouping as per the cluster analysis method.

The results pertaining to stratified random sampling from groups constituted by the three methods are presented in Table 1. It is clearly seen that the sampling variance of the pooled SDI of the core samples obtained from groups formed on the basis of geographical origin of the accessions had larger variance than those obtained from the other two methods for different sample sizes and frequency allocation methods. The stratification of the accessions using LEAV index resulted in only half the number of groups obtained by using the cluster analysis procedure. The results clearly indicated that the

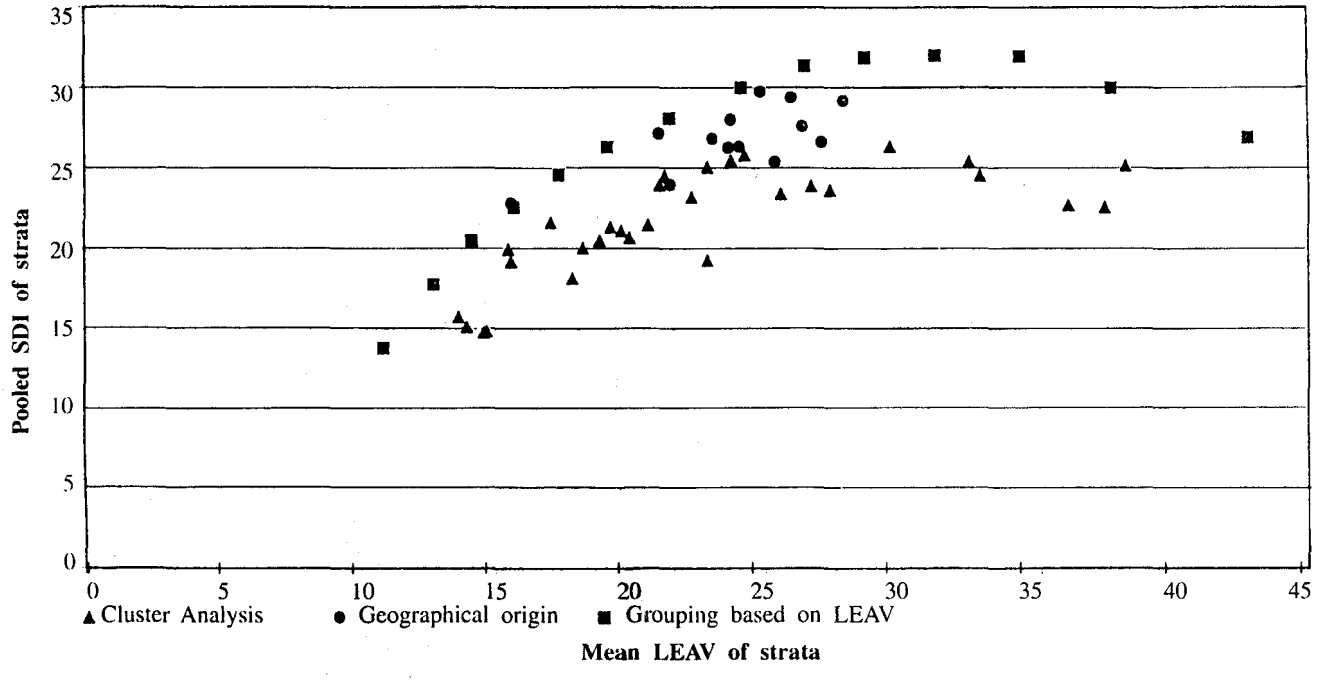

Fig 1. Relationship between mean LEAV and pooled SDI of strata obtained by three methods of grouping the accessions

Table 1. Mean Diversity and its sampling variance for the core samples drawn from the whole collection through stratified random sampling using different stratification procedures

Sl. No.	Sample Size	30 groups based on cluster analysis + geographical origin & Plant type		13 groups based on geographical origin		14 groups based on information measure (LEAV)	
		Mean SDI*	Variance (SDI)	Mean SDI	Variance (SDI)	Mean SDI	Variance (SDI)
1.	Simple random sampling						
	150	25.72	0.3876	Common to all the 3 methods of grouping			
	330	26.00	0.2163	—	—	—	—
	480	26.00	0.1230	—	—	—	—
	660	26.04	0.0900	—	—	—	—
2.	Frequency proportion method						
	150	25.97	0.1336	25.74	0.2899	25.78	0.0610
	330	26.07	0.0509	25.98	0.1152	26.00	0.0123
	480	26.13	0.0376	26.05	0.0865	26.03	0.0098
	660	26.00	0.0289	26.08	0.0499	26.10	0.0063
3.	Square root proportion method						
	150	28.28	0.1068	28.83	0.1694	28.38	0.0283
	330	28.50	0.0581	29.08	0.0676	28.62	0.0155
	480	28.58	0.0228	29.16	0.0313	28.67	0.0053
	660	28.62	0.0211	29.20	0.0258	28.73	0.0060
4.	Log frequency method						
	150	29.22	0.1147	29.40	0.1754	29.91	0.0402
	330	29.57	0.0335	29.68	0.0443	30.22	0.0108
	480	29.60	0.0209	29.75	0.0311	30.19	0.0112
	660	29.60	0.0130	29.62	0.0175	30.28	0.0044
5.	Diversity proportional method						
	150	26.98	0.1218	26.14	0.2777	27.50	0.0354
	330	27.08	0.0420	26.34	0.1563	27.78	0.0160
	480	27.08	0.0393	26.53	0.0807	27.75	0.0100
	660	27.11	0.0237	26.53	0.0709	27.85	0.0083
6.	Equal frequency method						
	150	29.85	0.0885	29.56	0.1350	30.65	0.0367
	330	30.03	0.0260	—	—	30.96	0.0145
	480	30.01	0.0223	—	—	31.07	0.0052
	660	—	—	—	—	31.06	0.0040

* – Pooled Shannon Diversity Index based on 28 descriptors

mean SDI of the core samples drawn from the groups constituted on the basis of LEAV index was comparable from those obtained from the other two methods of grouping. The most striking aspect was that this method yielded core samples whose sampling variance of the pooled SDI was very much smaller than that obtained by the other two methods of grouping.

In Table 2 the diversity measures of the core samples obtained by selecting the top ranked accessions based on the principal component scores evaluated on 10 quantitative descriptors are presented along with those of core samples obtained on the basis of ranked values of LEAV. The principal component scores method was mainly aimed at increasing the diversity of the core samples with respect to quantitative descriptors and the accessions in the core samples accounted for higher percentage of the GSS than those obtained by selecting the top ranked accessions on the basis of LEAV index. However, the core samples obtained by the latter procedure had higher pooled SDI in respect of qualitative and quantitative descriptors combined together. The core samples obtained on the basis of LEAV values had higher pooled SDI with respect to 18 qualitative descriptors and marginally lesser pooled SDI with respect to 10

Table 2. Diversity measures of the core samples obtained by selecting the top ranked accessions based on principal component scores evaluated on 10 quantitative descriptors and the LEAV index

Criterion	% Accessions Selected	%GSS accounted for by the Core Sample	Pooled SDI for 18 qualitative descriptor	Pooled SDI for 10 quantitative descriptors	Total pooled SDI[$]
Principal	Top 10%	37.70	12.82	18.39	31.21
Component	Top 15%	46.30	12.88	18.23	31.11
Score	Top 20%	53.80	13.04	18.13	31.17
Information	Top 10%	18.15	16.13	16.56	32.69
Measure	Top 15%	26.28	16.44	16.81	33.25
(LEAV)	Top 20%	34.03	16.24	16.89	33.13

$ Pooled SDI for the whole collection of 3250 accessions based on 28 descriptors = 26.14

quantitative descriptors. But both the methods yielded core samples that had much higher pooled SDI than that of the whole collection (= 26.14 nits).

In Table 3 the standardized SDI values for the individual descriptors in the core samples obtained by selecting the top ranked accessions based on principal component scores and the LEAV index are presented for a core sample size of 15% of the whole collection. The results indicated that the core samples by either of the two methods had significantly higher SDI than the whole collection with respect to almost all the descriptors. The SDI values in respect of qualitative descriptors were significantly higher in core samples obtained on the basis of LEAV index, except for 'growth habit' for which the SDI value was significantly lower. The SDI values for Shape of lower stem leaf and attitude of OIB to head were statistically at par in both the core samples. Also, in respect of descriptors that had low diversity in the whole collection, the core samples obtained on the basis of LEAV had substantially higher diversity than the whole collection. However, in the case of quantitative descriptors, except in the case of 'internode length' and 'main capitula diameter', the core samples obtained on the basis of principal component scores had significantly higher SDI. This was also evident from the results presented in Table 2, where these core samples had accounted for much higher GSS%. Same trends were observed for the core samples of 10% and 20% size.

Table 4 presents the relative frequencies of pairs of accessions with different degrees of phenotypic similarity for core samples drawn on the basis of ranked values of principal component scores and LEAV. The frequency patterns indicated that nearly 40% of accession pairs had a high degree of similarity (0.7 and above) in the case of core samples obtained on the basis of

Table 3. Diversity measure for individual descriptors in the core samples obtained by selecting the top ranked accessions based on principal component scores (PCS) and the LEAV index (15% sample size)

Descriptor Name	Whole Collection	Core sample based on PCS	Core sample based on LEAV
Shape of lower stem leaf	0.543	0.497	0.570
Margin of lower stem leaf	0.322	0.399	**0.571
Primary head shape	0.376	0.501	** 0.862
Texture of upper LEAVs	0.624	0.738	** 0.862
Shape of upper stem leaf	0.396	0.621	** 0.724
Margin of upper stem leaf	0.535	0.656	** 0.836
No. of Spines on upper stem leaf	0.520	0.638	**0.830
Attitude of OIB to head	0.731	0.918	0.900
OIB cross section shape	0.599	0.745	**1.000
Location of spines on OIB	0.249	0.325	**0.766
No. of spines on OIB	0.535	0.644	**0.964
Length of spines on OIB	0.607	0.727	**0.905
Bracts enclosing head	0.319	0.452	**0.928
Growth habit	0.893	0.921	*0.868
Branch Location on main stem	0.809	0.888	*0.939
Pollen production	0.822	0.903	**0.968
Pappus on the acheme	0.246	0.263	*0.355
Hull thickness	0.638	0.696	*0.796
Days to 50% elongation	0.682	0.839	**0.657
Days to primary branch initiation	0.704	0.809	**0.731
Days to 1st flowering	0.809	0.894	*0.860
Days to 50% flowering	0.808	0.906	*0.874
Days to physiol. Maturity	0.650	0.709	**0.647
Plant spread	0.705	0.870	**0.817
No. of primary branches	0.723	0.857	**0.817
No. of capitula/plant	0.684	0.882	**0.768
Internode length	0.559	0.730	0.691
Main capitula diameter	0.556	0.709	0.702
No. of accessions	3250	490	490

$: Diversity measure expressed as Shannon Diversity Index in standardized form

*,** SDI significantly different at 5% and 1% levels respectively (t-test)

Table 4. Relative frequencies of pairs of accessions with different degrees of similarity in core samples obtained on the basis of higher values of principal component scores (PCS) and the LEAV.

(Relative frequency as % of total number of all possible pairs of accessions)

Range of similarity coefficient	Top 10% (=325) accessions selected based on		Top 15% (=490) accessions selected based on		Top 20% (=650) accessions selected based on	
	PCS	LEAV	PCS	LEAV	PCS	LEAV
0.0-0.1	0.00	0.00	0.00	0.00	0.00	0.00
0.1-0.2	0.00	0.00	0.00	0.00	0.00	0.00
0.2-0.3	0.00	0.03	0.00	0.03	0.01	0.01
0.3-0.4	0.64	2.17	0.51	1.94	0.73	1.28
0.4-0.5	7.53	17.53	7.31	17.15	7.26	13.97
0.5-0.6	19.85	35.12	19.52	37.38	19.23	36.27
0.6-0.7	31.78	28.58	30.97	29.97	31.94	33.55
0.7-0.8	25.29	12.87	26.78	11.12	27.17	12.67
0.8-0.9	12.41	3.42	12.73	2.24	11.81	2.10
0.9-1.0	2.50	0.28	2.18	0.17	1.85	0.15

ranked principal component scores. In contrast, about 15% of the pairs of accessions had a high degree of similarity in the case of core samples obtained on the basis of ranked LEAV. This indicated that core samples obtained by the latter method are likely to contain lesser number of probable duplicates than the former method.

Our main objective was to classify the accessions based on the information contained in N x D attribute measurements. If there were not much diversity in the whole collection, then the accessions would be concentrated in a small region around the centroid of the collection. In such a case any random sample of desired size should constitute a good core sample. There would be scope for classification, if the accessions were distributed non-uniformly in groups and sets of accessions concentrated in a small area around the group centroids in the measurement space. In this context, the attributes' values for each accession in the collection may be regarded as a message about that accession. The messages here nominate the positions in the measurement space of the *N* points representing the attribute values of the entries. Shannon (1948) showed that information needed to record a series of such messages would be minimized if the messages were encoded such that the length of each message was proportional to minus the logarithm of the relative frequency of occurrence of the event what it represented. The message length is greatest when all the frequencies are equal. If the expected density of the points in the measurement space is everywhere uniform, the N x D points can not be encoded more briefly than by a simple listing of the attribute values. However, if the observed distribution of the *N* given points is markedly non-uniform, the average density distribution of the *N* points can be used as the basis for encoding the attribute messages. Given that the measurements for each accession is encoded on the basis of the average density distribution, equation (5) can be regarded as minus the logarithm of the probability that any arbitrary member of the collection would be found to have measurement x[d,s], be it a discrete or a continuous attribute (Wallace and Boulton, 1968). Accessions that have smaller LEAV would be concentrated near the centroid of the collection, whereas those with larger values would be concentrated farther away from the centroid. That is, the accessions that have relatively same values of LEAV are expected to be concentrated in a group or cluster. Hence, instead of the optimally encoded values for each accession about which we are not directly concerned, we could as well make use of the empirical value given by (5) to quantify each accession's dispersal from the centroid of the whole collection as an index for classification. In the present investigation the LEAV index has been viewed as one of the possible criteria for classification of the accessions apart from other criteria cited earlier.

One additional advantage with the proposed information measure as a criterion for classification is that it is computationally simpler than principal component analysis and it reduces to a single value combining several attributes that are both discrete and continuous. The group average for LEAV has a very high correlation with the group diversity when the accessions are stratified on this criterion. Fixing the stratum boundaries on the basis of LEAV values using Dalenius method is much simpler compared to other multivariate techniques where mainly attributes that are continuous in nature are

appropriate. Stratified random sampling of the accessions from strata constituted on the basis of LEAV resulted in pooled SDI with much smaller sampling variance. Purposive sampling of the accessions on the basis of ranked values of LEAV resulted in core samples having significantly higher levels of diversity for many qualitative attributes as compared to core samples selected on the basis of ranked principal component scores. This was due to the fact that LEAV index combined attribute values which were either discrete or continuous, whereas the principal component score was mainly concerned with quantitative descriptors. Again the core samples obtained on the basis of ranked values of LEAV had far less chances of containing duplicate accessions as seen from Table 4.

Conclusion

In the present investigation a new method has been proposed to stratify the accessions in a large germplasm collection based on an information measure that can be expressed as a single valued parameter. An optimum stratification strategy has been suggested to group the accessions based on this information measure. The grouping of the accessions based on this information measure resulted in core samples that had far less sampling variance for the pooled SDI as compared to groupings based on the other two methods. The proposed information measure could also be used as a criterion for purposive selection of core samples by ranking the accessions on the empirical value of LEAV and selecting a core sample of desired size.

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Confirmation of Occurrence of Natural Tetraploid Banana in India

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Exploration in North-eastern states of India has revealed the occurrence of a natural tetraploid of banana in India. Ploidy status was confirmed using flow cytometry while using morpho-taxonomic characterization, Bhat Manohar has been tentatively assigned the genomic status as ABBB. Being male and female fertile, this tetraploid has a good potential for use in breeding programmes.

Key words: Banana, Breeding, Characterization, Flow Cytometry, Genomic Status, *Musa*, Tetraploid

Banana and plantains (*Musa* spp.) are the oldest fruits cultivated by man. Evolution studies of present day bananas indicates its origin to Southeast Asia including Pacific Islands and India is the major centre of origin and diversification. Though South and South-east Asia are well recognized zones of *Musa* diversity, occurrence of large diversity for *Musa acuminata* ssp. *banksii, burmannicoides, siamea, microcarpa, malaccensis, truncata, zebrina* etc. in Malaysia, Thailand, and Indonesia are recorded in literature, while India and Myanmar have a wider diversity for *Musa balbisiana*. Due to movement and natural introgression among *acuminata* and *balbiasiana*, in Northeastern zones of India, a lot of variability occurs with respect to *acuminata- balbisiana* bispecific clones, especially for triploids like AAB and ABB (Singh *et al.*, 2001). Recent explorations conducted by NRCB, Trichy have revealed the occurrence of many unique clones from Northeastern India (Uma *et al.*, 1999-2000). Some of them exhibited tolerance to leaf spot diseases (Selvarajan, unpublished).

Materials and Methods

Three major explorations were conducted in North-eastern states of India including Assam, Arunachal Pradesh, Meghalaya, Mizoram and Tripura during 1998, 1999 and 2000. A total of 88 accessions were collected from various agroclimatic regions of North-eastern states.

The cultivar Bhat Manohar was collected during one of these explorations from the Namsai forest areas of Assam and Arunachal Pradesh border. Along with other accessions it was brought to NRCB field gene bank and planted under the prevailing wet-land conditions. It was evaluated for morphotaxonomic, other qualitative and quantitative traits like tolerance to Sigatoka leaf spot disease.

Assigning Tentative Genomic Status

Germplasm collected during such explorations were initially planted in 'Base Collection Block' where they were assigned tentative genomic groups using the Simmonds and Shepherd's (1955) fifteen character score card. In this, plant is scored from 1 to 5 as per descriptions available in Table 1. All the traits mentioned under *Musa acuminata* were given the score of 1 and those coinciding with *Musa balbisiana* were scored as 5. The variations between these two extreme characters were given the intermediary score based on experience. The total score ranged from 15-75 depending on the genomic groups. The total scores thus obtained were compared with the score card (Table 2) and corresponding genomic status was assigned to a particular accession.

Due to some of the lacunae like discontinuity and ambiguity with respect to score ranges in Simmond and Shepherd's score card, the modified score card developed by Silayoi and Chomchalow (1987) was referred. Hence at NRCB efforts were made to score 435 accessions belonging to various genomes and a modified score card has been proposed (Singh and Uma 1996). The trend of scoring for most of the accessions of a particular genome was used as the score range (Table 2).

Morphotaxonomy

Morpho-taxonomic characterization was carried out using IPGRI's (1996) banana descriptor for 117 traits.

Assignment of Ploidy Status

The ploidy status was determined using meiotic chromosome number and other morphological studies like stomatal density (no. of stomata per unit area),

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Table 1. Morpho-taxonomic scoring system for *Musa* genomic classification

S.No.	Character	*M. acuminata* Score 1	*M. balbisiana* Score 5
1.	Pseudostem colour	More or less heavily marked with brown black blotches	Blotches slight or absent.
2.	Petiolar canal	Margin erect or spreading with scarious wing below not clasping pseudostem	Margin inclosed, not winged below, clasping pseudostem.
3.	Peduncle	usually downy or hairy	Glabrous
4.	Pedicel	Short	Long
5.	Ovules	Two regular rows in each loculus	Four irregular rows in each loculus.
6.	Bract curling	Bracts reflex and roll back after opening	Bracts lift but do not roll back.
7.	Bract shape	Lanceolate or narrowly ovate, tapering sharply from the shoulder.	Broadly ovate, not tapering sharply.
8.	Bract apex	Acute	Obtuse
9.	Bract shoulder	Usually high (ratio less than 0.28)	Usually low (ratio more than 0.3).
10.	Bract colour	Red, dull purple or yellow outside and pink, dull and purple or yellow inside.	Distinctive brownish purple outside bright crimson inside.
11.	Colour fading	Inside bract colour fades to yellow towards base.	Inside bract colour continuous towards base.
12.	Bract scars	Prominent	Scarcely prominent
13.	Free tepal of male	Variably corrugated below flower	Rarely corrugated tip.
14.	Male flower colour	Creamy white	Variably flushed with pink.
15.	Stigma colour	Orange or rich yellow	Cream, pale yellow or pale pink.

Table 2. Modified score card for assigning tentative genomic groups

Genomes	Score card of		
	Simmonds & Shepherd (1982)	Silayoi and Chomchalow (1987)	Singh & Uma (1996)
AA/AAA	15-23	15-25	15-25
AAB	24-46	26-46	26-45
AB/AABB	49	59-63	59-49
ABB	59-63	59-63	59-65
ABBB	67	–	66-69
BB	70-75	70-75	70-75

stomatal measurements (length and breadth) and specific leaf weights.

Confirmation of ploidy status

The confirmation of ploidy was done using Flow Cytometry. For this, 10 cm^2 leaf bits were collected from the freshly and fully opened 3rd leaf from the top. Care was taken to collect the leaves without blemishes or spots caused by major and minor microbes. Such leaf samples were folded in wet paper and sealed in a polybag with labels. The sample were analysed at Vienna, Austria for ploidy using cytometry. The standard cultivars used as reference clones were, Pisang Lilin (2x), Rasthali (3x) and FHIA-01 (4x).

Sample Preparation for Ploidy Analysis Using Flow Cytometry

Ploidy level was analysed with a PA-I flow cytometer (Partec, Munster, Germany). Samples were prepared according to Dolezel *et al.*, (1997) with minor modifications. Briefly 20-30 mg of leaf tissue was chopped with a sharp razor blade in a plastic pertridish containing 0.5 ml Partec HR-A buffer. The sample was filtered through a 50um nylon mesh. Chicken red blood cell nuclei (CRBC) were prepared according to Dolezel *et al.* (2000) and added to the suspension of released nuclei as internal reference-standard. To stain nuclear DNA, 2ml Partec HR-B solution containing DAPI (4',6-diamidino-2-phenylindole) was added to the suspension of released nuclei. To avoid rapid tissue oxidation, 2µl/ml β mercaptoethanol was added to the HR-B solution just before use. The gain of the instrument was adjusted so that the Go/G1 peak of CRBC nuclei was approximately on channel 100. The relative DNA content of *Musa* accessions was then calculated by comparing peak positions of CRBC nuclei and nuclei of the sample. In each sample, a total of 5000-10000 nuclei were analysed. For each plant at least 8 measurements were made with 4

replicates and 2 repetitions. On observation, the accession of interest Bhat Manohar, collected from Namsai forest ranges exhibited very interesting morphological traits unlike other diploid and tetraploid clones.

Results and Discussion

Accession Bhat Manohar was evaluated for 15 characters as given by Simmond and Shepherd score card over three seasons (Table-1). The average score obtained was 68.8 out of the total score of 75. This was compared with the score card by Simmonds and Shepherd (1955) which, however, could not be used for allotting its genomic status specific into any particular group. It was then compared with the score card of Silayoi and Cham Chalow (1987) which too failed to provide a clear cut genomic status. Finally, the score card developed by Singh and Uma (1996) aided the classification of this accession tentatively under ABBB which has a score range of 66-69. The tetraploidy status of the accession was interesting since there are very few reports on the occurrence of banana tetraploids in nature (Simmonds, 1962). Klue teparod (4X), first reported natural tetraploid was later proved to be a triploid (3X) by Jenny *et al.* (1997). In general, tetraploids are less favoured in nature to their gigantic stature and long durations. Bhat Manohar has exhibited partial resistance to Sigatoka leaf spot disease with a YLS (Youngest Leaf Spotted) of more than 11.0 at shooting.

To confirm the tentative assignment of genomic and ploidy status, other preliminary tests were conducted like meiotic studies for chromosomal count, stomatal density, stomatal length, leaf thickness and specific leaf weights. Average leaf thickness of Bhatmanohar measured to be 3.91 as against 3.68-3.71 for triploids, and 3.23-3.38 for the diploids.

The per cent dry weight (83.2) was at par with other known synthetic tetraploids like FHIA-03(82.2), while triploids exhibited a range from 76.45 to 77.82 and diploid from 71.78-79.74. The stomatal density exhibited a lowest of 3.91 at par with other tetraploids (3.82 for FHIA-01 and 3.89 for FHIA-03) while stomatal density was as high as in diploids 40.5 to 43.6 followed by 35.7 to 38.3 in triploids. By nature, tetraploids exhibit a lower stomatal density (Simmonds, 1962) but comparatively larger stomata in size. This was also confirmed by the present observations of 32.3 μ in Bhat Manohar as against 28.4-29.1 μ in tetraploids and the smallest stomata were recorded in diploids (23.8-24.5 μ).

Chromosomal studies revealed the presence of more than 33 chromosomes but since the size of the chromosomes was very small, a final conclusion could not be reached. Hence, the use of Flow cytometry was sought. The results of Flow cytometry (Fig. 1), calculating the relative DNA content by comparing with peak positive of CRBC nuclei and nuclei of the sample confirmed the tetraploidy status of Bhat Manohar.

With all the preliminary and confirmatory tests, ploidy status of Bhat Manohar is determined to be 4x (tetraploid). Based on the morpho taxonomic scoring in comparison with Singh and Uma's score card (2000), the genomic status is tentatively assigned as ABBB. Though there was earlier reports of natural tetraploids, from Papua New Guinea, the genomic status was reported to be AAAB and AABB and Bhat Manohar is the first report of a natural banana tetraploid with ABBB genomic status. Doubts are also raised about the occurrence of pure natural tetraploid of *acuminata* and *balbisiana* origin (Horry *et al.* 1997).

In nature, tetraploids have been less preferred in the course of evolution with no satisfactory reason attached to it. No doubt that the tetraploids are one of the stepping stones in the evolution of present day commercial banana of tetraploidy status. The importance of tetraploids in target breeding was also envisaged as early as 1962 by Simmonds. Though lot of efforts have been diverted in developing a synthetic tetraploid, less emphasis is given for the search for natural tetraploids in the zones of evolution. Many pathogens are also expected to undergo co-evolution in such zones. This situation might have lead to the survival of only such tetraploids which have acquired resistant genes through introgression. Such tetraploids are very useful in breeding for improved triploids and secondary tetraploid. More attention is needed for cartography of natural habitats of wild germplasm, identification of tetraploids from potential co-evolution zones their collection and exploitation in genetic improvement programs.

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Combining Ability for Physiological Traits in Wheat (*Triticum aestivum* L.)

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Combining ability analysis was conducted in 9x9 parental diallel progenies for physiological traits, namely, flag leaf area, peduncle length and grain filling period, in wheat. Peduncle length was observed to be controlled by mainly gca variance while, both gca and sca variances were important for flag leaf area and grain filling period. However, flag leaf area had higher influence of additive gene effect as compared to the non-additive gene, whereas for grain filling period both additive and non-additive genetic components of variation were equally important. The parents DL-803-3, K-8708 and HD-2160 were observed to be good general combiners for flag leaf area, K-68 and HUW-81 for peduncle length and HP-1102, WH-542, HD 2402 and K-8708 for physiological grain filling period. Mean perforamnce of the lines was observed to be related with their gca effects in most of the cases. The cross combinations which showed high sca effects were involved in majority of the crosses both poor combiners and in some cases, one being good and the other being poor combiner.

Key words: Combining Ability, Physiological Traits, Wheat

Synthesis of the physiologically efficient plant type will help to convert maximum soil and solar energy in the form of biological energy and ultimately more productivity. In dwarf and semi-dwarf wheat varieties, the internodes usually remain very short as compared to the tall varieties, while the total numbers of leaves remain more or less same. Therefore due to shorter internodes, particularly in last internode (peduncle) and more numbers of leaves in a limited culm length, the sun-light does not properly penetrate through out the plant. In this situation longer peduncle will help the plant to receive more of sun-light resulting in, increased total photosynthetic area. In addition to the longer peduncle, broader and larger flag leaf with optimum plant foliage will be extremely helpful to receive more sunlight to produce more photosynthates and to translocate them properly to the sink (Barriga, 1979; Mackey, 1982; Singh and Rai 1991).

The final yield/spike of wheat is determined by the number and the weight of the grains it contains. The weight attained by any grain depends on duration of the grain filling period, rate of supply of assimilate to the grain and the rate of incorporation of these into its structure from anthesis onwards. The yield of late sown wheat is reduced mainly due to reduced grain filling period and not due to reduced rate of supply of assimilates. To evolve a physiological efficient and high productive genotype in wheat, the knowledge of the combing ability of the physiological traits would be helpful. Information on the nature of the genetic control of these physiological traits are lacking in wheat. Keeping this in view, the present investigation was conducted to obtain information on the genetic control of flag leaf area, peduncle length and grain filling period in wheat.

Materials and Methods

Nine diverse wheat varieties belonging to different height groups (tall, single dwarf, double dwarf and triple dwarf), were taken for this study. Non reciprocal F_1 crosses in diallel fashion were attempted in 1994-95. The final experiment consisting of 36 F_1s and 9 parental lines was conducted in a randomized block design with 3 replications at the research farm of C.S. Azad University of Agriculture and Technology, Kanpur in 1995-96. Each replication was divided into 5 traits to make more homogenous and compact replication. Each plot had a single row accommodating 15 plants spaced 15cm within and 30cm between rows. Guard rows were around the whole experiment to avoid border effect. Full plant population was maintained and recommended agronomic practices were followed to raise a good crop.

Leaving the border plants, data were recorded on 10 competitive plants/plots. Flag leaf area, peduncle length, 50% physiological maturity (days) and number of days taken to heading (50%) was recorded as grain filling period (days). Plot mean of the different characters were used for statistical analysis. The combining ability analysis was performed based on method II and model I of Griffing (1956).

Results and Discussion

Mean performance: Marked differences were observed in the mean performance of the different characters in the parental lines (Table 2). The varieties namely, HUW-81, DL-803-3, HD-2160, HP-1102 and K-8708 had high

flag leaf area. On the other hand, K-68 possessed low mean value for this trait. The tall variety HUW-81 had the longest peduncle length (51.89 cm) followed by single dwarf variety K-8708 (44.21cm) and tall variety K-68, which measured 43.89 cm, whereas, the variety HD-2160, a triple dwarf, recorded the shortest mean value (25.59 cm) for this attribute. As regards the grain filling period the varieties HD-2204, Hp-1102, K-8708, WH-542 and UP-115, had prolonged grain filing period while HD-2160 had a short grain filling period.

Combining ability: The estimates for the general combining ability mean squares were significant for all the characters studied, whereas these estimates, due to specific combining ability were significant only for flag leaf area and grain filling period, indicating the influence of both additive and non-additive components of variations for controlling the traits flag leaf area and grain filling period, whereas, peduncle length was mainly under the influence of additive gene action (Table 1).

In this investigation, flag leaf area was observed to be controlled by both additive and non-additive components. However, the magnitude of additive component was higher than that of the non-additive one, whereas, Dhonukshe and Rao (1979), and Ilyushechenko (1977) observed higher influence of non-additive component for flag leaf area in wheat.

Peduncle length is also reported to be predominantly under the control of additive genes (Jain and Singh 1976, Mackey 1982, Martin *et al.*, 1979. Singh and Rai 1991, Mann *et al.*, 1995 and Singh and Ravish 1997) as observed in the present investigation, Pandey *et al.*, (1983) suggested that non-additive component was more important for the control of this trait. However, Paroda and Joshi (1970), Sharma *et al.*, (1981), and Singh and Ravish (1997) observed the importance of both additive and non-additive components for peduncle length.

Table 1. Analysis of variance of combining ability for flag leaf area, peduncle length and grain filling period in wheat

Source of variation	D.F.	Mean squares		
		Flag leaf area	Peduncle length	Grain filling period
GCA	8	43.73**	184.26*	5.71**
SCA	36	18.49**	12.56	5.59**
Error	88	2.65	9.61	0.54

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

Grain filling period was under the control of additive and non-additive components of genetic variation, equally. Similar results were also obtained by Singh *et al.*, (1982), Singh *et al.*, (1985) and Virk and Aulakh (1975) in wheat.

Combining ability effects: The positive and significant gca effects were exhibited by DL-803-3, HP-1102, K-8708 and DL-2160, whereas, negative and significant effects were found in UP-115, HD-2204 and K-68 for flag leaf area. Parents, K-68 and HUW-81, both tall cultivars, were good general combiners for long peduncle, while dwarf parents, HD-2204 and HD-2160 were poor combiners (Table 2). The good general combiners for prolonged grain filling period were HP-1102, WH-542, HD2204, and K-8708, while DL-803-3, UP-115, K-68 and HD-2160 were poor combiners.

The mean performance of parents for different characters were observed to be related to their respective gca effects in a majority of the cases. Thus the selection of the lines for a breeding programme could be based on both mean performance and combining ability test. Considering the mean performance of gca effects for all the three characters together, the variety K-8708

Table 2. General combining ability effects and mean performance of nine parents for three characters in wheat

Parent	Flag leaf area		Peduncle Length		Grain filling period	
	Mean (cm)	gca effect	Mean (cm)	gca effect	Mean (cm)	gca effect
K-68	31.43	-3.52**	43.89	5.00**	40.35	-0.74**
HUW-81	50.99	0.03	51.89	6.91**	37.00	-0.17
HP-1102	49.10	1.07*	40.82	-0.37	45.27	0.81**
K-8708	48.89	1.29**	44.21	0.09	43.51	0.49
DL-803-3	50.91	2.78**	35.84	-1.40	43.37	-0.81**
WH-542	40.38	-0.46	39.27	-0.21	40.09	0.77*
UP-115	38.45	-1.85**	41.36	0.01	43.21	-0.58**
HD-2204	42.37	-1.01**	36.42	-2.70**	45.57	0.75**
HD-2160	48.28	1.70*	26.59	-7.12*	34.23	-0.51*
SE (gi)		±0.458		±0.879		±0.221

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

(single dwarf) was found to be best followed by another single dwarf variety HP-1102, whereas, UP-115 was observed to be the poorest for these traits. The varieties DL-803-3, HP-1102, K-8708 and HD-2160 have been intensively used in the breeding programme of this centre and a number of promising lines have been isolated from these varieties.

It is not necessary that parents having high estimates of gca effects would also give high estimates of sca effects (Table 3). In most of the cases it was observed that for almost all the characters, the crosses showing significant and positive as well as high sca effects combined both negative and poor general combiners. Apparently, the parents having low gca effects and a relatively high magnitude of non-additive gene effects and thus resulted in high sca effect when crossed. For instance, the crosses UP-115xK-8708 gave the maximum significant positive sca effects for flag leaf area while, both UP-115 and K-8708 had negative gca effects for this trait. Similar cases were also observed for other traits.

In few cases, the crosses showing significantly positive sca effect combined one good and poor general combiner. In most of the cases, the best F_1s were not cross combinations that showed the maximum sca effects. This may be so as it is a comparison of an absolute and a relative value. The absolute value (performance of F_1s) being similar, the relative values (sca effects) would increase with a decrease in the performance of the base (mean of two parents). The best F_1s had involved one of the high combiners as one of their parents.

The top combiners DI-803-3 and HUW-81 for flag leaf area also showed the best F_1 for this attribute. Thus, the choice of the parents, particularly for heterosis breeding, should be based on combining ability test. The crosses showing sea effects or high F_1 performance involving one good and one poor general combiner, could produce desirable transgressive segregants, if the additive genetic system present in the good combiner and the complimentary epistatic effects in F_1 acted in the same direction to maximise the desirable plant attributes.

Table 3. Top two combiners as parents, F_1S, general combiners and specific combinations for three characters in wheat

Characters	Parents	F_1s	General Combiners	Specific combinations
Flag leaf area	HP-1102	HP-1102xHUW-81	HP-1102	UP-115xWH-542
	HUW-81	UP-115xK-8708	HD-2108	UP-115xK-8708
Peduncle length	HUW-81	HuW-81xK-68	HUW-81	HD-2204xHD-2160
	K-8708	HUW-81xWH-542	K-68	HP-1102xK-68
Grain filling period	HD-2204	HP-1102xHUW-81	HP-1102	K-68xHD-2160
	HP-1102	HP-1102xHD-2204	HD-2204	UP-115xHD-2160
		HUW-81xWH-542		
		WH-542xHD-2160		

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Genetic Diversity in Cowpea [*Vigna unguiculata* (L.) Walp]

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One hundred cowpea genotypes were evaluated for eleven metric characters to quantify the genetic diversity existing among them by using Mahalanobis D^2 statistics. The genotypes fell into eleven clusters. Among the eleven quantitative characters studied, 100-seed weight contributed maximum (75.73%) towards divergence followed by plant height (8.28%) and seed yield (6.30%). Cluster VI had minimum days to first flower opening and days to maturity, and also had maximum number of pods per plant, pod length, number of seeds per pod and seed yield. Cluster IX exhibited lowest means for seed yield, 100 seed weight, number of seeds per pod, pod length, primary branches and plant height. The genotypes from Cluster VI and IX, which have high and low cluster means for the majority of the characters are suggested as parents for hybridization.

Key words: Cluster, Cowpea (*Vigna unguiculata*), D^2, Germplasm, Genetic Diversity

Genetic variability is the basic requirement for any crop improvement programme to be effective. When the existing variability is exploited by way of selection, for further improvement, the breeder has to resort to hybridization to succeed in evolving new recombinants with desirable traits of different genotypes. Accumulation of different desirable traits spread over the diverse genotypes into one genotype is important for the rapid advancement in yield improvement of any crop. To initiate hybridization, the genotypes are to be classified into clusters based on genetic divergence and the extent of genetic diversity between them need to be estimated so that the parents could be chosen from the clusters with wide genetic divergence. The characters for which the clusters excel and the objective of the breeding programme also need to be considered. In the present investigation, genetic diversity in a set of cowpea genotypes was assessed by Mahalanobis D^2 statistics for seed yield and related traits.

Material and Methods

In the present study, 100 cowpea genotypes were selected from those maintained at the All India Coordinated Research Programme (AICRP) on Arid legumes, University of Agricultural Sciences (UAS), Bangalore. These represented collections from different parts of India and Nigeria. The crop was sown in simple lattice design with two replications during summer season of 2000, with a spacing of 60x30 cm. Observations were recorded on ten randomly selected plants in each genotype, from each replication excluding the border plant, for eleven quantitative characters namely, plant height, primary branches, secondary branches, days to first flower opening, days to 50 per cent flowering, days to maturity, number of pods per plant, pod length, number of seeds per pod, seed yield per plant and hundred seed weight (test weight). The analysis of variance was carried out for all the characters individually and then the data were subjected to multivariate analysis of Mahalanobis (1936). The genotypes were grouped into different clusters following Teachers method (Rao, 1952).

Results and Discussion

The analysis of variance (ANOVA) exhibited significant differences among the varieties for all the eleven characters studied (Table 1). Based on D^2 values, 100 cowpea genotypes were grouped into 11 clusters (Table 2). The cluster strength varied from single/ solitary genotype (cluster X and XI) to 25 genotypes (cluster I). The pattern of distribution of these germplasm lines into 11 clusters confirmed the existence of diversity among the genotypes indicated by ANOVA.

Table 1. Analysis of variance for quantitative characters in 100 cowpea genotypes

Source of variation	D.F.	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
Genotypes	99	145.9**	2.09**	5.17**	7.59*	6.02*	10.57*	31.15*	5.68*	5.74*	33.6*	6.41**
Replication	1	-0.03	2.42	0.58	1.44	1.44	6.5	1.74	6.83	1.76	3.23	0.003
Error	99	3.89	0.14	0.48	0.52	0.439	1.91	1.79	0.56	0.68	1.05	0.01
S.E.		1.97	0.37	0.09	0.72	0.65	1.38	1.33	0.75	0.82	1.02	0.11
C.V.		5.11	9.69	9.28	1.32	1.13	1.76	9.27	5.79	7.44	11.05	1.10

X_1 = Plant height; X_2 = Primary branches; X_3 = Secondary branches; X_4 = Days to first flower opening; X_5 = Days to 50% flowering; X_6 = Days to maturity; X_7 = Number of pods/plant; X_8 = Pod length; X_9 = Number of seeds/pod; X_{10} = Seed yield per plant; X_{11} = 100 seed weight

Table 2. Composition of genotypes in cluster

Cluster	No. of Genotypes	Included of Genotypes
I	25	KAB-13,CAS-15,CAP-8,CAS-11,KAP-7, CAP-2, KAB-9, TAP-1, TAP-3, TAS-21, TAP-2, CAS-5, TAP-8,APC-401,APC-966,TVX-944,C-152,APC-455, APC-988, TAS-13, ITTA-958, C-40, MS-2, C-27, C-66.
II	22	A-4-3-3, C-130, APC-217, P-695, EC-394822, ITTA-784, VCP-9, GC-89322, GC-8929, APC-68, C-30, TCM-101-4, Lolitha, Pattambi, A-4-4-1, KAB-12, CAB-6, CAP-6, KAB-32, CAP-4, KAB-36, TA-9, APC-331.
III	21	APC-97C11, CAZC-11, LD-SP, CAZC-3, BDC-547-46, KBC-1, TCM-121-9, APC-121-132-P, TCM-42-1, V-585, V-422, APC-105-TVX-2460, CS-88, CAB-3,CAB-7,CAB-7,KAP-2,TAP-12, CAS-6, TAP-7, TAP-4.
IV	12	GC-2, CA2C-10, TCM-75-3, APC-565-56, V-16, S-488, APC-578-57, APC-946, TAS-12, CAS-8, CAP-13, KAP-2.
V	9	TCM-77-4, CPT-10,ITTA-1010, V-585, V-130, APC-645, CAP-5, KAP-1, KAP-5.
VI	2	APC-855-Sel 46, KBC-2.
VII	3	APC-384, APC-949, TCM-14-1.
VIII	2	APC-748, KAB-3.
IX	2	APC-332, APC-379 (C0-1)
X	1	ITTA Cowpea Black.
XI	1	KAB-2

The average intra- and inter-cluster distances are given in Table 3 and Figure 1. The intra-cluster distance ranged from 0.00 (X and XI) to 363.90 (IX) and did not transgress the limits of any of the cluster distances. Maximum inter-cluster distance (4509.19) was recorded between Cluster II and Cluster IX, revealing that these two clusters were most diverse, followed by Cluster IX and XI (4160.82).

The average cluster mean for different characters (Table 4) showed that the genotypes included in Cluster VII had maximum plant height, Cluster XI had maximum primary and secondary branches. Cluster VI had minimum days to first flower opening and days to maturity in addition to maximum number of pods per plant, pod length, number of seeds per pod and seed yield. Cluster X had maximum 100-seed weight. The Cluster IX exhibited lowest means for plant height, primary branches, pod length, number of seeds per pod, seed yield and 100-seed weight. Based on the earlier reports, heterosis and better recombinants were obtained by crossing parents between clusters of high and low means (Shweta *et al.*, 1972, Usha Kumari *et al.*, 2000). Selection of parents is most critical to isolate desirable recombinants. It can be suggested that for creating variability and to get better heterosis, the genotypes from Cluster VI (KBC-2 and APC-855-sel46) and Cluster IX (APC-332 and APC-379) with high and low cluster means respectively for majority of the characters, may be selected for

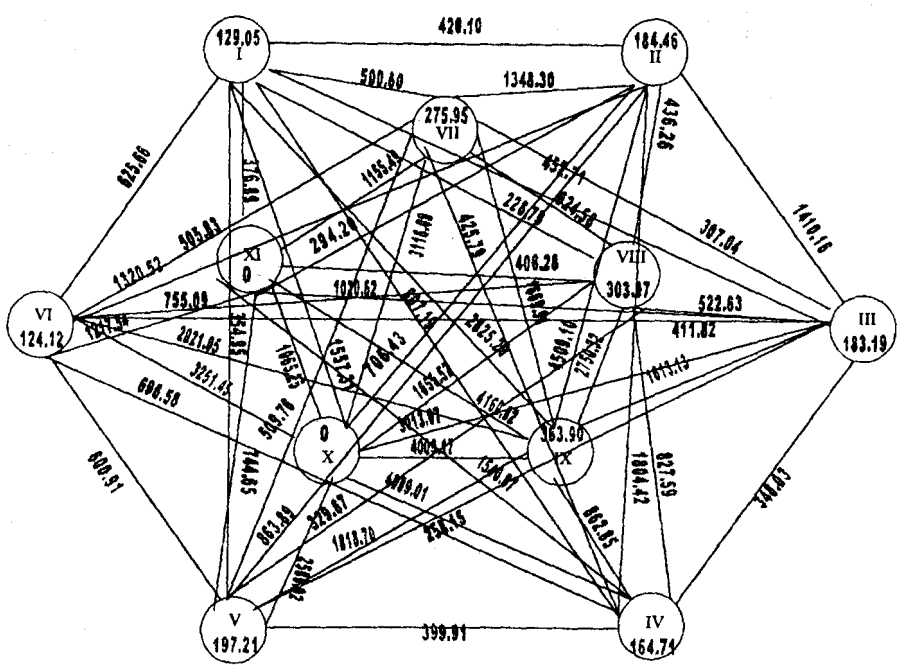

Fig. 1: Intra- and inter-cluster distance (D) in the cowpea germplasm

Table 3. Intra and Inter cluster distance (D^2) in the cowpea genotypes

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	129.05	420.10	452.71	807.19	354.95	625.66	500.60	226.79	2825.29	1557.31	376.89
II		184.46	1410.16	1804.42	863.89	1320.52	1348.30	463.26	4509.10	706.43	294.20
III			183.19	348.03	285.15	411.82	307.04	522.63	1613.13	3013.07	1020.62
IV				164.71	399.91	696.58	425.79	827.59	862.85	4089.01	1540.67
V					197.21	600.91	509.76	329.67	1818.70	2589.92	744.65
VI						124.12	505.83	755.09	2021.05	3251.45	1217.54
VII							275.95	624.58	1669.91	3116.09	1155.49
VIII								303.07	2750.32	1655.52	406.28
IX									363.90	4009.17	4160.82
X										0	1065.25
XI											0

Table 4. Cluster means for 11 characters of cowpea

Cluster	Plant height (cm)	Primary branches (No)	Secondary branches (No)	Days to first flower opening	Days to 50% flowering	Days to maturity	No of pods/plant	Pod Length (cm)	No of seeds/pod	Seed yield (g)	100 seed weight (g)
I	42.06	3.87	7.26	55.10	58.32	79.10	12.63	12.97	10.99	8.16	11.02
II	34.60	4.08	7.47	54.36	58.10	77.36	12.97	13.72	11.36	10.24	12.56
III	41.74	3.55	7.18	53.57	55.60	78.37	13.67	13.71	11.77	10.36	9.36
IV	33.90	3.57	7.27	55.50	58.75	79.16	13.23	11.56	9.98	7.95	8.33
V	33.39	4.14	7.49	54.38	58.05	78.05	13.71	13.39	11.40	6.64	9.78
VI	48.97	4.04	12.25	52.50	56.00	75.25	22.57	15.33	13.39	25.25	9.60
VII	55.90	3.71	9.48	54.50	57.16	79.16	17.85	12.76	11.36	8.11	9.33
VIII	38.27	4.22	7.37	55.00	59.00	79.00	20.50	11.20	9.73	8.84	11.05
IX	26.34	2.64	6.58	55.00	58.25	78.25	21.92	9.435	7.23	6.49	5.75
X	34.40	2.78	5.05	52.50	56.50	78.50	8.25	11.94	8.91	7.64	15.16
XI	39.83	8.25	13.20	56.50	59.50	80.50	12.94	12.75	10.88	8.95	12.06

hybridization, in achieving improvement in yield in cowpea.

In addition to classifying the genotypes into clusters based on genetic divergence, this study also provided information on the characters that contributed maximum to the total divergence among genotypes (Table 5). Test weight was the trait, which contributed for maximum genetic distance. Plant height, seed yield, days to first flower opening, primary branches and number of pods per plant were the next important traits responsible for the divergence recorded. Similar results were observed by Thiyagarajan *et al.*, (1988) in cowpea. Number of seeds per pod contributed minimum to the genetic divergence among the genotypes studied leading to the inference that in general, the variability for this character is less in cowpea genotypes used in this study.

Table 5. Contribution of each character to divergence

Character	Number of times D^2 values scored	% Contribution of each character
Plant height	402	8.28
Primary branches	111	2.28
Secondary branches	18	0.35
Days to first flower opening	123	2.53
Days to 50 % Flower opening	34	0.70
Days to maturity	10	0.2
Number of pods per plant	107	2.20
Pod length	58	1.19
Number of seeds per pod	9	1.18
Seed yield	306	6.30
100 seed weight	3674	75.73
Total	4851	100.00

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Collection and Electrophoretic Characterization of Genetic Diversity in Muskmelon (*Cucumis melo* L.)

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Seed storage protein profiles of muskmelon genotypes were analysed on single seed basis by Sodium Dodecyl-Polyacrylamide gel electrophoresis (SDS-PAGE) under reducing condition. The seed protein of 32 germplasm lines could be resolved into 18 bands distributed in 3 zones A, B and C zone. In general there was very high similarity between genotypes of muskmelon, apart from some minor differences in the B region while the seed proteins of different cucurbit species show polymorphism. This shows that SDS-PAGE is not very effective for distinguishing muskmelon genotypes and it will be desirable to use DNA-based markers.

Key words: Electrophoresis, Muskmelon, Protein

Muskmelon (*Cucumis melo* L. $2n=2x=14$) is one of the most important cucurbits grown as a 'desert crop' throughout the warmer regions the globe. The genus *Cucumis* comprises about 30 species. The place of origin of muskmelon is not known with certainty but as the wild species of *Cucumis* exist in Africa, it is likely that it is originated in the African continent. Secondary centres of origin are now in India, China, Persia and South Russia (Chadha and Lal, 1993).

In India, at present Akola, Ludhiana, Hissar, Modipuram, Anand, Delhi, Faizabad and Durgapur are the centres which are participating in the research programme of muskmelon. By the efforts of these stations, a number of varieties namely Hara Madhu, Punjab Sunehri, Arkajeit, Arka Rajhans, Durgapur Madhu, Pusa Sharbati, Pusa Madhuraas, Punjab Hybrid and Pusa Rasraj etc. have been released by ICAR as reported by Nandpuri (1989) and Ram (1997). Identification of cultivar by examination of morphological features sometime becomes difficult due to limited variation. The problem of cultivar identification has been simplified to a great extent by use of biochemical markers such as protein/isozyme profile (Brewbaker, 1966 and Ladizensky and Hymowitz, 1979). In recent years DNA markers are being used for the identification of plant genotypes (Dwelikat *et al.*, 1993) but there is no work on muskmelon in this direction. The aim of the present work was to investigate the extent of variation in the protein profiles of diverse cultivars of muskmelon.

Materials and Methods

Thirty two lines of muskmelon were collected from muskmelon growing areas of different parts of western Uttar Pradesh. Seed proteins of these genotypes were extracted in the sample buffer (Tris Base, SDS, glycerol and mercaptoethenol) and were subjected to SDS-PAGE in vertical slab gels (Laemmli, 1979). The cotyledon half of single seeds were crushed between folded butter paper with a hammer on metal plates. Sample were defatted with 1ml of petroleum ether in Eppendorf tubes and centrifuged for 10 min at 10000 rpm. Supernatant was discarded and whole process was repeated once again. Finally the supernatant was drained out and residue was dried completely. The defatted seed extract was transferred into a fresh Eppendorf tube and, added with 200 µl of distilled water, 200 ml of (2x) sample buffer and 8 µl of 2 mercaptoethanol in each tube to make 400 µl of 1x sample buffer containing 2% mercaptoethnol. Samples were centrifuged for 10 minute at 10,000 rpm just before loading 10 µl of supernatants in the gel slots. The run was performed at a constant current of 40mA/gel. Afterwards gel was stained in staining solution (0.25%) w/v Commassie Brilliant Blue R 250 + 6% w/v Trichloroacetic acid +18% (v/v) methanol + 60% (v/v) glacial acid. The destaning was performed in NaCl solution (3%) (Sreeramulu and Singh 1995). Gel was washed in distilled water, photographed and electrophoregrams of the seed protein profile were prepared.

Results and Discussion

The protein banding pattern of the muskmelon genotypes were characterised by three distinct zones, namely A, B and C in the increasing order of electrophoretic mobility (Fig. 1). The protein bands were stacked according to their molecular weight i.e. high molecular weight protein in upper region and low molecular weight protein in middle to lower region of the gel, respectively. The 'A'

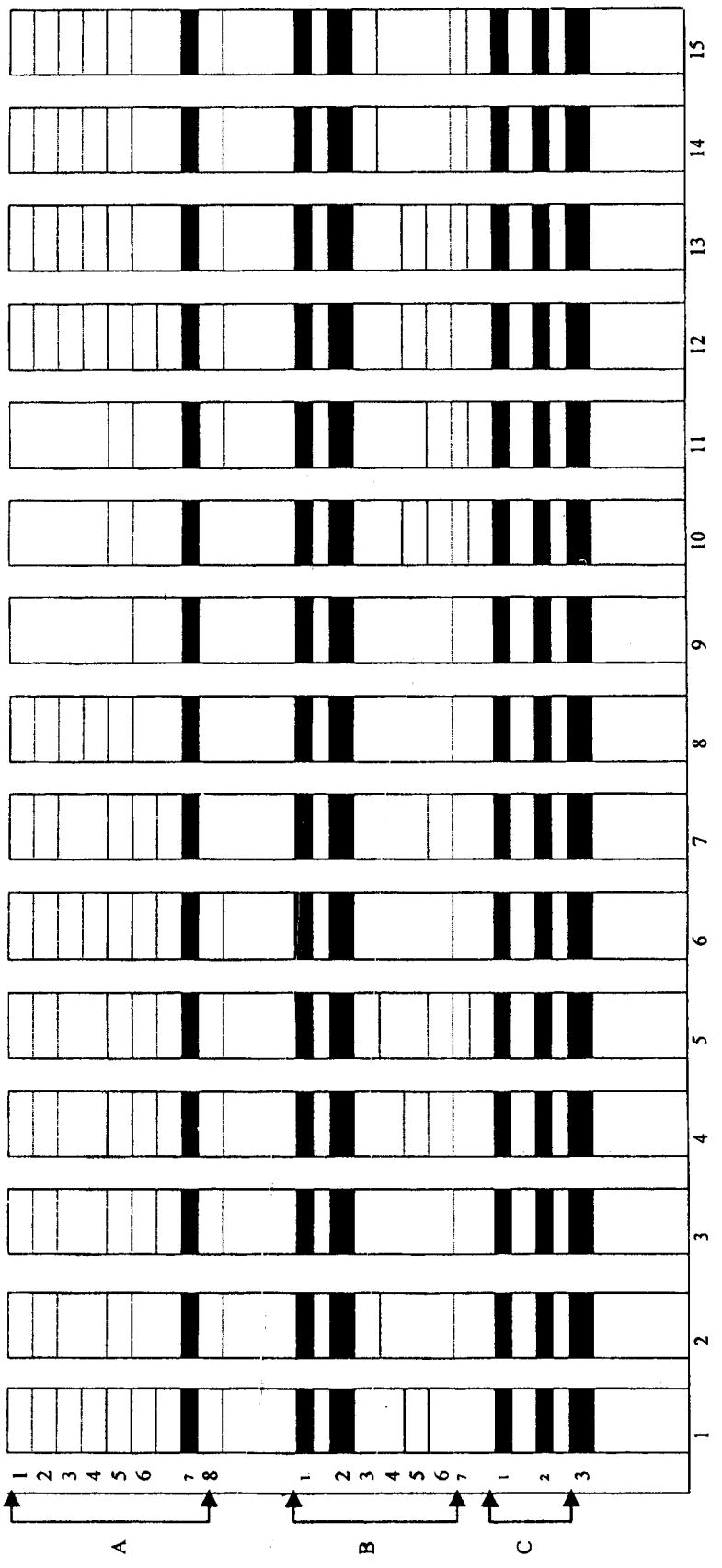

Fig. 1. Schematic diagram of the seed protein electrophoretic banding pattern in some muskmelon genotypes

region comprised of heaviest molecular weight proteins and had eight bands namely, A1-A8. Zone B represented seven bands namely B1- B7 and zone C had three bands namely C1-C3. All the 32 genotypes showed very similar banding patterns in the three zones. Only minor differences were present, particularly in zone B. The similarity index for different pairs of the genotypes is given in Table 1.

The similarity index gave an idea of genetic/ evolutionary relationship between cultivar pairs. The similarity index greater than 90 per cent indicate that two cultivars are very closely related.

Most cultivar pairs had similarity index in a narrow range of 44.0 to 99.9 percent which clearly indicated that all genotypes were closely related as far as their seed storage protein is concerned. The cultivar MM 45-B is very closely related with MM-58 having a similarity index of 94.4 percent, although morphologically they are different. MM-58 is closely related with MM-96-69 (SI.94.4 per cent) while MM-96-69 is similar to MM-96-77 (SI.94.4 per cent), and MM.96-91, MM-96-93, MM96-94, MM96-95, MM-96-96 and MM 96-97 having similarity index of 94.4%

MM-96-82 is closely related with MM96-84 (S.I. 94.4%), MM 96-85 (S.I. 99.9%) MM-96-86 (S.I. 99.9%), MM-96-88 (S.I. 94.4%), MM-96-89 (S.I. 99.9%), MM-96-91 (S.I. 94.4%) MM-96-95 (S.I.94.4%), MM-96-96) (S.I. 94.4%), MM-96-97 (S.I. 94%). MM-96-84 is similar to MM-96-85, MM-96-89, MM-96-92 and MM-96-99 having similarity index of 94.4%.

MM-96-85 is closely related with Mm-96-86 (S.I. 99.9%)s, MM-96-88 (S.I. 94.4%), MM-96-89 (S.I. 99.9%),

Table 1. Protein banding pattern in 32 germplasm of muskmelon

Genotype	Bands																	
	A_1	A_2	A_3	A_4	A_5	A_6	A_7	A_8	B_1	B_2	B_3	B_4	B_5	B_6	B_7	C_1	C_2	C_3
MM-41	+	+	+	+	+	+	+	+	+	+	–	+	+	–	–	+	+	+
MM-45B	+	+	–	+	+	–	+	+	+	+	+	–	–	+	–	+	+	+
MM-58	+	+	–	+	+	–	+	+	+	+	–	–	–	+	–	+	+	+
MM-96-69	+	+	–	+	+	+	+	+	+	+	–	+	+	+	–	+	+	+
MM-96-70	+	+	–	+	+	+	+	+	+	+	+	–	+	+	+	+	+	+
MM-96-71	+	+	+	+	+	+	+	+	+	+	–	–	–	+	–	+	+	+
MM-96-72	+	+	–	+	+	+	+	–	+	+	–	–	+	+	–	+	+	+
MM-96-73	+	+	+	+	+	–	+	–	+	+	–	–	–	+	–	+	+	+
MM-96-74	–	–	–	–	–	–	+	–	+	+	–	–	–	+	–	+	+	+
MM-96-75	–	–	–	–	+	–	+	–	+	+	–	+	+	+	+	+	+	+
MM-96-76	–	–	–	+	+	–	+	+	+	+	–	–	+	+	+	+	+	+
MM-96-77	+	+	+	+	+	+	+	+	+	+	–	+	+	+	–	+	+	+
MM-96-79	+	+	+	+	+	–	+	+	+	+	–	+	+	+	+	+	+	+
MM-96-80	+	+	+	+	+	–	+	+	+	+	+	–	–	+	+	+	+	+
MM-96-81	+	+	+	+	+	–	+	+	+	+	+	–	–	+	+	+	+	+
MM-96-82	+	+	+	+	+	+	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-83	–	–	–	+	+	–	+	–	+	+	–	+	+	–	–	+	+	+
MM-96-84	+	+	+	+	+	+	+	+	+	+	–	–	–	–	–	+	+	+
MM-96-85	+	+	+	+	+	+	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-86	+	+	+	+	+	+	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-87	+	+	–	–	–	–	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-88	+	+	–	+	+	+	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-89	+	+	+	+	+	+	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-90	+	+	+	+	+	–	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-91	+	+	+	+	+	–	+	–	+	+	–	+	+	–	–	+	+	+
MM-96-92	+	+	+	+	+	+	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-93	+	+	+	+	+	–	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-94	+	+	+	+	+	–	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-95	+	+	+	+	+	–	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-96	+	+	+	+	+	–	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-97	+	+	+	+	+	–	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-98	+	+	+	+	+	–	+	–	+	+	–	–	–	–	–	+	+	+
MM-96-99	+	+	+	+	+	–	+	+	+	+	–	–	–	–	–	+	+	+

+ = present; – = absent.

MM-96-91 (S.I. 94.4%), MM-96-92 (S.I. 94.4%), MM-96-93 (S.I. 94.4%) MM-96-94 (S.I. 94.4%0, MM-96-95 (S.I. 94.4%, MM-96-96 (S.I. 94.4%) and MM-96-97 (S.I. 94.4%). MM-96-86 is similar to MM-96-88 (S.I. 94.4%), MM-96-89 (S.I. 94.4%, MM-96-94 (S.I. 94.4%), MM-96-95 (S.I. 94.4%), MM-96-96 (S.I. 94.4%) and Mm-96-97 (S.I. 94.4%).

MM-96-88 is closely related to MM-96-89, MM 96-91, MM-96-92, MM-96-93, MM-96-94, MM-96-95, MM-96-97 having similarity index of 94.4%. MM-96-89 is similar to MM-96-92 MM-96-93, MM-96-94, MM-96-95, MM -96-96, MM-96-97 and MM 96-98 having similarity index of 94.4%.

MM-96-91, Mm-96-92, MM-96-93, MM-96-94, MM96-95, Mm-96-96 and Mm-96-97 are closely related to each other with a similarity index of 99.9%.

The above results with the SDS-PAGE of 32 genotypes suggest that there is very limited variation for seed storage protein among the muskmelon genotypes. In contrast, these genotypes were selected on the basis of their diverse morphological traits and origin (Table 2). This may be due to limited number of genes of a common origins for the major seed storage proteins in muskmelon. Similar SDS-PAGE analysis of seed storage protein of different cucurbit species showed extensive variation between species (Fig. 2). This clearly shows that SDS-PAGE to distinguish seeds of different varieties of the same species as similar results have been obtained with different variety of cucumber. Hence it will be desirable to make use of new DNA markers such RAPD and RFLP for the cataloguing of muskmelon germplasm.

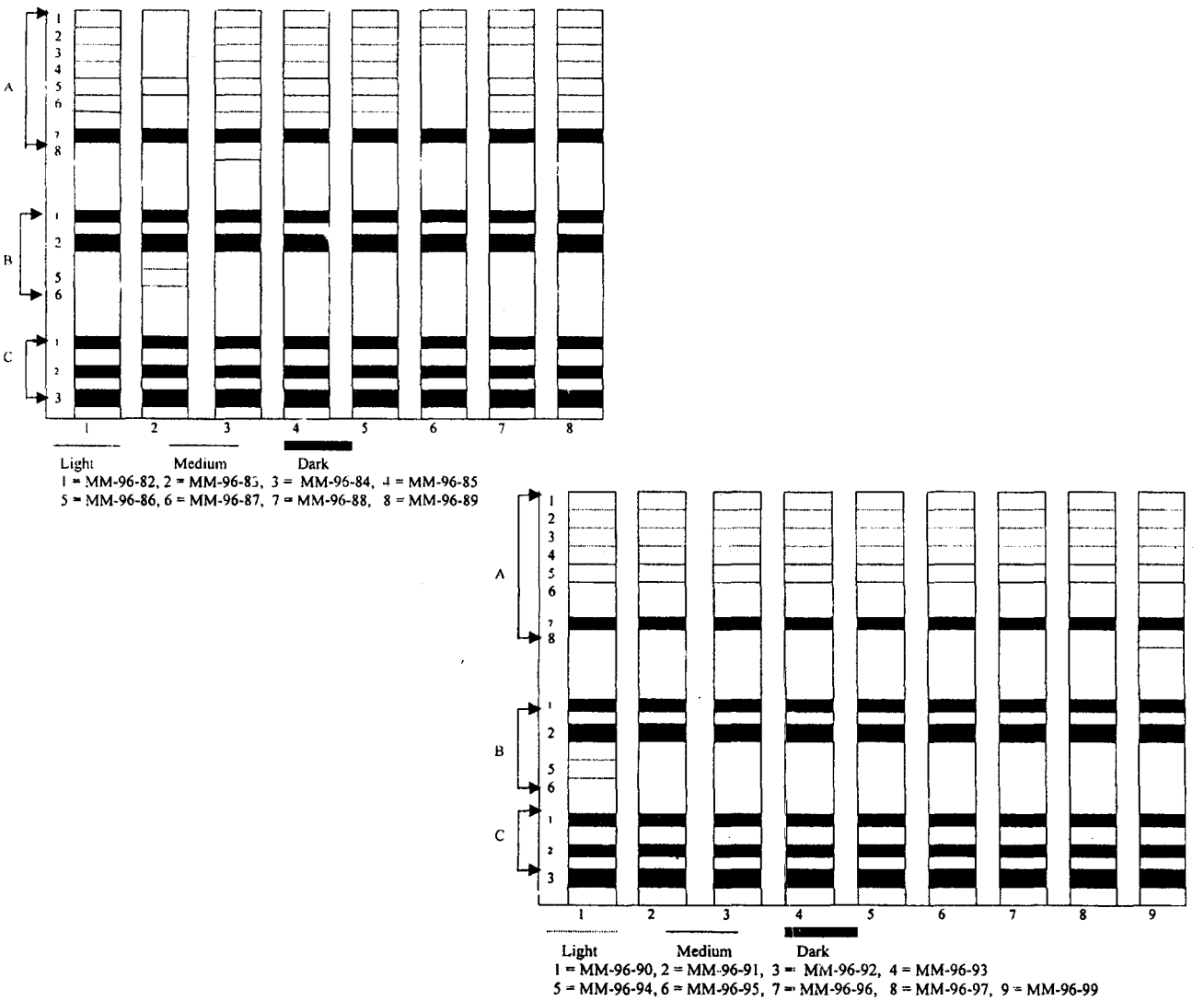

Fig. 2. Schematic diagram of the seed protein electrophoretic banding pattern in some muskmelon genotypes

Table 2. Mean values of 16 morphological characters

Geonotype	Days to Seed Germination	No of days to first male flower	No. of days to first female flower	Inter nodal length (cm)	Days to first fruit harvest	Fruit weight (gm)	No. of fruits per plant	Polar diameter (cm)	Latitudinal diameter (cm)	No of strips	Blossom and scar size (cm)	Peduncle scar size (cm)	Flesh thickness (cm)	Seed cavity size (cm)	T.S.S.	Yield per plant (cm)
MM-58	11.40	42.00	46.66	6.20	78.00	851.33	1.61	11.16	12.38	9.66	1.33	1.39	2.39	7.57	9.0	1646.40
MM-41	10.33	40.33	44.66	6.96	78.00	953.33	2.96	11.12	13.60	9.91	1.65	1.62	2.30	8.87	6.70	2705.60
MM-45 B	12.66	47.33	52.00	6.76	81.66	509.33	2.64	8.88	10.83	10.0	2.52	1.36	2.33	7.26	6.83	2186.60
MM-96-69	11.13	43.33	47.33	7.43	81.66	800.00	1.91	102.6	11.93	10.00	1.44	1.56	2.28	7.58	6.66	1832.83
MM-96-70	10.00	38.33	46.00	7.33	83.00	805.00	1.96	10.46	11.96	9.66	2.60	1.81	2.95	6.68	7.00	1685.83
MM-96-71	11.66	45.66	48.33	5.96	81.66	766.66	2.17	10.69	12.07	9.23	1.63	1.50	2.95	7.55	9.00	2429.73
MM-96-72	11.16	42.3.	42.00	6.00	79.33	1015.00	2.32	11 73	11.32	9.66	1.46	1.63	2.35	8.36	9.50	5268.00
MM-96-73	11.60	42.6	47.33	7.00	8150	1048.33	1.69	10.06	12.56	9.90	2.30	1.65	2.06	8.50	8.66	1740.93
MM-94-74	12.26	43.00	49.00	7.66	81.00	941.66	1.66	9.04	12.83	10.00	2.45	1.33	3.06	7.83	8.16	1619.16
MM-96-75	11.06	42.66	47.33	6.23	81.33	690.00	1.47	8.53	11.33	10.20	1.86	1.55	2.16	8.53	7.75	3773.16
MM-96-76	12.86	44.66	49.33	5.64	82.00	1020.00	2.85	9.57	14.16	9.06	2.05	1.52	2.56	7.30	10.00	2789.00
MM-96-77	11.00	42.66	47.33	6.13	82.66	510.00	2.06	7.30	10.50	6.43	1.91	1.90	3.03	6.60	9.66	1169.60
MM-96-78	11.33	42.66	46.33	4.53	83.00	893.33	2.53	11.23	10.90	10.00	1.88	1.60	2.51	8.53	11.66	2810.81
MM-96-79	11.66	44.00	48.33	5.26	76.33	631.66	2.36	10.05	13.16	10.16	1.93	1.44	2.35	7.37	9.43	1493.38
MM-96-80	10.80	44.33	47.66	5.56	78.33	1081.66	1.63	10.42	12.26	10.50	2.10	1.45	2.40	8.39	10.21	2362.78
MM-96-81	11.20	45.00	48.66	5.80	84.00	669.66	3.32	8.36	10.33	9.33	1.68	1.05	2.53	6.43	9.50	2159.86
MM-96-82	11.13	43.00	50.33	6.13	79.33	993.33	1.46	11.21	13.69	11.00	2.70	1.19	2.16	9.58	7.00	1831.06
MM-96-83	20.43	45.66	49.00	5.53	83.70	1155.00	2.12	16.50	13.93	10.00	2.13	1.42	3.02	9.29	10.13	2172.96
MM-96-84	11.00	44.00	45.33	5.26	80.56	578.00	1.43	8.96	10.18	10.00	1.22	1.02	1.76	7.18	10.50	841.08
MM-96-85	11.73	44.33	49.00	6.43	81.53	1007.33	1.55	10.28	12.18	9.50	2.35	1.54	2.37	8.91	9.80	1870.50
MM-96-86	11.33	43.00	48.33	5.33	78.66	787.00	2.82	11.71	12.52	9.86	2.10	1.43	2.38	8.90	6.66	2062.66
MM-96-87	12.13	45.00	49.00	6.73	82.76	703.33	2.92	10.45	9.97	9.66	1.04	1.36	1.85	6.53	8.66	1894.66
MM-96-88	10.93	44.66	49.00	5.66	80.66	3480.00	2.24	9.93	13.35	10.33	1.82	1.86	2.32	8.34	9.84	1643.98
MM-96-89	11.13	44.33	48.33	7.86	79.00	713.33	1.81	8.21	11.02	10.20	2.73	1.43	1.66	6.68	8.00	583.16
MM-96-90	11.13	44.00	49.00	6.90	78.26	623.33	3.36	9.68	11.61	12.00	2.04	1.32	2.80	7.48	9.00	5105.00
MM-96-91	11.33	48.33	52.66	5.73	82.80	690.00	1.62	9.44	11.16	10.00	1.94	1.26	2.41	1.13	10.08	580.49
MM-96-92	11.66	46.33	50.33	6.30	80.70	821.66	1.66	10.30	10.54	10.00	2.56	1.60	2.70	7.30	10.33	1503.05
MM-96-93	13.13	45.66	50.66	7.13	81.33	688.66	1.97	10.36	12.03	9.66	2.25	1.28	2.46	7.85	8.00	1564.77
MM-96-94	13.10	42.66	50.66	5.73	84.33	610.00	3.66	9.64	11.39	40.00	2.21	2.08	2.21	7.22	10.20	2876.66
MM-96-95	10.80	41.66	45.66	5.90	79.96	681.66	2.26	9.32	11.40	9.66	1.63	1.28	2.33	7.27	8.96	1208.33
MM-96-96	12.83	44.00	48.00	5.30	79.26	590.00	1.47	9.76	9.46	10.00	1.80	1.12	1.98	6.64	10.33	961.33
MM-96-97	12.83	45.33	50.33	6.00	82.33	605.00	2.36	9.37	11.20	9.66	1.58	1.32	2.39	7.32	9.53	1809.08
MM-96-99	13.00	45.33	49.00	6.23	82.33	916.66	2.38	10.53	12.56	9.66	2.18	1.76	2.68	8.48	11.00	2497.50

Table 3. Similarity Index (S.I.) for seed protein profile in different genotypes of muskmelon

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
1.	100	88	72.2	88.8	72.2	83.3	72.2	72.2	44.4	44.4	55.3	83.3	83.3	66.6	66.6	83.3	55.5	83	83.3	83.3	61	78	72.2	89	78	83	78	78	78	78	77.7	83.3
2.			94.4	77.7	83.3	83.3	77.7	83.3	66.6	55.5	72.2	72.2	66.6	72.2	72.2	72.2	55.5	78	72.2	72.2	72	72	72.2	67	78	72	78	78	78	78	77.7	83.3
3.				94.4	77.7	88.8	77.7	88.8	72.2	61.1	77.7	77.7	77.7	83.3	83.3	77.7	66.6	83	72.2	72.2	78	83	72.2	72	83	72	83	83	83	83	83.3	83.3
4.					83.3	83.3	88.8	72.2	55.5	66.6	72.2	94.4	83.3	66.6	66.6	72.2	66.6	78	72.2	72.2	61	78	72.2	78	67	72	67	67	67	67	66.6	72.2
5.						77.7	88.8	66.6	50	61.1	77.7	77.7	77.7	83.3	83.3	66.6	55.5	72	66.6	66.6	56	67	61.1	61	61	67	61	61	61	61	61.6	66.6
6.							83.3	94.4	61.1	50	55.5	88.8	77.7	83.3	83.3	88.8	50	94	88.8	88.8	67	83	88.8	72	83	89	83	83	83	83	83.3	88.8
7.								83.3	66.6	66.6	72.2	83.3	72.2	66.6	61.1	83.3	72.2	78	83.3	83.3	72	89	83.3	78	78	83	78	78	78	78	77.7	72.2
8.									72.2	55.5	66.6	77.7	77.7	83.3	83.3	88.8	66.6	83	88.8	88.8	78	83	83.3	83	78	83	94	94	94	66	94.4	61.1
9.										55.5	72.2	50	50	55.5	55.5	61.1	72.2	56	61.1	61.1	83	61	61.1	56	94	61	67	67	67	56	66.7	50.0
10.											83.3	61.1	72.2	55.5	55.5	50	83.3	56	61.1	61.1	83	61	50.0	67	67	50	56	56	56	61	55.5	66.6
11.												66.6	77.7	72.2	72.2	55.5	72.2	61	55.5	55.5	67	61	55.5	61	56	56	61	61	61	72	61.1	77.7
12.													88.8	72.2	72.2	77.7	66.6	73	77.7	77.7	56	72	77.7	83	61	78	72	72	72	72	72.2	77.7
13.														83.3	83.3	66.6	66.6	72	66.6	66.6	56	61	66.6	67	72	67	72	72	78	78	77.7	83.3
14.															99.9	72.2	50	78	72.2	72.2	61	67	72.2	67	78	72	78	78	78	78	77.7	83.3
15.																72.2	44.4	78	72.2	72.2	61	67	72.2	67	78	72	78	78	94	94	94.4	88.8
16.																	66.6	94	99.9	99.9	78	94	99.9	83	94	94	94	94	72	72	72.2	66.6
17.																		61	44.4	44.1	67	72	66.6	83	72	67	72	72	89	89	88.8	94.4
18.																			94.4	94.4	72	89	94.4	78	89	94	89	89	94	94	94.4	88.8
19.																				99.9	78	94	99.9	83	94	99	94	94	94	94	94.4	88.8
20.																					78	94	99.9	83	94	94	94	94	83	83	83	77.7
21.																						83	77.7	72	83	78	83	83	94	94	94.4	83.8
22.																							94.4	83	94	94	94	94	94	94	94.4	88.8
23.																								83	94	94	94	94	89	89	88.8	83.3
24.																									89	83	89	89	100	100	99.9	88.8
25.																										94	95	100	94	94	94.4	88.8
26.																											94	94	100	100	99.9	94.4
27.																												100	100	100	99.9	94.4
28.																														100	99.9	94.4
29.																															99.9	94.4
30.																																94.4
31.																																94.4

1= MM-41, 2=MM-45-B,3=MM-58, 4=MM-96-69, 5=MM-96-70, 6 = MM-96-72, 8= MM-96-73-9= MM-96-74, 10= MM-96-75, 11=MM-96-76, 12=MM-96-77, 13=MM-96-79, 14=MM-96-80, 14= MM-96-80, 15= MM-96-81, 16= MM- 96- 82, 17 = MM – 96- 83, 18=MM-96-84, 19=MM-96-85, 20-MM-96-86, 21=MM-96-87, 22=MM-96, 23= MM-96-89, 24= MM-96-89, 24=MM-96-90, 25=MM-96-91, 26= MM-96-92, 27= MM-96-94, 29=MM-96-94, 29=MM-96-95, 30=MM-96-96, 31=MM-96-97, 31=MM-96-98, 32=MM-96-99.

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Collection and Characterization of Walnut (*Juglans regia* L.) from Himachal Pradesh

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The physico-chemical variation in nut and kernels of walnut germplasm collected from Himachal Pradesh was studied. The promising accessions identified for high kernel/nut ratio, shell softness, high oil and protein content and kernel sweetness were NIC-20110, NIC-20942, NIC- 20109, NIC-20118, NIC-20116 and NIC-20111. These genotypes can serve as useful parents in genetic improvement programme as most of the traits described are highly heritable.

Key words : Characterization, Germplasm, *Juglans regia*, Physico-Chemical, Walnut

The potential of *Juglans regia* (locally known as *akhrot*) as an important nut fruit has been recognized globally. This species is widely distributed through out the dry, cold and alpine regions of Himachal Pradesh, including hills of Uttaranchal and Jammu and Kashmir in India. The major walnut production comes from seedling trees of primitive populations from natural forest and plants raised in farmers backyards without any standard cultural operations and agro-techniques. Walnut cultivation has not changed from the practices used for centuries and seed propagation is still common. Many of these local plantings have evolved through natural and human selection and represent distinct ecotypes or landraces. No efforts, whatsoever, are made to conserve these genetic resources (Srivastava *et al.*, 1977; Joshi and Pandey, 1996). Low productivity due to seedling habit biotic and abiotic stresses (spring frosts, hailstorms, rain) during flowering and sparse fruiting through terminal bearing behaviour are the main causes of low productivity which has led to dis-interest amongst the walnut growers. Thus there is strong need to conserve this important germplasm and to explore the possibilities to select the viable cultivars to promote walnut plantation as a commercial proposition in Himalayan regions of India (Joshi and Pandey, 1966).

Materials and Methods

A survey of Himachal Predesh (30° 34N latitude and 74°79E longitude) was made to collect indigenous walnut seedling trees for *ex situ* conservation. Sufficient nuts and bud wood of 33 accessions were collected in the month of September-October during the year 1994 from the forest, farmers backyards as well as seedling plantation. The places covered were Sahi, Anni in Kullu; Mooring, Sangla, Jangi, Pooh, Tangling in Kinnaur; Purthi, Lunj (Pangi valley) in Chamba and Udaipur in Lahaul and Spiti district of Himachal Pradesh. The scion wood collected were budded/grafted on walnut seedlings. Fifteen nuts of each accession were characterized for physico-chemical traits (Table 1). The oil content of kernel at 5 per cent moisture level of each accession was measured by non-destructive method using Newport NMR analyser, model-4000 from Oxford Analytical Instruments Ltd. Nitrogen content of the digested material was determined by conventional Kjeldahl method in Kjeltec Auto 1030 analyser from Tecator, Sweden. The factor 6.25 was used to convert nitrogen into protein.

Results and Discussion

Nut Characters

Significant differences for all the physical characters amongst the germplasm accessions were recorded. The nut length ranged from 2.85 cm (NIC-20068) to 4.20 cm (NIC-20114) whereas fruit diameter varied from 2.71 cm (NIC-20059) to 4.02 cm (NIC 20939). The maximum fruit weight (19.67g) was recorded for the accession NIC-20939 collected from Moorang and minimum (5.70g) for the accession NIC-20073 from Sangla. The minimum and maximum fruit weight were recorded for the collection from Kinnaur. Three different nut shape namely round, oval and oblong with slightly pointed at the distal end were observed in 33 accessions studied. Shell colour intensity varied from light brown, brown, slightly blackish to light golden colour. Similar observations have been recorded in nut and kernel characters of seedling walnut trees grown in Chakrata hills of Uttar Pradesh (Lal and Singh, 1978).

Table 1. Physico-chemical characteristics of walnut germplasm

Accessions	Nut length (cm)	Nut width (cm)	Nut weight (gms)	Kernel (%)	Kernel oil(%)	Kernel protein (%)	Kernel/ nut ratio	Taste	Shell Characters
NIC-20105	3.29	3.14	12.38	24.49	43.81	13.19	0.59	Good	Thin shell
NIC-20106	3.38	3.21	11.76	50.16	67.15	22.73	0.87	Good	Thin shell
NIC-20107	3.89	3.51	15.19	27.22	65.76	18.21	0.9\60	V. Good	Thin shell
NIC-20108	3.72	3.15	13.03	29.76	67.36	16.46	0.59	V. Good	Thin shell
NIC-20109	3.40	3.05	12.12	28.72	72.37	13.75	0.57	Good	Thin shell
NIC-20110	3.43	3.01	11.79	38.19	72.27	16.20	0.68	V. Good	Thin shell
NIC-20111	3.45	3.15	11.31	30.93	66.57	18.77	0.92	V. Good	Thin shell
NIC-20112	3.78	3.30	15.58	29.11	52.36	17.47	0.59	V. Good	Thin shell
NIC-20113	3.61	3.15	10.55	43.70	69.12	18.59	0.62	V. Good	Thin shell
NIC-20114	4.20	2.89	12.40	42.84	69.71	15.69	0.70	V. Good	Semi hard
NIC-20115	3.93	3.45	17.05	32.82	68.97	16.46	0.73	Good	Semi hard
NIC-20116	3.42	3.22	13.17	46.94	72.09	15.67	0.97	Good	Thin shell
NIC-20117	3.63	3.42	12.50	32.26	70.45	15.71	0.68	Good	Thin shell
NIC-20118	3.52	2.80	8.64	46.78	72.82	14.29	0.79	V. Good	Thin shell
NIC-20119	3.64	3.19	12.49	33.92	68.69	19.28	0.75	V. Good	Thin shell
NIC-20057	3.70	2.90	15.52	26.07	68.67	13.81	0.36	Good	Hard shell
NIC-20059	3.63	2.71	6.96	41.72	53.18	23.39	0.72	V. Good	Thin shell
NIC-20065	3.65	3.36	9.50	26.44	52.54	17.52	0.38	V. Good	Semi hard
NIC-20066	3.44	2.88	13.59	12.73	46.30	26.89	0.24	Good	Thin shell
NIC-20068	2.85	2.85	7.96	32.19	65.77	13.68	0.63	V. Good	Thin shell
NIC-20069	3.21	2.92	10.46	6.46	44.75	24.48	0.26	V. Good	Hard shell
NIC-20070	3.11	3.22	12.82	27.45	64.19	18.32	0.30	V. Good	Hard shell
NIC-20071	3.93	3.24	11.59	34.21	62.22	20.28	0.57	Fair	Semi hard
NIC-20073	2.87	2.79	5.70	46.37	63.36	19.22	0.73	V. Good	Thin shell
NIC-22075	3.34	3.24	14.49	20.75	61.08	19.32	0.30	V. Good	Thin shell
NIC-20939	4.17	4.02	19.67	27.44	69.66	17.86	0.48	Good	Thin shell
NIC-20940	3.49	2.78	7.77	45.95	70.68	16.68	0.85	V. Good	Thin shell
NIC-20941	3.62	3.31	13.39	34.23	69.79	15.38	0.48	Good	Semi hard
NIC-20942	3.45	3.29	13.92	19,50	74.92	11.81	0.33	Fair	Semi hard
NIC-20943	4.15	3.82	12.58	37.55	67.84	16.31	0.80	V. Good	Thin shell
NIC-20944	3.82	3.37	14.80	24.71	64.94	17.68	0.28	Good	Hard shell
NIC-20945	3.16	3.18	15.34	13.65	71.24	14.21	0.20	Fair	Hard shell
NIC-20946	3.69	3.48	16.33	17.76	63.32	19.24	0.27	Good	Semi hard
S. Em+	0.05	0.02	0.14	0.40	0.21	0.06	0.01		
Range									
Min.	2.85	2.71	5.70	6.46	43.81	11.81	0.20		
Max.	4.20	4.02	19.67	50.16	74.92	26.89	0.98		
C.D. at 5%	0.14	0.07	0.39	0.12	0.59	0.15	0.03		

Kernel Characters

Significant differences were recorded amongst the accessions for kernel percentage and kernel/nut ratio. The maximum kernel percentage (50.16%) alongwith very good kernel/nut ratio (0.87%) was observed in NIC-20106 and minimum kernel percentage (6.46%) coupled with poor kernel/nut ratio ((0.26%) was recorded in NIC-20069. Kernel/nut ratio (as depicted by weight of kernel/weight of shell) was lowest (0.20) in NIC-20045 and highest (0.97) in NIC-20116.

Kernel Oil and Protein Characterization

Significant differences in kernel oil and kernel protein were recorded amongst the 33 accessions studied. Highest kernel oil (74.92%) was recorded in NIC-20942 which is significantly higher than the NIC-20118 (72.82%), NIC-20109 (72.37%) and NIC-20110 (72.27%). The lowest kernel oil was recorded in NIC-20105 (43.81%). The highest (26.89%) and lowest (11.81%) protein was recorded in the accessions NIC-20066 and NIC-20942 respectively. It is evident from the Table-1 that higher oil content in the accession coupled with lower protein and vice versa. All the 33 germplasm accessions studied could easily be divided into three distinct group of shell softness, namely thin shell, semi hard and hard shell. Organoleptic taste of kernel was fair to very good in different accessions studied and in most of the cases was sweet except for few bitter (NIC-20071) and few mildly bitter (NIC-20945).

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Correlated Response in Amaranth

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The present study was done to test the suitability of direct and indirect selection of grain yield in amaranth through nine component traits. The selection gain among yield components was high for number of inflorescence/plant (110.55%) followed by number of nodes/plant (83.63%), leaf size (72.9%) and number of primary branches/plant (68.76%). The correlated response for grain yield was maximum on selection of plant height (4.18%), leaf size (3.25%), number of inflorescence/plant (3.14%) and number of spikelets /spike (2.90%). The estimate of correlated response (CRY) and relative selection efficiency (RSE) were in proportion with each other, though relative selection efficiencies were less than one. The selection of plant types with medium plant height, large number of inflorescence/ plant and spikelets/spike, and big leaf size is suggested to enhance the grain yield.

Key words: Amaranth, Correlated Response, Genetic Advance, Heritability

Amaranth is an important pseudocereal as human food, and has been grown by people since long. The current interest in amaranth resides in the fact that it exhibits a high nutritional value, a C_4 photosynthetic pathway, a great amount of genetic diversity and phenotypic plasticity. It has rapid growth due to its remarkable capacity for biosynthesis and low rate of photorespiration. To increase its yield potential, several efforts for genetical improvement have been done (Pandey and Pal, 1988; Gupta and Gudu, 1990, 1991; Lehmann *et al.*, 1991; Joshi and Rana, 1995; Katiyar *et al.*, 2000). The selection based on phenotypic performance does not lead to expected genetic advance. Hence, the knowledge of indirect selection is necessary to estimate the proximity of component traits favoring or linked to grain yield. The correlated response is resultant effect of heritability, genetic advance, genotypic correlation and selection intensity; it has an added advantage in selection of suitable characters over others. Studies on this aspect are meagre, though some studies on genetic association were made (Pandey, 1981; Ganeshaiah *et al.*, 1999). The present investigation is an attempt to extend the earlier studies to test the suitability of component characters for making direct and indirect selection for high grain yield.

Materials and Methods

The material comprised 66 genotypes, including 60 distinct lines obtained from two species of amaranthus *i.e. Amaranthus hypochondriacus* and *A. cruentus* and six cultivars of *A. hypochondriacus*. The crop was sown in 1997-98 in a randomized block design with 3 replications at National Botanical Research Institute, Lucknow located at 26.5^0N, 80.5^0E and 120 m above the sea level. The rows were 3m long and 45 cm apart. In each row plant to plant distance was maintained at 15 cm. Data on 5 randomly selected plants from each entry and replication were recorded for plant height (cm), number of spikelets/ spike, number of nodes/plant, leaf size $(cm)^2$ and gain yield/plant (g). The correlated response (CRY) and relative selection efficiency (RSE) were estimated as per procedure suggested by Searle (1965). Heritability (Δh) and genetic advance (ΔG) were calculated according to Allard (1960).

Results and Discussion

The different direct and indirect parameters *i.e.* heritability, genetic advance, genotypic correlation and correlated response are presented in Table 1. The heritability estimates in broad sense were high for all the characters, while genetic advance (ΔG) among yield components was high for number of inflorescence / plant (110.55%) followed by number of nodes/plant (83.63%), leaf size (72.90%) and number of primary branches/plant (68.76%), indicating that these characters are more responsive to selection. The correlated responses for grain yield was maximum on selection of plant height (4.18%), leaf size (3.25%), number of inflorescence/plant (3.14%) and number of spikelets/spike (2.90%). These components also had medium to high heritability and positive significant genotypic correlation with grain yield. The high relative selection efficiency (RSE) of these component traits indicated that selection of genotypes for grain yield for these traits would be more effective. The high correlated response of leaf size and positive significant genotypic correlation revealed that leaves are responsible for photosynthetic activity, so increase in leaf size may increase the production of grain, as it is an end product of biochemical activity in plants.

Table 1. Correlated response for grain yield in amaranth

Characters	Grain yield				
	ΔG	Δh	rgh	CRY	RSE
Days to flowering	20.93	0.96	0.152	1.158	0.025
Days to maturity	10.32	0.80	0.172	1.190	0.026
Plant height (cm)	52.49	0.89	0.572*	4.180	0.092
No. of primary branches/plant	68.76	0.82	0.220	1.539	0.034
No. of inflorescence/ plant	110.55	0.72	0.475*	3.139	0.069
Inflorescence length (cm)	49.13	0.69	0.199	1.284	0.028
No. of spikelets/ spike	56.86	0.69	0.450*	2.904	0.064
No. of nodes/plant	83.63	0.89	0.250	1.827	0.040
Leaf size (cm^2)	72.90	0.62	0.530*	3.255	0.071
Grain yield (g)	45.57	0.53	x	x	x

*Significant at 5%
ΔG, genetic gain; Δh, heritability (coefficient value);
rgh, genotypic correlation; CRY, correlated response;
RSE, relative selection efficiency.

The high correlated response for number of inflorescence/plant towards grain yield and it's positive significant genotypic correlation with high genetic advance (110.55%) suggest that the selection of plant genotypes with multiple number of inflorescence may provide more grain yield. The relative selection efficiency of each trait towards grain yield was less than unity. It might be due to high expected selection response on grain yield and thus denominator being higher than numerator CRY/ΔG, hence the ratio will naturally be less than one.

From the present findings it is concluded that medium plant height, large number of inflorescence/ plant and number of spikelets/spike and big leaf size should be considered to build up a novel plant type in amaranth to enhance the grain yield.

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Genotype x Environment Interaction and Stability Studies in Late Sown Bread Wheat (*Triticum aestivum* L. em Thell)

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Forty nine genotypes of wheat were evaluated in three different environments for number of seeds/spike, 1000-grain weight, number of productive tillers/m^2 and grain yield/plot. Mean performances between genotypes and environments were significant indicating substantial variability among genotypes and environments for all the characters except number of productive tiller/m^2. Highly significant variance due to environment + (GxE) revealed that genotypes interacted considerably with environmental conditions. Though both linear and non-linear components of GxE interaction played important role in the expression of number of seeds/spike and 1000-grain weight, the linear component was larger in magnitude. Number of productive tiller/m^2 and grain yield/plot showed highly significant variance due to non-linear component. Considering the three parameters of stability for each character, the genotypes namely PS 461, DW 1104, DL 97-8, DW 1106 and HP 1744 were found to be stable across the environments for yield as well as component traits.

Key words: GxE Interaction, Stability, Wheat

Late sown wheat is frequently affected by heat stress in early vegetative stage and during grain filling. With this background, breeders continually strive to broaden the genetic base of crop species to prevent their vulnerability to changing environments. Understanding the genetic basis of differential responses to environments and broadening the genetic base for such traits are extremely important in crop breeding programmes. Differential genotypic responses to different environments are collectively called 'Genotype x Environment (GxE) Interaction'. Besides, stability reflects the suitability of a genotype for cultivation over a range of environments. The breeder's objective should be to produce genotypes that are better adapted over a range of environments. Hence, studies of GxE interaction and stability analysis of grain yield and its component characters are important.

Materials and Methods

The experimental material consisted of 49 genotypes of wheat suited for late sowing contributed by different breeders of Indian Agricultural Research Institute (IARI), New Delhi and its regional research stations alongwith four check varieties. They were evaluated in a randomised block design with three replications in three different environments during *rabi* seasons of 1997-98 and 1998-99 at IARI, New Delhi under late sown irrigated conditions. The three different environments were artificially created by changing the dates of sowing, irrigation and fertilizer levels. Each genotype was planted in a plot having a gross area of 6mx1.08 m, with 6 rows at 18 cm spacing. The recommended cultural and agronomic practices for late sown irrigated condition were followed to raise the crop. Five random plants/plot/replication were labelled and observations were recorded for four characters *viz.* number of seeds/spike, 1000-grain weight, number of productive tillers/m^2 and grain yield/plot. The data were subjected to analysis of stability as per the method proposed by Eberhart and Russell (1966).

Results and Discussion

For estimating GxE interaction, multi-location and multi-year testing of genotypes are essential. However, the difficulty in handling the material at different locations with the required precision imposes a restriction on the number of locations. A possible way to overcome this bottleneck is to create artificial environments at the same location by changing the agronomic treatments such as levels of fertility and irrigation, fertilizer doses, sowing dates etc. The reliability of unilocational testing of genotypes by creating artificial environments as mentioned earlier has been reported by Gupta (1971) and Luthra *et al.*, (1974).

The pooled analysis of variance over environments is presented in Table 1. The differences among the genotypes and environments were significant in respect of all the characters namely number of seeds/spike, 1000-grain weight and grain yield/plot except number of productive tillers/m^2. This indicated that number of productive tillers/m^2 exhibited less GxE interaction as compared to the other characters. Since the formation of tillers in short duration genotypes follows a rapid vegetative phase, there is possibility that most of the

Table 1. Pooled analysis of variance for 4 characters

Source	d.f.	Mean sum of squares for different characters			
		No. of productive tillers/m^2	No. of seeds/ spike	1000-grain weight	Grain yield/ plot
Genotypes	48	149.33**	28.71**	20.35**	0.18**
Environments	2	725.46**	3840.01*	94.94**	1.42**
GxE	96	122.97	16.11**	6.93**	0.09**
Pooled error	288	113.94	12.52	2.41	1.35

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

genotypes which represent early maturity strains, have responded uniformly under different environments.

A perusal of Table 2 for analysis of variance for stability revealed highly significant variance due to environment + (GxE) which indicated that genotypes interacted differentially with environmental conditions that existed in different seasons for all the four characters. Highly significant pooled deviations suggested that the genotypes differed considerably with respect to their stability for all the four characters. The GxE interaction was further partitioned into linear and non-linear components. Since linear and non-linear components were significant for the two characters namely number of seeds/spike and 1000-grain weight, practical usefulness of prediction would depend on relative magnitudes of two variances. The other two characters namely number of productive tillers/m^2 and grain yield/plot revealed non-significant variance due to linear component and highly significant variance due to non-linear component indicating the unpredictable performance of genotypes across the environments for number of productive tillers/m^2 and grain yield/plot. In case of number of seeds/spike and 1000-grain weight, linear component played an important role in the expression of these characters because the linear component was 1.76 and 3.88 times higher than the non-linear component for these characters, respectively indicating that the performance of genotypes may be predicted across the environments for these characters. In prediction of performance, the non-linear component may have a role since it is also significant.

Different measures of stability have been used by various workers. Earlier Finlay and Wilkinson (1963) considered linear regression slope as a measure of stability. Eberhart and Russel (1966) emphasized the need of considering both the linear and non-linear components of GxE Interation in judging the stability of genotypes. According to Eberhart and Russell (1966), a variety with unit regression coefficient (b=1) and the deviation not significantly different from zero ($S^2_{di}=0$) and high mean ($\bar{x}$) is said to be stable. All the three parameters of stability for number of seeds/spike, 1000-grain weight, number of productive tillers/m^2 and grain yield/plot are presented in Table 3.

In case of number of productive tillers/m^2, out of 49 genotypes, 37 were significant for linear component and 12 were significant for non-linear component of GxE interaction, indicating thereby that for most of the genotypes, GxE was linear in nature suggesting that the prediction can be possible for number of productive tillers/m^2 across the environments. These findings are in agreement with Singh and Chatrath (1995), Menon *et al.* (1997) and Deswal *et al.* (1996). Considering the individual parameters of stability, it is evident that the genotypes *viz.* PS 465, DL 97-11, DW 1123, PS 467,

Table 2. Analysis of variance for stability

Source	d.f.	Mean sum of squares for different characters			
		No. of productive tillers/m^2	No. of seeds/ spike	1000-grain weight	Grain yield/ plot
Genotypes	48	149.33	28.71	20.35**	0.18*
Environment + (GxE)	98	135.07**	94.15**	8.72**	0.12**
Env. (Linear)	1	1450.67**	7680.10**	189.99**	2.85**
Genotype x Env. (Linear)	48	128.86	20.41	10.97**	0.06
Pooled deviation	49	114.30**	11.57**	2.83**	0.12**
Pooled error	288	37.98	4.17	0.80	0.0045

*Significant at 1%, ** significant at 5%

Table 3. Estimation of stability parameters - mean ($\bar{x}$), regression coefficient (bi) and deviation from regression (S^{-2}_{di}) for 4 characters

Strain	No. of productive tillers/m²			No. of seeds/spike		
	$\bar{x}$	bi	S^{-2}_{di}	$\bar{x}$	bi	S^{-2}_{di}
PS 458	74.22	-3.86*	-30.14	29.56	0.62	18.25*
Ind 98-35	90.89	2.42	902.99**	31.78	1.19	0.97
DW 1105	81.44	2.14	-19.38	33.33	0.80	14.86
PS 470	70.67	0.09	-37.98	36.44	1.52	13.29
DL 97-9	86.87	1.06	363.60**	239.56	0.85	21.88*
NIAW 34	68.56	0.78	-26.05	36.56	0.85	21.88*
Ind 98-33	76.78	0.55	21.73	32.89	1.34	1.81
DW 1093	90.67	-1.57	309.88**	37.11	1.12	24.94*
DW 1120	76.22	1.45	74.39	40.11	1.82**	1.30
PS 461	71.89	1.12	14.97	39.33	0.93	3.44
DW 1114	80.44	-0.22	314.89**	33.56	1.32	22.45*
HW 2045	72.11	-0.08	45.01	35.11	1.33	14.14
PS 465	85.00	0.83	-37.98	40.33	1.08	27.48*
DW 1102	87.44	2.20	278.89**	34.56	1.12	0.00
DL 97-11	89.11	-0.48	-24.84	39.00	0.34*	2.38
DW 1123	91.44	1.45	34.32	33.89	0.90	25.45*
PS 467	81.67	-2.61	-37.64	37.89	1.67*	1.27
Ind 98-36	73.78	2.03	18.41	38.00	1.29	2.90
DW 1092	75.67	-0.41	-36.85	33.89	0.93	27.03*
PS 462	79.56	3.02	-12.51	39.56	0.89	3.61
DL 97-10	83.33	2.12	101.96	43.56	0.81	35.64**
DW 1104	80.78	1.82	-0.99	41.22	1.38	-4.13
DL 97-8	83.44	0.56	-27.54	37.33	0.49	-3.96
PBW 373	82.56	2.32	244.20*	41.00	0.86	13.21
PS 456	80.33	-0.94	29.52	34.78	0.43*	-3.12
DW 1097	75.11	-1.23	157.00*	38.33	1.27	-2.26
PS 463	71.11	-2.29	36.25	34.67	0.96	15.81
WR 821	78.22	-0.63	29.31	36.78	1.47	0.75
PS 469	70.78	2.82	59.61	32.89	0.87	-3.11
DL 97-12	79.44	1.52	-37.98	38.89	0.68	-0.34
DW 1106	74.11	0.35	48.24	35.89	1.44	49.08**
GW 173	92.00	1.67	159.66*	34.67	0.44*	3.55
DW 1119	65.67	0.99	243.46*	38.44	1.32	-3.12
PS 460	80.56	2.48	-24.81	33.78	0.66	22.78
DW 1117	78.11	1.90	-37.74	39.00	1.34	6.37
PS 468	70.22	-1.83	228.15*	39.44	0.68	31.39**
PS 459	96.44	2.11	-97.00	35.11	0.85	-0.95
DW 1111	82.56	1.59	-10.74	37.78	0.95	-3.49
PS 464	70.67	5.54*	-19.50	44.11	0.83	6.69
HP 1744	74.11	0.44	-37.97	40.67	1.35	20.15*
PS 457	70.56	-0.52	435.55**	34.33	0.28**	1.18
PS 466	83.44	-1.63	-34.25	33.44	0.78	-1.47
Ind 98-32	76.33	0.29	-36.17	34.11	1.09	-3.21
DW 1115	83.56	3.82	-28.66	35.11	0.77	-4.01
PS 455	83.78	3.71	16.21	35.44	0.80	-3.66
DW 1122	79.89	4.61	207.10*	36.56	0.83	-2.53
Ind 98.37	69.78	-1.69	1.52	32.89	1.45	15.45
Population mean = 79.295	SE(Mean)=7.56			Population mean = 36.58	SE(Mean) = 2.40	
Mean of bi = 1.0001	SE of bi = 1.96			Mean of bi = 1.000	SE of bi = 0.27	

Strain	1000 grain weight			Grain yield/plot		
	$\bar{x}$	bi	S^{-2}_{di}	$\bar{x}$	bi	S^{-2}_{di}
PS458	37.84	2.07	2.26	1.63	-1.58	2.06**
Ind 98-35	38.29	0.53	0.69	1.68	1.98	0.10**
DW 1105	42.06	5.80**	5.74**	1.89	2.47	0.00
PS 470	40.35	2.10	3.01	1.97	0.58	0.07**
DL 97-9	38.47	-0.56	-0.36	2.02	2.63	0.05**
NIAW 34	42.34	2.42	-0.07	1.85	1.81	0.19**
Ind 98-33	35.48	-1.92**	12.51**	1.56	0.87	0.00
DW 1093	34.62	0.28	-0.37	1.88	1.35	0.00
DW 1120	26.02	1.64	-0.74	1.88	2.27	0.03
PS 461	36.82	0.17	0.84	2.25	0.88	0.00
DW 1114	37.83	5.47**	5.53**	1.65	3.41	0.04**
HW 2045	42.83	0.13	-0.19	2.15	2.88	0.37**
PS 465	39.66	1.71	-0.14	2.17	0.49	0.52**
DW 1102	41.09	2.10	-0.38	2.08	1.68	0.09**
DL97-11	37.44	1.36	6.91**	2.18	0.58	0.08
DW 1123	40.43	-1.00*	9.10**	1.81	-0.09	0.36**
PS 467	42.25	-0.47	1.93	2.14	1.44	0.25**
Ind 98-36	42.28	-1.60**				
DW 1092	38.78	1.35	-0.31	1.76	1.72	0.02*
PS 462	43.94	-0.09	-0.70	2.39	0.81	0.12**
DL 97-10	37.59	3.84**	13.26**	2.27	0.95	0.03*
DW 1104	38.69	2.36	0.00	2.62	0.75	0.01
DL 97-8	38.32	0.30	1.84	2.06	0.28	0.00
PBW 373	36.01	0.82	0.26	2.29	0.14	0.02
PS 456	44.45	0.54	-0.71	2.01	-0.64	0.16**
DW 1097	38.56	0.83	1.61	1.71	1.17	0.07**
PS 463	40.66	-1.67**	2.38	1.57	0.15	0.18**
WR 821	39.20	1.27	-0.72	2.34	-0.03	0.11**
PS 469	40.90	2.52	6.82**	2.19	1.80	0.10**
DL 97-12	37.62	1.33	-0.67	2.44	1.51	0.10**
DW 1106	37.56	1.94	-0.39	2.15	1.92	0.00
GW 173	43.39	0.53	-0.01	2.22	1.24	0.06**
DW 1119	40.14	-0.23	3.54*	1.94	0.43	0.15**
PS 460	38.02	1.87	-0.17	0.05	1.13	0.02*
DW 1117	37.27	2.31	-0.80	1.71	1.13	0.34**
PS 468	42.11	1.69	-0.33	2.34	1.00	0.00
PS 459	41.23	0.67	-0.80	1.98	-0.84	0.31*
DW 1111	39.85	0.06	0.79	2.16	-0.13	0.21**
Ind 98-34	39.004	-0.01	-0.80	1.98	-0.84	0.02*
DW 1118	38.37	2.77*	4.41*	2.17	1.87	0.03
PS 464	42.72	-1.88*	1.23	1.97	1.81	0.03
HP 1744	40.55	1.14	0.07	2.07	1.39	0.00
PS 457	44.44	-1.99*	-0.06	2.15	0.74	0.07**
PS 466	42.72	2.52	0.72	2.12	1.97	0.01**
Ind 98-32	40.55	0.98	-0.34	1.97	0.08	0.00
DW 1115	39.81	-0.15	2.36	2.20	-0.43	0.47**
PS 455	42.63	-0.65	0.54	2.10	-0.56	0.05**
DW 1122	45.95	3.04*	4.03*	2.52	0.89	0.09**
Ind 98-37	43.31	0.74	-0.79	1.77	3.16	0.40**
Population mean = 40.01	SE (Mean) = 1.19			Population mean = 2.047	SE (Mean) = 0.24	
Mean of bi = 0.99	SE of bi = 0.85			Mean of bi = 0.0001	SE of bi = 1.41	

PS 462, DL 97-10, DW 1104, DL 97-8, DL 97-12, PS 460, PS 459, DW 1111, Ind 98-34, PS 466, DW 1115 and PS 455 were specifically adapted to unfavourable (poor) environments for number of productive tillers/ m^2 while the genotype DW 1118 was found to be specifically adapted to favourable (rich) environments for this character.

In case of number of seeds/spike, 38 genotypes were significant for linear components and 11 genotypes were significant for non-linear components indicating thereby the predominance of linear GxE interaction for this character. The present results are in consonance with Singh and Chatrath (1995). On examination of individual parameters of stability, it reveals that the genotypes DL 97-9, DW 1114, Ind 98-36, PS 462, DW 1104, DL 97-8, DW 1097, WR 821, DL 97-12, DW 1117, DW 1111 and PS 464 were specifically adaptable to unfavourable environments for number of seeds/spike and the genotypes DW 1120, DL 97-11 and PS 467 were specifically adaptable to favourable environments for this character.

In case of 1000-grain weight, 38 genotypes were significant for linear component and 11 genotypes were significant for non-linear GxE component, indicating thereby the preponderance of linear GxE interaction. Similar findings have been reported by Thete *et al.* (1987), Patil *et al.* (1992), Singh and Chatrath (1995) and Deswal *et al.* (1996). On consideration of individual parameters of stability, the genotypes namely PS 470, NIAW 34, HW 2045, DW 1102, PS 467, PS 462, PS 456, GW 173, PS 468, PS 459, HP 1744, PS 466, Ind 98-32 and PS 455 were found to be specifically adapted to unfavourable environments while the genotypes PS 464 and PS 457 were specifically suited to favourable environments for 1000-grain weight.

In case of grain yield/plot, 13 genotypes were significant for linear component while 36 genotypes were significant for non-linear GxE component, indicating the predominance of non-linear GxE interaction. This indicated that variation among genotypes for yield was largely unexplained by regression slopes and performance across the environments was mostly governed by unpredictable component. These results are in consonance with Maloo *et al.* (1993). On examination of individual parameters of stability, the genotypes *viz.* PS 461, PS 467, DW 1104, DL 97-8, DW 1106, PS 468, HP 1744 and PS 466 were found to be specifically adaptable to unfavourable environment in case of grain yield/plot.

From the ongoing discussion, it can be concluded that out of 49 genotypes, the genotypes namely PS 461, DW 1104, DL 97-8, DW 1106 and HP 1744 were found to be stable across the environments for yield as well as its component traits.

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Effect of Paclobutrazol Drenching on Growth of Micropropagated and Seedling Plantlets of 12 Citrus Cultivars: Principal Component Analysis

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Paclobutrazol was applied to soil (0,5,25,50 and 100 mg/plant) in potted plants of 12 citrus cultivars propagated by tissue culture and seedlings. Required quantity of active ingredient of paclobutrazol was applied in 200 ml of water around the base in polythene bags and control plants were given 200 ml of water only on 4 month old seedings. Six random plants were selected for morphological observations at the age of one year. Results indicated that all citrus types were sensitive to paclobutrazol. Micropropagated plants seems less responsive to paclobutrazol than seedlings which might be due to increase in secondary roots of seedlings at early stage than micropropagated plantlets, which helped plants in absorption of paclobutrazol. Principal component analysis indicated that the cultivars, JL, AL and P registered very high positive loading in PC1 which indicated that response of paclobutrazol was least on these species where as distinct response on growth reduction was observed in *Citrus indica*, KM, SAT, SOB, SLS and CV. All the variables have very high positive loading except per cent of thick roots, which registered negative loading indicative of one of the most important parameters to be used. It was observed that application of paclobutrazol significantly affect the root morphology particularly root thickness.

Key words : Citrus, Micropropagation, Paclobutrazol, Principal Component Analysis

Citrus is a major fruit crop of north-eastern hill region of India. There is huge demand for planting material. Non availability of scientifically propagated planting material from elite clones for plantation are the main constraints in citrus cultivation. In recent years, tissue culture techniques (micropropagation) are increasingly used for rapid clonal propagation of several economic plants, restoration of vigor and yield and preservation of germplasm. However, information on performance of tissue culture plants are lacking. Besides, bioregulant like paclobutrazol (PCB) play a very important role in fruit production. Its application has been consistently documented as an effective retardant of vegetative growth in citrus (Monelise, 1986; Yelenosky *et al.*, 1995; Minger and Sanyu, 1996 and Matta and Tominga, 1998). Therefore, the present experiments were planned and the effect of various treatments were investigated.

Materials and Methods

A large number of micropropagated and seedling plants of 12 citrus cultivars were transplanted in polythene bag containing 1:1 soil and FYM mixture after 40 days of rooting/germination. Weeding and spraying of insecticides were done at regular intervals to protect the plants from the insect pests. The experiment was conducted at ICAR Research Complex for NEH Region, Umiam, Meghalaya, on 4-month old plant of 12 citrus cultivars kept in open sky after hardening. The experiment consisted of 5 concentrations of paclobutrazol (0, 5, 25, 50 and 100 mg/plant) as soil drench. The required quantity of active ingredient PCB was dissolved in water and 100ml of water was applied around the stem base in each polythene bag as soil drenching and control plants were given an application of 100ml water only. The experiment was laid out in factorial design replicated 3 times. Six plants were randomly selected for morphological observations at the age of one year. Plant characters were recorded for shoot length, root length, number of leaves, number of tap roots, number of secondary roots, shot weight, root weight and plant weight. The data were subjected to principal component analysis (Adams and Wiersma, 1978).

Twelve important citrus cultivars, mostly indigenous to NEH region, were selected for this study, including *Citrus volkameriana* as control.

Results and Discussion

A perusal of the data presented in Table 1 indicates

S.No.	Cultivars (Species)	Abbreviations
i.	Satkara (*Citrus macroptera* Mont.)	SAT
ii.	Khasi papeda (*Citrus latipes* Tanaka)	LAT
iii.	Sweet lime (*Citrus limettioides* Tanaka)	SLS
iv.	Soh Bitara (*Citrus sinensis* Osbeck)	SOB
v.	Indian wild orange (*Citrus indica* Tanaka)	I
vi.	Ada Jamir (*Citrus assamensis* Dutta & Bhatnagar)	ADA
vii.	Khasi mandarin (*Citrus reticulata* Blanco)	KM
viii.	Soh myndong (*Citrus jambhiri* Lush)	JL
ix.	Jaintia lemon (*Citrus limon* Burm)	JL
x.	Pummelo (*Citrus grandis* Osbeck)	P
xi.	Assam lemon (*Citrus limon* Burm)	AL
xii.	Volkamer Lemon (*Citrus volkameriana* Pasq.)	CV

marked variation in growth of planting material due to paclobutrazol drenching. Plant height was significantly reduced by paclobutrazol (PCB). Highest per cent of thick roots were observed with 100mg paclobutrazol drenching. The increasing concentration of paclobutrazol significantly influenced all the characters except root length, number of secondary roots and total dry weight of plant. In general, response of PCB was more pronounced on seedling than micropropagated plants. This may be because at initial stage, growth of seedlings was more than micropropagated plants. Seedling had more number of secondary roots at the time of application, which may absorb more PCB. However, at the age of one year, maximum secondary roots were observed in micropropagated plantlets.

Principal Component Analysis (PCA)

The data pertaining to principal component analysis is presented in Table 2. All the cultivars showed very high positive loading in PC1 and PC2. JL and P registered very high postive loading in PC1, which indicated that response of paclobutrazol was least on these species where as distinct response on growth reduction was observed in *C. indica*, KM, SAT, SOB, SLS and CV.

Data pertaining to PCA presented in Table 3 indicates that all the variables have very high positive loading for PC1 except per cent of thick roots which registered negative loading in PC1 indicative of one of the most important parameters to be used. It was observed that application of paclobutrazol significantly affect the root morphology particularly root thickness. PC1 contributes 52 per cent variance towards the total variability by recording higher loading. Leaf area recorded negative loading in PC2 which showed that this is also an important variable. Number of secondary roots and length of internode showed negative loading in PC3 which

Table 1. Interaction between paclobutrazol drenching and method of propagation

S.No.	Paclobutrazol	Method of propagation	Plant height (cm)	No. of leaves	Root length (cm)	Stem diameter (mm)	length of internode (mm)	Leaf area (cm^2)	No. of secondary roots	%of thick roots	Plant dry wt. (g)			
											stem	leaves	roots	total
1	0	S	22.54	23.9	23.14	3.69	8.71	19.94	66.39	0.00	1.06	1.42	1.29	3.77
		M	27.76	27.17	25.13	3.80	8.81	20.60	79.14	0.00	1.23	1.55	1.51	4.29
2	5mg	S	21.72	22.77	22.20	3.66	8.26	19.36	64.39	64.39	17.02	0.93	1.24	3.25
		M	26.27	26.16	24.46	3.74	8.36	19.81	76.29	15.39	1.04	1.34	1.26	3.64
3	25mg	S	17.89	20.39	20.32	3.31	6.83	16.86	53.16	38.32	0.75	0.91	0.82	2.48
		M	21.63	23.14	22.39	3.42	7.16	17.29	57.16	35.49	0.84	1.01	0.92	2.77
4	50mg	S	14.76	17.47	18.28	2.96	5.96	14.64	45.53	52.23	0.58	0.74	0.66	1.98
		M	18.25	20.32	20.95	3.09	6.29	15.45	48.24	49.06	0.67	0.83	0.75	3.00
5	100mg	S	9.97	13.8	14.24	2.38	4.19	9.59	30.22	63.37	0.34	0.54	0.50	1.38
		M	14.01	17.49	17.37	2.51	4.52	10.76	32.99	54.48	0.42	0.62	0.59	1.63
	SEm ±		0.18	0.15	1.70	0.17	0.07	0.11	2.95	4.73	0.01	0.012	0.011	0.16
	C.D. (P=0.05)		0.49	0.41	NS	0.47	0.19	0..30	NS	13.10	0.03	0.033	0.03	NS

S= Seedling, M=Micropropagation

Table 2. Principal component scores for citrus growth as influenced by paclobutrazol drenching

Sl.No.	Cultivars	PC1	PC2	PC3	PC4	PC5	PC6
1	SAT	27.11	58.91	1.89	-12.15	-2.815	2.76
2	LAT	45.81	60.25	3.70	5.67	-1.57	4.03
3	SLS	34.91	67.82	14.67	-1.90	-1.37	1.01
4.	SOB	31.19	82.02	7.08	1.21	-7.65	4.19
5.	I	28.68	42.72	4.76	0.45	-4.88	3.74
6.	ADA	41.38	59.92	22.83	-9.30	-3.45	4.40
7.	KM	24.97	68.45	0.39	-7.14	-3.38	2.36
8.	SM	47.77	70.06	3.18	-4.87	2.30	4.62
9.	JL	67.35	63.91	5.83	-1.90	-4.35	2.10
10	P	54.69	57.64	5.65	-4.42	-5.54	3.75
11	CV	39.78	60.09	9.13	2.83	-2.82	1.25
12	AL	57.88	63.48	2.80	-11.14	-5.28	2.45

Table 3. Latent vectors and Latent roots for different variables under influence of paclobutrazol drenching

Sl.No.	Variables	Principal Component					
		PC1	PC2	PC3	PC4	PC5	PC6
1	Plant height	0.45	0.15	0.05	0.40	0.34	-0.40
2	No. of leaves	0.15	0.18	-0.10	0.37	0.52	0.41
3	Root length	0.17	0.19	0.13	0.61	-0.72	0.14
4.	Stem diameter	0.05	0.01	0.03	0.02	0.05	0.07
5.	Length of internode	0.17	0.02	-0.07	0.17	0.15	-0.3
6.	Leaf area	0.25	-0.04	0.93	-0.20	-0.07	0.04
7.	No. of secondary roots	0.66	0.41	-0.27	-0.51	-0.02	0.04
8	% of thick roots	-0.46	0.86	0.15	-0.05	0.08	-0.11
9	Stem dry wt.	0.03	0.02	0.01	-0.00	0.05	0.21
10	Leaves dry wt.	0.02	0.02	0.01	-0.01	0.05	0.17
11	Roots dry wt.	0.02	0.02	0.01	0.01	0.02	0.21
12.	Plant dry wt.	0.08	0.06	0.01	0.00	0.11	0.62
	Latent roots	178.37	86.12	39.51	31.79	6.36	1.52
	Percentage variance	51.76	24.99	11.47	9.23	1.85	0.44
	Cumulative variance	51.76	76.76	88.22	97.45	99.30	99.74

contributed 12 per cent variance. It can be concluded that per cent thick root is the most important variable to be taken into account followed by leaf area, number of secondary roots and internodal length.

It is evident from Table 4 that 50 and 100 mg/l paclobutrazol registered negative loading in PC1 indicating that these are the best treatment to reduce the overall growth of citrus. However, 100mg/l paclobutrazol drenching showed complete suppression of growth. The PCA presented in Table 5 shows that among all the variables, per cent of thick root registered negative loading in PC1 which indicate the importance of treatment. PC1 contributes 99 per cent variance towards total variability which again confirms the importance of this PC.

The principal component scores using correlation matrix for different cultivars propagated by tissue culture and seedling and influenced by paclobutrazol drenching

Table 4. Principal component scores for paclobutrazol drenching

Sl. No.	Paclobutrazol levels	PC1	PC2	PC3	PC4
1.	Control	49.45	70.46	-9.66	5.39
2.	05mg/plant	34.41	76.87	-11.91	4.93
3.	25mg/plant	8.28	75.80	-10.98	6.15
4.	50mg/plant	-8.48	76.56	-8.38	5.17
5.	100mg/plant	-33.68	71.25	-11.41	5.20

Table 5. Latent vectors and latent roots for variables under influence of paclobutrazol levels

	Variables	Principal Component			
		PC1	PC2	PC3	PC4
1.	Plant Height	0.16	0.17	-0.15	0.27
2.	No. of leaves	0.12	0.11	-0.13	0.59
3.	Root length	0.09	0.38	0.88	-0.13
4.	Stem Diameter	0.02	0.04	-0.00	0.09
5.	Length of internode	-0.05	0.07	0.02	0.1
6.	Leaf area	0.12	0.27	0.15	0.63
7.	No. of secondary roots	0.51	0.66	-0.37	-0.37
8.	% of thick roots	-0.82	0.54	-0.16	-0.01
9.	Stem dry wt.	0.01	0.00	0.00	0.04
10.	Leaves dry wt.	0.01	-0.01	-0.01	-0.04
11.	Roots dry wt.	0.01	-0.02	-0.01	0.03
12	Plant dry wt.	0.03	-0.05	-.0.04	-0.06
	Latent Roots	1101.09	9.48	2.06	0.22
	Percentage variance	98.94	0.85	0.19	0.02
	Cumulative variance	98.94	99.79	99.98	100.00

are presented in Table 6. All the cultivars recorded highest loading for factor 2 followed by factor 1. The latent vectors presented in Table 7 indicate that the first three principal component cumulatively contributed 87.17%, 28.11% and 10.38% respectively for factor 1, factor 2 and factor 3.

Table 6. Principal component scores for interaction between cultivar and methods of propagation under influence of paclobutrazol drenching

Sl. No.	Cultivars	Method of propagation	PC1	PC2	PC3	PC4
1.	SAT	S	25.59	55.79	-5.53	-14.54
		M	31.70	59.65	-2.98	-11.44
2.	LAT	S	43.47	59.42	6.05	3.13
		M	49.99	59.55	4.05	2.46
3.	SLS	S	35.88	50.13	9.25	-9.79
		M	32.71	84.44	13.78	-7.65
4.	SOB	S	28.36	80.94	6.66	-1.58
		M	36.89	81.25	2.74	-5.32
5.	I	S	24.36	42.03	5.39	-1.97
		M	34.58	42.00	2.22'	-2.56
6	ADA	S	39.80	59.58	16.79	-18.57
		M	39.34	58.65	16.63	-18.29
7.	KM	S	15.71	63.40	0.84	-5.09
		M	37.52	71.40	-9.14	-8.82
8.	SM	S	45.11	67.66	-0.14	-8.82
		M	53.30	70.41	0.89	-4.95
9.	JL	S	66.25	61.79	4.46	-5.39
		M	70.76	63.21	5.35	-4.24
10	P	S	53.42	55.60	3.18	-7.42
		M	57.60	56.84	3.64	-6.86
11.	CV	S	36.95	58.63	9.23	-2.07
		M	44.24	60.29	8.12	-1.92
12.	AL	S	55.21	59.81	-2.12	-14.66
		M	63.61	63.58	-0.95	-10.03

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Table 7. Latent vectors and latent roots for variables under influence of cultivar and method of propagation

Sl. No.	Variables	Principal Component PC1	PC2	PC3	PC4
1.	Plant height	0.43	0.18	0.24	0.36
2.	No. of leaves	0.16	0.21	0.05	0.37
3.	Root length	0.16	0.18	0.33	0.49
4.	Stem diameter	0.04	0.00	0.04	0.01
5.	Length of internode	0.15	0.01	0.02	0.18
6.	Leaf area	0.22	-0.02	0.79	-0.54
7.	No. of secondary roots	0.69	0.36	-0.44	-0.37
8.	% of thick roots	-0.45	0.87	0.07	-0.13
9.	Stem dry wt.	0.02	0.01	0.01	0.00
10.	Leaves dry wt.	0.02	0.02	0.01	-0.01
11.	Roots dry wt.	0.02	0.02	0.01	0.01
12.	Plant dry wt.	0.07	0.05	0.02	0.00
	Latent Roots	192.44	110.00	40.63	33.94
	Percentage variance	49.17	28.11	10.38	8.67
	Cumulative variance	49.17	77.28	87.67	96.34

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Resistance in *Kalanamak* against Panicle Blast Caused by *Magnaporthe grisea*

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Kalanamak is one of the most important small and medium grained indigenous aromatic rices of India. Panicle blast, caused by *Magnaporthe grisea*, is one of the most serious problems of *Kalanamak*. Susceptibility of 37 germplasm of Kalanamak was tested against panicle blast under field conditions during the years 1999 and 2000. These germplasm showed wide variation in their susceptibility towards panicle blast. Ten *germplasm* were resistant to panicle blast. Some *germplasm* exhibiting moderate to high resistance towards panicle blast were also superior in yield and other quality traits.

Key words: Aromatic Rice, *Kalanamak, Magnaporthe grisea*, Panicle Blast, Resistance

Among small and medium grained Indian aromatic rice varieties, '*Kalanamak*' is one of the most important. For more than 2500 years it is being cultivated in districts of Siddharth Nagar, Basti and Gorakhpur of Uttar Pradesh (U.P.). Except for grain length, it is superior to Basmati in all other quality traits like aroma, elongation after cooking, fluffiness, taste etc. (Singh US and Singh RK, unpublished). In local markets, it fetches higher price than even Basmati varieties (Singh *et al.*, 2000). *Kalanamak* faced serious attack of panicle blast, caused by *Magnaporthe grisea*, during 1998 and 1999 resulting in decline in cultivation of this prime scented rice variety from 10 per cent to less than 1 per cent during the year 2000 in district Siddharth Nagar. In the absence of any seed production and/or improvement programme farmers have been using their own seed for hundreds of years. This has resulted in a high degree of impurity in this variety. An extensive survey of *Kalanamak* fields in district Siddharth Nagar, showed that it is now a mixture of lines sharing black husk colour, tall stature and relatively similar maturity durations. Wide variability within seed lot is resulting in decline in quality and yield. However, this variability can be exploited to improve the variety. Thus, the panicle blast susceptibility of 37 germplasm of *Kalanamak* were tested under field condition in order to identify resistant material, which could be either used as donor in breeding programme or can be promoted directly for the cultivation.

Materials and Methods

Plant Material

Thirty-seven germplasm of *Kalanamak*, collected from Siddharth Nagar, Basti and Gorakhpur districts of Uttar Pradesh and West Champaran district of Bihar, were purified by single plant selection at Rice Research Station, Nagina, which is in the aromatic rice growing belt of U.P. Seedlings of these germplasms were raised in field nursery during the years 1999 and 2000. Thirty-five-day old seedlings were used for transplanting. Five one-meter rows were transplanted with each germplasm. Plant to plant and row to row distances were 15 cm and 20 cm, respectively. Basal fertilizer application was @ 10 kg N+ 50 kg P_2O_5 + 40 kg K_2O + 25 kg $ZnSO_4$ per ha. Two more applications of N was done @ 10 kg per ha after 40 days of transplanting and at panicle emergence.

Incidence (proportion of panicles infected) and severity of panicle blast were assessed by following the standard procedure described by IRRI (1998-2000). Ten panicles were selected diagonally per plot (per germplasm) for the assessment. Panicle blast incidence was assessed as:

$$(\Sigma \text{ \% infected panicles from hill 1 to 10}) \div (10)$$

where, % infected panicles for each hill is calculated as: [(number of infected panicles per hill) ÷ (total number of panicles per hill)] *100

Observation on severity was recorded on 5 infected panicles for each sample hill. In case 5 infected panicles are not available, data was recorded only on available

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infected panicles. Severity was recorded using 0 to 9 scale: 0 = no visible lesion; 1 = < 5% of pedicels/ secondary branches of a panicle affected; 3 = 5 to 25 % of pedicels/secondary branches of a panicle affected; 5 = 26 to 50% of pedicels/secondary branches of a panicle affected; 7 = 51 to 75 % of pedicels/secondary branches of a panicle affected; 9 = > 75% of pedicels/ secondary branches of a panicle affected lesion completely around panicle base or uppermost internode or panicle axis near the base.

Disease severity on plot basis is calculated as:

(Σ of disease severity from hill 1 to 10) ÷ (10)

where, mean disease severity for each hill is calculated as:

(Σ of disease severity from panicle 1 to n) ÷ [(9) * (n)]

where, n is number of infected panicles assessed per hill and 9 is maximum disease grade.

Percent panicle blast index (PBI) was calculated as:

(Percent incidence)* (severity)

Based on panicle blast index, germplasm were categorized as Resistant (R; PBI <5), Moderately Resistant (MR; PBI 6 to 10), Moderately Susceptible (MS; PBI 11 to 20) and Susceptible (S; PBI > 20).

Results and Discussion

As shown in Table 1 and Figure 1, a wide variation in susceptibility of different germplasm of *Kalanamak* was observed under field condition. Out of 37 germplasm screened, ten exhibited a high degree of resistance against panicle blast. Although, screening was done under natural condition, incidence of panicle blast in some of the germplasm was as high as 100 %, indicating high degree of reliability of the data.

Details of the yield, agronomic and quality traits of some of the blast resistant and moderately resistant germplasm are given in Table 2. Yields varied from 1.3 t/ha to as high as 2.5 t/ha. These are quite high yields, if one compares with the farmers' average yields of approx. 1.0 t/ha. Large variation was observed for plant height, panicle length and grains per panicle. With a view to test the performance, these lines are being evaluated at several farmers' fields in the districts of Siddharth Nagar and Gorakhpur of Uttar Pradesh during the year 2001 and the observations are recorded on their disease and pest tolerance/resistance, yield and other traits. Based on their performance in these multi-location trails, we hope to promote a couple of them for commercial cultivation.

Table 1. Reaction of *Kalanamak* germplasm towards panicle blast

Disease Reaction	Germplasm
Resistant (R)	3114, 3121, 3128, 3130, 3131, 3213, 3216, 3220, 3259, 3320
Moderately Resistant (MR)	3081, 3089, 3119, 3120, 3126, 3130, 3168, 3214, 3215, 3256, 3266
Moderately Susceptible (MS)	3113, 3117, 3125, 3129, 3202, 3327, 3329
Susceptible (S)	3121, 3122, 3124, 3168, 3212, 3219, 3222, 3257, 3319

Table 2. Characteristics of some selected germplasm of *Kalanamak*

Germplasm	Plant height (cm)	Duration (days)	Tillers/ hill	Panicles/ hill	Panicle length (cm)	Grains per panicle	Grain characteristics			Paddy yield (t/na)*
							Length (L) (mm)	Breadth (B) (mm)	L/B	
3114	116	160	8.8	8.6	24	218	5.1	1.6	3.2	2.5
3119	136	160	8.4	8.4	24	205	4.6	1.6	2.9	2.5
3120	141	160	9.8	9.2	24	247	4.8	1.6	3.0	1.6
3130	107	160	9.4	8.8	30	203	5.9	1.9	2.6	2.4
3131	108	160	11.8	11.6	27	227	4.7	1.8	2.7	2.0
3216	125	165	8.2	8.0	22	202	4.7	1.6	2.9	1.3

*Based on 20 m^2 plot

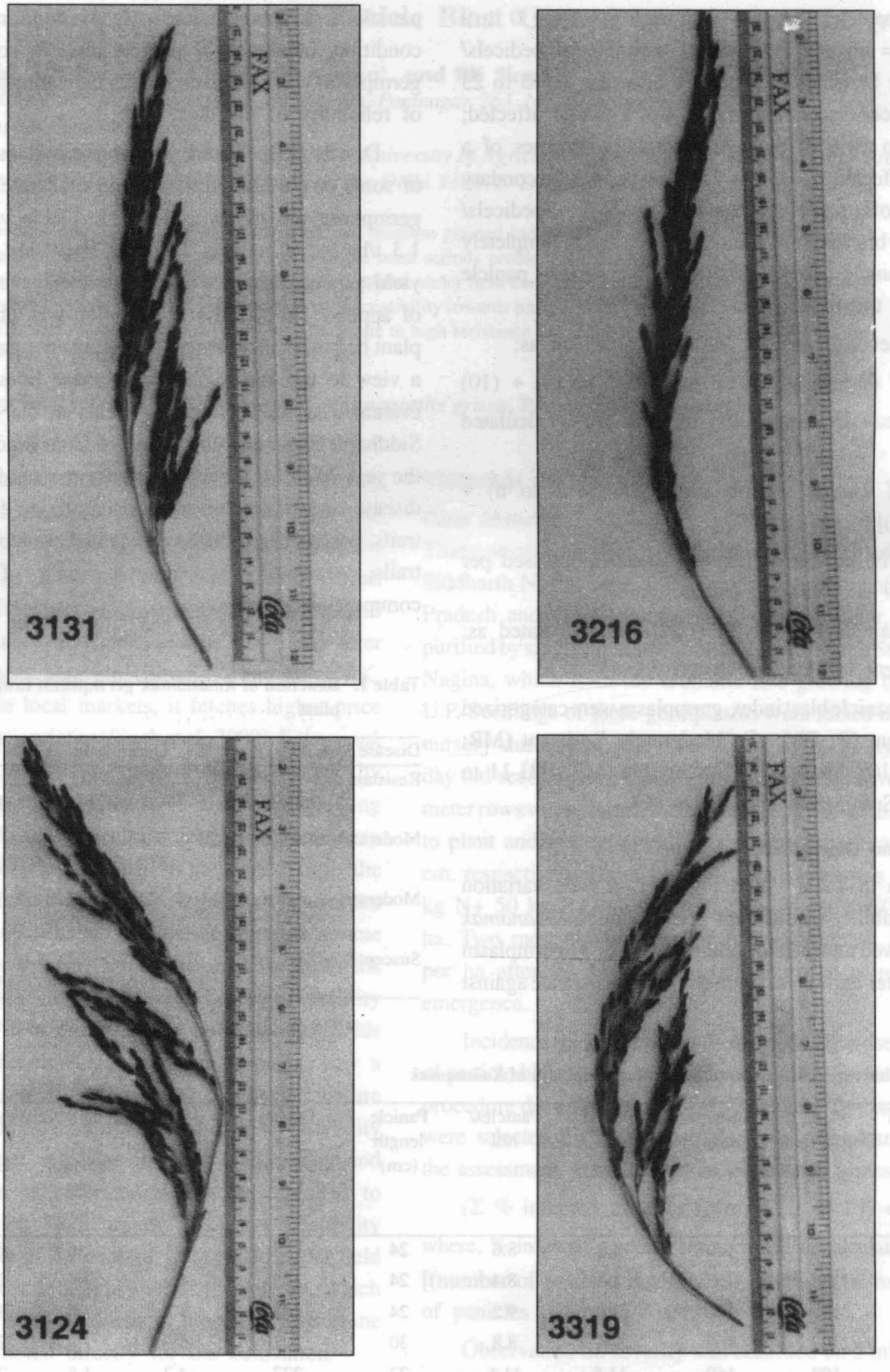

Fig 1. Panicles of two blast resistant (3131 and 3126; incidence 0 %) and two susceptible (3124 and 3319; incidence 100%) germplasm of Kalanamak. *Panicles of germplasm 3124 and 3319 are infected by panicle blast*

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Promising Wild Orchids of Andaman and Nicobar Islands and their Conservation

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Andaman and Nicobar group of islands are one of the three major habitats of orchids in India. A great diversity is observed in the flora of orchids, growing wild in the territory. Considering its importance, a survey was conducted in some potential forest areas of these islands and a germplasm collection of about twenty species of orchids made over a period of three years. Some of the promising species have been listed along with its description, status, occurrence and importance in this paper. The collected germplasm will be very useful in the breeding programme, besides ornamental values.

Key words : Andaman and Nicobar Islands, Conservation, Occurrence, Status, Wild Orchids

Floriculture trade has increased many folds in the recent times, considering its vast scope in the international and domestic market. Among the flowers, orchids occupy the premier place in the global market, contributing nearly 8 per cent by establishing a large spectrum of commercial potentialities. Orchids have immensely contributed to the economy of many developed and developing countries in the form of cut flower and pot plant.

Orchids are known for their diversity in forms, colours, appearances, size, shape and fragrance. Endowed exotic and delicate beauty with the long-lasting qualities are lured by scientists and layman alike. This majesty of nature represents the most highly evolved family *Orchidaceae,* among cotyledons, which is one of the largest groups in the plant kingdom. They are distributed throughout the world, right from tropical to temperate climates with more than 20,000 species in 800 genera. However, majority of orchids presently under cultivations are native to the tropical countries.

Many of our Indian species of orchids have contributed considerably for evolving famous hybrids as progenitors in Europe and USA. Still, there is a preference for hybrids endowed with beauty and novel color in the floriculture trade, where many of our native species can stand as competitors with them. India is the origin for the species like *Cymbidium,* ranking one of the top ten important plant in the floriculture trade of international market.

The climate conditions prevailing in Andaman and Nicobar group of islands are very much conducive for the luxuriant growth and development of various ornamental species, including flowering and foliage plants. A number of trees, shrubs, climbers, herbs, creepers, ferns, and other ornamental plants are found growing in the wild state. Among these, orchilds share as one of the largest groups in these islands, among the flowering plants. The tropical rain forests of these island ecosystem harbor over 110 species of orchids in wild state, of which most of them are epiphytic in nature except a few. Out of 110 species occurring in these islands, 25 species from 19 genera are reported to be endemic (Rao, 1996) and nine species in the rare and threatened category (Nayar, 1994).

Materials and Methods

Botanical explorations were conducted over a period of three years in the forest areas of Andaman and Nicobar group of islands, which have lead to a collection of about twenty species of indigenous orchids. All the collected species were subjected to cataloguing, description and evaluation in the wild natural forest ecosystem and also under the low-cost orchidanium. Based on the morphological and characters, it was found that most of the species are having ornamental values.

Among the collections, some of the promising wild species of orchids occurring in the Andaman and Nicobar Islands are listed below along with its botanical description, distribution, status and importance.

Results and Discussions

Eulophia andamanensis Reichb. f

It is a rare, terrestrial, sympodial type of orchid arising from stout pseudobulb with several clustered leaves. It is an endemic species distributed in the forest floor of Andaman group of islands especially in little Andaman reserved forests areas. The spike is arising from the side of pseudobulb, erect with about 24 florets in a

length of 70-100 cm, each flower measuring 3.0 to 3.7 cm across. Flowers are pale green with maroon streaks, white to pale green lip. Flowering is in November-March. Usually 3-4 spikes are produced from one pseudobulb and it remains on the plant for at least $1^1/_2$ months. It can be used as cut flower and pot plants due to its long-lasting quality.

***Dendrobium formosum* Roxb.**

It is an epiphytic orchid found in the trees, growing at higher altitude. It is the largest flower among the wild orchid flora of Andamans, bearing 4-5 flowers, each measuring 8-10 cm across at the tip of the cane. Flowers-white fragrant with yellow throat and attractive. Flowers last for about 5 weeks in the plant. It is distributed only in the Andaman group of islands in the forest area of Mount Harriet (South Andaman). Flowers during November-January and May-July. It can be used as cut flower and pot plant due to its attractive flower and long-lasting quality.

***Dendrobium Crumenatum* Sw.**

This is an epiphytic herbaceous orchid commonly seen in 'rain tree' (*Samania saman)* and mango tree as its hosts along the roadside. The plant grows fast and forms a bushy appearance in short time. Flowers borne in single usually; rarely in two or three produced at nodes, 3-4 cm across, white with yellow throat and highly fragrant. Blooms at least 4-5 times in a year, each flower remains for 2-3 days in the plant. Flowers look like bat. It is growing wild in the interior forest areas of Andaman and Nicobar group of islands. Owing to its fragrance, it can be grown as pot plant in the garden as well as at home.

***Dendrobium aphyllum* Roxb.**

An epiphytic orchid found in the branches of the trees in the hanging position. Flowers white with light maroon streaks in the light yellow base, usually 10-12 flowers per long spike. Flowers appear in the stem alternatively at leafless condition. Flowers during March-April. Each flower is short-lived for 2-3 days only. It is distributed only in Andaman group of Islands. It can be used as pot plant in the hanging basket for being its drooping spike.

***Dendrobium anceps* Sw.**

A small epiphytic, monopodial type of orchid found growing in the tree trunks of the forest areas. Stems flattened, leaves arranged very closely with pointed edges. Flowers small, light yellow with while lip and dark yellow throat appearing at the terminal of the stem as single usually, rarely in two or three, and also at node as single, thus number of flowers per stem varies from 1-3. Flower remains as fresh for nearly one week. Flowering season is April-July and September-November. This peculiar plant is distributed in Andaman and Nicobar group of islands. Being its dwarf and miniature stature, it can be grown as pot plants in hanging baskets.

***Dendrobium secundum (Bl.)* Lindl.**

It is an epiphytic orchid with slender stem generally seen in the branches of 'rain tree' along the road sides as well as in the forest areas. Flowers pinkish in color with dark pink lip, appears in the distal end of the stem during December-February in the leaf shed condition. It is distributed in the Andaman group of Island only so far. It can be used as potential pot plants for its beautiful 'tooth brush' like small flowers.

***Cymbidium aloifolium (Linn.)* Sw.**

An epiphytic, sympodial type orchid found growing in the tree trunks, is the largest of the orchids in the territory of the bay islands. It produces the cluster of leathering linear leaves with good anchorage on the tree trunks. Pendulous inflorescence appears from the base of the plant with 15-25 flowers, in a drooping manner. Flowers creamish yellow in color with eqi-distance in the inflorescence during November-March. This majestic look herbaceous plant is distributed only in the Andaman group of Islands. Due to its long-lasting quality and showy appearance of inflorescence, it can be suitable for growing as cut flower and garden plants in pots. Even, it can be grown in hanging baskets for its attractive drooping nature of the inflorescence.

***Bulbophyllum lepidum (Bl.)* J.J. Sm.**

It is an epiphytic, sympodial type of orchid with small pseudobulbs, each bearing solitary leaf of fleshy green and glossy appearance. Flowers during November-December with many in crimson red color having white lip at the terminal cluster in long erect, reddish peduncle. The small orchid is found in tree trunks at higher elevation in the seashore and interior forests of Andaman group of islands, particularly in South and Little Andamans. It can be grown as pot plants in hanging baskets for its small stature and attractive flower.

***Eria andamanica* Hook. f.**

A small, endemic, epiphytic orchid seen growing in

the trunks of "rain trees" along the roadsides. It bears ovoid pseudobulbs having 3-4 leathery leaves with linear lanceolate in shape. Flowers are very attractive, yellowish brown with purple batches, produced in 7-10 nos. on peduncle, measuring 15-25 cm in length. No of spikes per pseudobulb vary from 1 to 2. The flowers are thick with pubescence, which mimics the miniature birds. Flowering is in April-June. It is occurring only in Andaman group of islands, particularly Sourth Andamans. Owing to its attractiveness and longer shelf-life, it can be used both as cut flower and pot plant.

***Papilionanthe teres* (Roxb.) Schlech**

A large epiphytic orchid with thick, slender, leafy monopodial stems, found growing in the branches of Pyima *(Lagestromeia hypholeuca)* in the forests area and also in mango tree along roadsides in criss-crossed manner as thick mass like mat. Slender pencil thickness leaf is a peculiar phenomenon in the plant. Inflorescence is auxiliary, sub-erect or drooping with 5-7 showy flower with large size petals. Flowers are light pink with rich purple lip and reddish orange deeper inside. Flowers during February-May. It is very well distributed in the Andaman group of islands particularly in the forest area on host trees. Being attractive and brilliant in color, it is found suitable for growing as cut flower and pot plant.

***Agrostophyllum planicaule* (Wall ex. Lindl/Rchb.f.)**

This is a rare epiphytic orchid with crowded flat stems with one or two lanceolate leaves per stem. Found in inland forests of Andaman Islands. Inflorescence is auxiliary with very minute flowers appearing in clusters, bearing 10-20 in numbers. Flowers are yellowish white in color with dark yellow throat but not showy. Flowers during September-November. Due to its rare occurrence, it can be conserved for further improvement.

***Pholidota imbricata* Lindl.**

An epiphytic orchid with cluster of pseudobulbs, each producing a large size leaf, furrowed and wrinkled in age. Inflorescence arising from the base of the pseudobulbs, each in which small white flowers are arranged in two rows in drooping manner. Both the flowers and pinkish brown bracts together offer the splendor. Flowering is in May-September, found in shady trees like 'rain tree' *(Samania saman)*, tamarind and Pyima *(Lagestromia hypholeuca)* along the roadsides and in the forest areas of Andaman and Nicobar group of Islands. It can be grown as pot plants in hanging baskets due to its minute flowers in long pendulous raceme.

***Rhyncostylis retusa* Bl.**

It is commonly known as "fox-tail orchid". An elegant epiphytic orchid found growing wild in the shady trees of seashore sides and also in the forest area. Plants are erect with 6 to 9 pairs of leaves arranged on either side of thick short stem. Individual flowers arranged in the long pendulous inflorescence (40-50 cm) in a densely packed manner along the stalk gives attractive appearance like garland. The flowers are purple spotted white with pale mauve lip, which last for long time in the plant itself. Flowers during March-June. It is widely spread in the South Andaman and also in Nicobar group of Islands. Due to its droping pendulous inflorescences, long-lasting quality and attractive color, it can be grown as cut flower and pot plants in hanging baskets.

***Luisia teretifolia* Gaud**

A small epiphytic orchid with slender leaf. Flowers auxiliary in cluster of 7-10 numbers, greenish yellow with light green lip, conspicicuous. Flowering is in June-September and January-March. Flowers are not showy. It is distributed in the forest areas of Andaman and Nicobar group of islands. Since the flowers are not showy, it can be grown as pot plants in hanging baskets due to its slender leaf and dwarf stature.

***Oberonia iridifolia* (Roxb.) Lindl.**

It is a small epiphytic orchid with sword like flat, thick leaf, seen in the branches of shady-trees like Mango and Pyima in the inland forest areas of Andaman group of Islands particularly South Andaman. Inflorescence arises from the base of the plant in drooping pendulous manner. Flowers are minute with whitish yellow in color arranged compactly. Flowers during October-November. Flowers are not showy due to its minute (microscopic) nature. It can be used only as port plant for its flat leaf and dwarf stature.

***Spathoglottis plicata* Bl.**

A beautiful terrestrial orchid, grows to a height of 90-100 cm. It is a herbaceous plant, which produces attractive, showy lilac flowers at the terminal point on a long, erect peduncles during January-March. It is wide spread in the forest areas of Great Nicobar and Car Nicobar group of Islands. Also introduced into the houses and offices of Port Blair city as garden plant. Because of its attractive color, it is found suitable for growing as pot plant.

***Vanilla andamanica* Rolfe**

It is only climbing orchid found in the Andaman and

Nicobar group of islands, particularly in South Andaman, Great Nicobar and Katchal island. It grows up to a height of 2-3 meters on the tree trunks with thick, glossy, green leaves. Occurrence of this orchid is rare in these islands. It bears large, white, fragrant flowers with pink lip having white patches on it during December-April, which also sets fruits in the island conditions around July. Being its large, white, fragrant flowers and thick fleshy leaves, it can be grown as garden plant on the shady trees.

Utility

Some of the species can be used as genetic base material in breeding programme for evolving hybrids with attractive colour and long-lasting quality. Few of them can serve as donor plant for producing pest and disease resistant hybrids/varieties. Besides, some of the wild species are also reported to have medicinal values.

Conservation

Due to injudicious over- exploitation of natural resources and excessive intervention owing to human settlement, the survival of many species becomes threatened and as a consequence many got extinct or brought under rare and endangered category, which calls for immediate action plan to conserve such species in these islands.

As a part of *ex-situ* method, all the collected germplasm of wild indigenous orchids are being multiplied and maintained at indigenous low-cost orchidarium of Horticulture experimental farm of Central Agriculture Research Institute, Port Blair, Andamans. Utmost care is also taken to protect and conserve the rare and threatened species. Efforts are also being made to conserve them in *in-vitro* conditions.

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SHORT COMMUNICATION

Rapid Biochemical Method for Screening the Fenugreek Germplasm Against Powdery Mildew Disease

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Fenugreek (*Trigonella foenum-graecum* L.) is an important multi-purpose cash crop of India grown during winter season. It is prone to many diseases and amongst them, powdery mildew caused by *Erysiphe polygoni* DC is the most devastating and serious which alone causes more than 50 per cent yield losses. Breeding resistant varieties to this disease is of *priori* consideration, for which screening of germplasm is a pre-requisite for the identification of resistant sources. Certain biochemical compounds like phenols and oxidative enzymes have been reported to impart resistance to many diseases in various crops but this information is lacking in fenugreek. Screening of germplasm at early stages on the basis of phenolic contents may be a good criterion in fenugreek also. Keeping this in view, total phenols and ortho-dihydric phenols in healthy and diseased leaves of resistant and susceptible genotypes to powdery mildew were estimated at different growth stages for the establishment of biochemical basis of screening the fenugreek germplasm.

The fourth leaf from the top were collected from the plants of two resistant (NLM and HM 350) and two susceptible genotypes (T 8 and HM 65) which were grown under two environmental conditions *i.e.* artificially

Table 1. Total phenols (mg g^{-1}) in healthy and diseased leaves of fenugreek genotypes at different stages of growth

Genotypes	40 DAS		80 DAS		100 DAS	
	E_1	E_2	E_1	E_2	E_1	E_2
NLM(R)	36.61±0.38	36.30±1.27	44.80±0.48	45.03±0.30	42.14±0.23	38.93±0.41
HM 350 (R)	36.77±0.17	37.65±0.87	44.23±0.19	44.49±032	41.62±0.99	39.24±0.26
T8(H)	29.73±0.50	29.27±0.48	31.85±0.31	31.74±0.82	31.67±0.73	29.62±0.47
T8(50% D)	–	–	35.78±0.64	36.75±1.36	32.31±0.13	31.08±0.54
T8 (100%D)	–	–	39.18±0.68	39.03±0.28	36.85±0.18	33.40±0.54
HM 65 (H)	30.98±0.63	31.33±0.69	32.11±0.33	32.25±0.29	31.18±0.51	30.80±0.19
HM 65 (50% D)	–	–	35.44±0.41	35.13±0.63	34.98±0.18	32.01±0.08
HM 65 (100% D)	–	–	37.78±0.18	38.17±0.53	36.76±0.46	34.50±0.09
C.D. 5%	–	–	2.13	1.98	1.77	2.09

DAS = Days after sowing; E_1 = Inoculated environment; E_2= Natural Environment; R= Resistant; H= Healthy; D= Diseased

Table 2. Ortho-dihydric phenols (mg g^{-1}) in healthy and diseased leaves of fenugreek genotypes at different stages of growth

Genotypes	40 DAS		80 DAS		100 DAS	
	E_1	E_2	E_1	E_2	E_1	E_2
NLM (R)	6.37±0.04	6.54±0.06	7.61±0.04	7.54±0.02	6.46±0.09	6.22±0.06
HM 350 (R)	6.42±0.03	6.37±0.04	8.53±0.12	8.37±0.03	7.12±0.05	6.34±0.07
T8 (H)	4.28±0.04	4.41±0.07	4.38±0.02	4.44±0.06	4.30±0-.04	3.82±0.05
T8 (50% D)	–	–	5.69±0.06	5.88±0.07	5.14±0.06	5.08±0.10
T8 (100% D)	–	–	6.30±0.06	6.26±0.13	5.90±0.06	5.49±0.49
HM 65 (50% D)	4.91±0.07	4.87±0.87	4.89±0.02	4.97±0.06	4.14±0.07	3.63±0.03
HM 65 (50% D)	–	–	5.61±0.10	5.53±0.02	5.25±0.16	4.77±0.09
Hm 65 (100%D)	–	–	5.88±0.04	5.94±0.04	5.75±0.14	4.93±0.09

inoculated (E_1) and natural (E_2). The leaf samples were collected at three growth stages *i.e.* before appearance of disease at 40 days after sowing (DAS), after infection, 80 DAS and at severity, 100 DAS. These samples were categorised as healthy (having no visible symptoms of powdery mildew) and disease (having 50% and 100% leaf area mildewed). The samples were first sun-dried, then oven dried at 60°C and ground to fine powder. Total phenols were extracted and estimated by the method of Swain and Hillis (1959), while ortho-dihydric phenols were determined as per Johnson and Schaal (1952).

The pattern of total phenols and ortho-dihydric phenols (Table 1 and 2) clearly indicates that resistant genotypes exhibited significantly higher contents of both these compounds in comparison to healthy and infected leaves of susceptible genotypes at all the growth stages under both the environments (E_1 and E_2). These findings are in close agreement to those obtained by Parashar and Sindhan (1986), Kalia and Sharma (1988) and Rathi *et al.* (1998) for powdery mildew disease in peas. In the defense response to pathogen, the contents of both the compounds increased from 40 to 80 DAS and then uniformly decreased at last stage (100 DAS) in all the genotypes in both E1 and E2. Moreover, all the genotypes exhibited higher contents of both the phendies in E1 and E2. Moreover, all the genotypes exhibited higher contents of both the phendies in E1 than in E2 at 100 DAS, whereas such trend was not observed at 40 and 80 DAS. Sempio *et al.* (1975) reported that resistance in plants is expressed by oxidation of phenols to quinones which are more toxic to pathogen. In susceptible genotypes the fungus got enough time for its growth, whereas in resistant cultivars higher accumulation of phenols at initial stages might have succeeded in restriction of the pathogen. Moreover, higher contents of phenolics in resistant genotypes might have resulted in *estrification* of cell walls restricting, thus the entry of the pathogen as suggested by Fry (1987). Therefore, it can be concluded that higher contents of both total and ortho-dihydric phenols in resistant genotypes at initial stages might have imparted resistant to powdery mildew disease in fenugreek. By using estimation of any one of these phenolics, germplasm in fenugreek can be screened against powdery mildew even before the appearance of the diseases. Moreover, this technique is quicker, simpler, reliable and also there is no need to create artificial inoculated conditions for screening the germplasm.

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SHORT COMMUNICATION

Estimation of Combining Ability Effects of Parental Lines in Upland Cotton *(Gossypium hirsutum)*

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High yielding parents may not necessarily transmit their superiority to their progenies in crosses. Therefore, in a systematic breeding programme it is essential to identify the elite parents for hybridization and superior crosses to expand the variability reservoir for selection of superior genotypes. The line x tester mating design is very useful and simple procedure for preliminary evaluation of genetic studies through hybridization programme. Accordingly, the present investigation has been undertaken to determine combining ability for seed cotton yield and its component traits in *G. hirsutum* cotton.

Hybrid material for the study was generated from 10 selected diverse genotypes of *G. hirsutum* cotton. Two sets of 16 hybrids each were sown during *kharif* 1996-97 in randomized block design along with 10 parents. Spacing for hybrids and parents were kept 67.5x60 cm and 67.5x30 cm, respectively. In the first set of hybrids two female lines: K 34007 and F 891 and eight male testers: LRA 5166, F 505, LRK 516, H 777, F 1184, HS-6, LH 900 and F 1183 were used. Second set of hybrids consisted of eight females (testers and males of first experiment) and two males (lines and females of first experiment). The observations were recorded on ten plants for seed cotton yield per plant (g), boll weight (g), mean fibre length (mm), G.O.T.%, and seed index. Data were analysed following Kempthorne (1957).

Genotypes differed significantly from each other in both the sets of experiments. For the first set of experiment variance due to both GCA and SCA were highly significant for males and females except for mean halo length and seed index for females. In the second experiment both GCA and SCA variances were significant except mean halo length for females and boll weight and G.O.T. for males. This indicated importance of both additive and non-additive gene effects in the two sets of hybrids.

For the first set of hybrids, from the estimates of GCA effects it was revealed that, for seed cotton yield the best combiner female was F 891 and males were, LH 900, LRK 516, H 777, LRA 5166. For boll weight H 777, HS-6, LRK 516 and F 1183 males were the best combiners. F 891 and F 1184 were the best combiner female and male for G.O.T. and seed index respectively.

In general F 891 as female and H 777, LRK 516, LH 900, F 505, F 1184, HS-6 as males were found to be the best combiners. Further, it was also observed that parents showing significant GCA effects were also having medium to high *per se* performance for the respective traits in majority of cases.

In the second set of hybrids for seed cotton yield gca effects of the females: HS-6, LRK 516, F 1183; for boll weight of the females; LRK 516, F 1183; for G.O.T. of female HS-6 and for seed index of female HS-6, male K 34007 were significant and positive. This indicated that these male and female parents were the best combiners for their respective traits. *Per se* performance of parents showing significant gca effects were medium to high trait in most of the cases.

In the first set of hybrids for seed cotton yield/ plant the cross F 891xL H900 manifested highest sca effect followed by K 34007xLRA 5166, K 34007xH 777, F 891xF 505 and F 891xLRK 516. From the results, it is revealed that good general combiners may not necessarily produce specific combinations for this character. It is also revealed that the good combining line F 891 and testers LH 900, LRA 5166, H 777, LRK 516 exhibited high sca effects in their combinations for this trait. Such combinations may be expected due to contribution of favourable alleles by their parents. A number of earlier workers have also observed high sca effects for good combining parents

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in seed cotton yield (Bhatade, 1982; Bhatade and Bhale, 1983 and Tomar and Singh, 1992).

Minutes of sca effects were significant only in cross K 34007xLRA 5166 for boll weight. Male and female parents involved in this cross were poor combiner for the trait. This cross also exhibited significant positive heterosis for seed cotton yield. Cross K 34007xLRK 516 showed highest positive sca effects for mean fibre length and seed index, whereas cross K 34007xLRA 5166 manifested lowest sca effect for ginning out turn. It is revealed that those superior crosses for boll weight, mean fibre length, G.O.T. and seed index involved K 34007 poor combiner line parent.

Additive gene action for seed index, fibre length has been reported by Nadarajan and Rangaswamy (1990) and Khajjidone *et al.* (1984) and both additive and non-additive gene effects for ginning per centage and mean fibre length (Duhoon *et al.*, 1984). While for other characters additive gene action was found prevalent which is contradictory to the earlier reports of Nadarajan and Rangaswamy (1990) and Duhoon *et al.*, (1984). This might be due to the different genotypes contribution of the parents used in the present and earlier studies. The presence of non-additive gene action as exemplified by the equal proportion of sca effect will hinder the process of selection in the earlier generation and selection has to be postponed to later generation (Nadarajan and Rangaswamy, 1990).

In the 2nd hybrid set, for seed cotton yield crosses LRK 516xF 891 manifested highest sca effect (20.44), followed by F 1184xK 34007 (16.73), H 777xK 34007 (5.56) and HS-6xK 34007 (4.56). Like the hybrid set these crosses with high sca effects did not necessarily involve good combiner parents. High sca effect cross HS-6xK 34007 seed cotton also exhibited highest sca effects for G.O.T. (2.15) and Seed Index (21.54). For mean halo length none of the parent showed significant sca effect.

It was revealed from the study that K 34007 manifested high gca effect both as line and tester for seed cotton yield and its component traits. Four parents F 891, LRK 516, HS-6 and H 777 exhibited high gca effects for seed cotton yield both as line and tester.

The magnitude of gca effects for male and female parents were lower than the sca effects indicating the preponderance of non-additive components of genetic variance although additive component also present in sizable proportion. Therefore, it is suggested that in a cotton breeding programme aiming to improve yield, a three way or double cross involving possibly K 34007, F 891, LRK 516, HS-6 and H 777 may be produced and further handled through some form of recurrent selection procedure.

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SHORT COMMUNICATION

Selection of Parents for Heterosis Breeding through Line x Tester Analysis in Upland Cotton *(Gossypium hirsutum)*

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In the modern era of synthetic fibres, cotton continues to occupy top position as king of fibres and accounts for more than 60 per cent consumption in the World's textile industry. A study on heterosis will therefore have a direct bearing on the breeding methodology to be employed for varietal improvement. Hybridization is an important tool to exploit the genetic variability and breaking linkages as well as to create new genetic variability. Looking to the importance of the hybrid in increasing productivity as well as quality of cotton, present investigation was undertaken to measure heterosis for yield and its component traits.

Two experiments were conducted on 16 hybrids in each set. First experiment consisted of the crosses of two females (K 34007 and F 891 lines) and eight males (LRA 5166, F 505, LRK 516, H 777, F 1184, HS-6, LH 900 and F 1183 as testers). The second experiment consisted of eight females (testers and males of first experiment) and two males (lines and females of first experiment). These hybrids were grown along with ten parents in randomized block design with three replications during *kharif* 1995-96 and 1996-97. Hybrids and parents were grown at spacing of 67.5x60 cm and 67.5x30 cm, respectively. Data were recorded for seed cotton yield/plant (g) and its four component traits namely, boll weight (g), mean fibre length (mm), G.O.T. (%) and seed Index (g) and lint index on five randomly selected plants in each genotype from each replication. Heterosis was measured over better parent and the best parent.

The mean squares due to genotypes were significant in both the sets of experiment for all the traits indicating that there was enough genetic variability present in the experimental material selected for the study.

Seed Cotton Yield per Plant

In the first experimental set, three hybrids, K 34007xLRA 5166, F 891xLRK 516 and F 891x LH 900 showed more than 20 per cent positive heterosis (over better parent). The maximum heterosis observed over better parent was 52.71 per cent for the hybrid K 34007 x LRA 5166. Over the best parent, hybrid F 891 x LH 900 gave 29.69 per cent heterosis and 36.39 per cent over better parent.

In the 2nd experimental set the hybrids F 1184 x K 34007, HS-6 x K 34007 and HS 6 x F 891 gave the heterosis of 24.14 and 31.03 per cent over better parent, respectively. None of the hybrids could give more than 20 per cent heterosis over the best parent in this experimental set. Results indicated that crosses involving K 34007 and F 891 as male and female parents could give positive heterosis with other parents for seed cotton yield.

Boll Weight (g)

Six crosses for boll weight showed more than 20 per cent heterosis (22.77 to 42.04 per cent) over better parent in the first experimental set. The cross F 891 x HS-6 had maximum positive heterosis followed by F 891 x K 34007 and F 891 x F 505. None of the cross could show more than 20 per cent positive heterosis over best parent. Three crosses, H 777 x F 891, HS-6 x F 891 and LH 900 x F 891 had positive heterosis of 63.29, 48.23 and 22.35 per cent, respectively over better parent in the second experiment. Like for the first experiment, none of the cross in the 2nd experiment had more than 20 per cent heterosis over the best parent for boll weight. Results suggested that in crosses using F891 and HS-6 either as male or female with other parents give positive heterosis for boll weight.

Mean Fibre Length (mm)

In the first experimental set, hybrids F 891 x HS-6 (28.01%) and F891 x F 1183 (22.69 %), gave positive heterosis for mean fibre length over better parent. Over the best parent none of the hybrids gave positive heterosis. In the second experiment none of the cross combinations

had more than 20 per cent positive heterosis over either better or the best parents.

Ginning Out Turn (%)

The highest positive heterosis was observed for the crosses K 34007xH 777 (10.00) followed by K 34007 x LH 900 (8.33) and K 34007 x F1183 (7.39) over better parent in the first experiment. All the crosses gave negative heterosis over best parent. For crosses LH 900 x K 34007, F1184 x K 34007 and H 777 x K 34007 heterosis over better parent were 14.44, 8.03 and 7.78 per cent, respectively in the second experiment. The cross HS-6 x K 34007 showing heterosis over better parent was the only hybrid which also showed positive heterosis of 5.4 per cent over the best parents. For ginning out turn K 34007 could be used either as male or female for desirable heterosis.

Seed Index (g)

Only two crosses K 34007 x LH 900 (8.33) and K 34007 x F1183 (7.39) showed positive heterosis over better parent in the first experiment. Hybrids F1184xF891 and HS-6 x F891 gave positive heterosis of 8.64 and 6.17 per cent, respectively over better parent in the second experiment.

These results are in agreement with the findings of many workers who recorded significant heterosis for boll weight (Patil *et al.*, 1991; Tuteja *et al.*, 1993 and Ahuja and Tuteja, 2000) and for yield of seed cotton (Kalsy and Garg, 1989; Bhale and Bhat, 1990; Koodalingam *et al.*, 1991; Singh *et al.*, 1995; Tuteja *et al.*, 1993 and Ahuja and Tuteja, 2000) and quality traits like mean fibre length (Gupta and Singh, 1987; Wang and Pan, 1991) ginning out turn by (Rao *et al.*, 1977; Tuteja *et al.*, 1993 and Tiwari *et al.*, 1987), seed index (Mirza, 1986; Gupta and Singh, 1987; Rathinavelu and Premsankar, 1990). Results discussed clearly indicate that positive heterosis values were higher for experimental set involving two females and eight males (2x8) in comparison with eight female and two males (8x2).

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SHORT COMMUNICATION

Genetic Variability for Seed Yield and Component Traits in Newly Collected Germplasm of Yellow Sarson (*Brassica rapa* L. syn. *Brassica campestris* L. spp. yellow *sarson*)

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Rapeseed breeding strategy involve assembling or generating variable germplasm for selection of superior genotypes for utilizing them in hybridization programme to develop a superior variety. Assessment of genetic variability, heritability and genetic advance are necessary pre-requisite. The present study was undertaken to estimate the magnitude of genetic variability, heritability and genetic advance to determine breeding strategy and select superior genotypes from newly collected germplasm of yellow sarson.

Thirty seven germplasm of yellow sarson (*Brassica campestris* L. var. yellow *sarson*) collected form different districts of Uttar Pradesh under NATP on Sustainable Management of Plant Biodiversity including one standard variety Type-151 were grown in Randomised Block Design (RBD) with three replications during *rabi* season 2000-2001. Each treatment consisted of one row of three-meter length and 45 cm spaced apart. An approximate distance of 15 cm between plants was maintained by thinning after 15 days of sowing. Observations were recorded on five randomly selected plants in each replication for nine characters, namely days to flowering, number of primary branches/plant, number of siliquae on main raceme, number of siliquae/plant, length of siliqua (cm), number of seeds/siliqua, days to maturity, 1000 seed weight (g), and seed yield (g). Data recorded on 37 entries were subjected to analysis of variance for RBD according to standard procedure (Panse and Sukhatme, 1978). Genotypic and Phenotypic coefficients of variation were calculated according to method of Burton (1952). Heritability in broad sense (Burton and deVane, 1953), and expected genetic advance (Johnson *et al.*, 1955) were also estimated.

The differences among the germplasms were highly significant for all the characters under study. A wide range of variation was noticed in days to flowering, number of primary branches, number of siliquae on main raceme, number of siliquae/plant, length of siliqua, number of seeds/siliqua, days to maturity, 1000 seed weight and seed yield/plant (Table 1). High genotypic coefficient of variation was found for number of primary branches, number of siliquae/plant, length of siliqua and

Table 1. Range, mean, variance and coefficients of variation for seed yield and component traits in yellow sarson germplasm

Characters	Range	Means	SE	Variance		Coefficient of Variability,%		
				Phenotypic	Genotypic	Phenotypic	Genotypic	Environmental
Days to flowering	36.93-54.2	47.22	0.64	7.50	16.26	8.59	8.54	2.36
Number of primary branches/plant	4.93-15.07	9.85	0.47	7.21	6.52	27.27	25.93	8.43
Number of siliquae on main racemes	26.8-61.6	38.02	0.27	50.26	50.09	18.65	18.60	1.27
Number of siliquae/plant	89-252.6	161.33	5.44	1344.71	1255.64	22.72	21.96	5.85
Length of siliqua (cm)	2.98-7.5	4.42	0.04	1.08	1.074	23.51	23.43	1.89
Number of seeds/siliqua	26.8-46.0	86.07	0.53	19.78	18.92	12.33	12.06	2.57
Days to maturity	106.4-118.07	112.58	0.78	13.16	11.30	3.22	2.99	1.21
1000 seed weight (g)	2.13-5.13	3.787	0.40	0.82	0.46	23.96	17.85	15.97
Seed yield/plant (g)	11.3-22.75	17.31	0.34	7.11	6.61	15.40	14.85	4.09

1000-seed weight. Moderate genotypic and phenotypic coefficients of variation were observed for number of seeds/silique and seed yield/plant. Gupta and Singh (1998) reported high estimates of genotypic coefficient of variation for yield/plant followed by pods on main shoot, plant height and number of branches. The coefficient of variation indicated high magnitude of variability in the germplasm. Selection may, therefore, be effective for these characters. Days to maturity showed low genotypic and phenotypic coefficient for this character. Hussain *et al.* (1998) observed highest phenotypic coefficient of variation and genotypic coefficient of variation alongwith high estimates of heritability and genetic advance for secondary branch number, biological yield per plant and number of seeds per siliqua. High heritability was observed for all the characters except 1000-seed weight, which showed moderate estimate of heritability (Table 2). Number of seeds/siliqua and days to maturity showed very low genetic advance.

High heritability with high genetic advance were observed for length of siliqua (cm), number of primary branches and number of siliqua/plant. Moderate heritability and genetic advance were observed for 1000 seed weight. Phenotypic and genotypic coefficient of variability together with heritability estimates revealed selection will be more effective for number of seeds/ siliqua and seed yield/plant. This is in conformity with the finding of Bagrecha *et al.* (1972).

The genotypes having high heritability with high genetic advance for length of siliqua (cm), number of primary branches, number of siliquae/plant, seed yield/ plant (g) indicated that additive gene effects were more important for these characters and selection pressure could be applied on these for yield improvement. A wide range of variation was noticed for phenoytypic coefficient of variability, genotypic coefficient of variability, environmental coefficient of variability, heritability and genetic advance.

Table 2. Estimate of genetic parameters in yellow sarson

Characters	Heritability (%)	Genetic advance	Genetic advance in percent of mean
Days to flowering	92.92	7.93	16.78
Number of primary branches	90.43	4.98	50.53
Number of siliquae on main raceme	99.54	14.46	38.02
Number of siliquae/plant	93.38	70.25	43.59
Length of siliqua (cm)	99.35	4.37	98.66
Number of seeds/siliqua	95.65	0.73	1.94
Days to maturity	85.85	6.34	5.62
1000-seed weight (g)	55.93	0.27	29.18
Seed yield/plant (g)	92.98	5.05	27.13

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SHORT COMMUNICATION

Screening of Maize Germplasm for Multiple Disease Resistance

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Maize is predominantly grown during *kharif* season in tropical and sub-tropical environments in an area of 6.4 million hectares and production of 11.47 million tonnes is third important cereal crop in India (Anonymous, 2001). The productivity in the country (1.8t/ha) against 7.0 t/ha in temperate areas and world average (3.8t/ha) is very low. Diseases such as Bacterial stalk rot (*Erwinia chrysanthermi* pv. Zeae), Maydis leaf blight (MLB), (*Dreschslera maydis)* and brown stripe downy mildew (BSDM) (*Sclerophthora reyssiae* pv. Zeae) are important bottlenecks causing significant reduction in grain yield (Sharma *et al.,* 1993). These diseases can be partially managed by biocides. High rainfall during the crop season restricts the resource starved farmers to use costly chemicals. Under these conditions the cultivation of resistant varieties is economically viable, practically feasible and cost effective alternative. Keeping this in view some Indian hybrids and composites were evaluated against these diseases and resistant stocks against widely prevalent diseases in northern parts of the country are reported herein.

Two hundred sixty six hybrid and composite stocks of Advanced Breeding Material received from Directorate of Maize Research, New Delhi, were planted during Kharif 2000 at experimental farm of RRS Dhaulakuan, following recommended agronomic practices (Anonymous, 2000). Bacterial stalk rot epiphytotics were created by inoculating 75-100 plants/entry using hypodermic syringe method (Anonymous, 1983). The field is inoculum sick with brown stripe downy mildew (*Sclerophthora rayssiae* pv zeae), however, to avoid disease escape, 30 days old plants were whorl inoculated with brown stripe downy mildew infected maize leaf bits (Anonymous, 1983). The evaluations against Maydis leaf blight were on natural infection basis. The data were recorded on per cent wilted plants in case of *Erwinia* stalk rot, 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 (Anonymous, 1983). The balanced seed of each entry was evaluated during the subsequent *kharif* (2001) season to confirm their reactions.

The hybrid and composite stocks showing resistance against *Erwinia* stalk rot, brown stripe downy mildew and maydis leaf blight during the year 2000 and 2001 are given in Table 1. None of the entries were free from *Erwinia* stalk rot, brown stripe downy mildew or maydis leaf blight. Stocks Agri MH-101, AH01135, AH-1139, BH-1620, BISCO 103, JK 2002, JH 3773, PAC 70002, Rasi MH-102, Sneha, UMC 12 and WH-1 were resistant with less than 10% stalk rot incidence, 22 entries with disease reaction <2 to BSDM and 24 stocks with 1-2 disease reaction were resistant to maydis leaf blight. In addition 31 hybrids with 10-20% disease incidence, 24 and 26 stocks with disease reaction 2.0-2.5 were moderately resistant to *Erwinia* stalk rot, BSDM and MLB, respectively. It has been observed that frequency of entries resistant to *Erwinia* stalk rot was more frequent in stocks of full season maturity. In case of MLB and BSDM resistance was more frequent in early maturing entries. Sources of resistance among inbreds, hybrids and composites have also been reported against *Erwinia* stalk rot (Thind and Payak, 1985; Ebron *et al* 1987; Basandrai *et al* 200), *maydis* leaf blight (Khan *et al* 1992, Liu *et al* 1990; Sharma and Payak 1990; Basandrai *et al* 2000) and brown stripe downy mildew (Bains *et al* 1989; Basandrai *et al* 2000).

It has been observed that hybrids AH 1103, AH 1135, AH 1139, BISCO 103, BH 1718, BH 1542, BIO 9681, D 996, Ganga 11, JC 1441 (FS)C_1, JH 3773, JH 10044, JH 10054, JH 10056, NMH 99503, Nardi 216, PHS 4790, Rasi MH-1093, Sneha Gold, Seed Tach 204 and Z-13346 showed multiple resistance against all the three diseass. Hybrid BH 1680, FH 3146, JH 3776, PAC 70002, PGM 411, Rasi MH 102, R. 9801, Sneha, Surya 116 and Agri MH 101, BH 1620, BIO 91119, F 2784, HKH 1170, KH 2002, JH 10070, JH 3861, PAC 70002, Rasi MH 102, Sneha, UMC 12, WH 1 showed combined resistance against *Erwinia* stalk rot and brown stripe downy mildew and *Erwinia* stalk rot and maydis leaf blight, respectively. Stocks D-994, F-8007, JH 3861, PAC 70004, 70002, 70005, PGM 411, PHS 4755, 4787, PRO 348, SYN 1(y), Sneha, Seed Tech Surya 11 and X 3342 were resistant to maydis

Table 1. List of maize stocks resistant to *Erwinia* stalk rot (*E. chrysanthemi* pv zeae), downy mildew (*Sclerophtora rayssiae*) and *maydis* leaf blight (*Drecheslera maydis*).

Erwinia Stalk rot

Resistant (<10%)	Moderately resistant (10-20%)
Agri MH-101, AH-1135, AH-1139, BH 1620, BISCO 102, JK 2002, JH 3773, PAC 70002, Rasi MH 102, Sneha, UMC 12, WH 1	AH-1103, BH 1680, -1718, -1542, BIO 9681, -52331, 091119, D 996, F 2784, FH 3146, Ganga 11, HKH 1170, JC 1441 (FS) CI, JH 10056,-10044,-10054,-10070, -3778,-3861, NMH 99503, Nardi 216, PHS 4790, PGM 411, PRO 347, 311, Rasi MH 1093, R 9801, Surya 116, Sneha Gold, Seed Tech 204, X-13346

Brown stripe downy mildew

Resistant (<2)	Moderately resistant (2.1-2.5)
AH 1103,-1135, BISCO 103, BIO 52231, D 994, F 8007, JH 3861, 3773, 3776, 10054, JC 1441 (FS)C_1, PGM 411, PAC 70004, PHS 4755, 4787, R 9801, Rasi MH 102, 1903, Syn 1(Y), Sneha, Seed Tech Surya 11, Seed Tech 204	AH 1139, BH 1680, 1718, 1542, BIO 9681, D 996, FH 3146, Ganga 11, JH 10056, 10044, NMH 99503, Nech 108, Nardi 216, PRO 348, 311, PAC 70002, 70005, PHS 4754, 4790, Surya 116, Seed Tech 101, Sneha Gold, X 3342, 13346

Maydis leaf blight

Resistant (<2)	Moderately resistant (2-2.5)
AH 1103, BIO 9681, D 994, 996, F 2784, GK 3030, JC 1441(FS)C_1, JH 10044,-10054, -10056, -10070,-3773, -3861, PGM 411, PRO 347,-348, PHS 4787,-4790, Surya 116, Seed Tech 101, Seed Tech Surya 11, UMC 12, WH 1, X 3342	Agri MH 101, AH 1135, 1139, BH 1718, -1620,01542, BIO 91119, BISCO 103, F 8007, Ganga 11, HKH 1170, JK 2002, Nech 108, NMH 99503, Nardi 216, PAC 70005, 70004,-70002, PHS 4755, Rasi MH 102, 1093, Sneha, Syn 1(Y), Sneha Gold, Seed Tech 204, X 13346

leaf blight and brown stripe downy mildew. Sources with muliple resistance have been reported against *maydis* leaf blight and brown stripe downy mildew (Dey *et al.* 1983), *Turcicum* leaf blight, *Maydis* leaf blight and brown spot (Kaiser and Pradhan, 1990) and *Erwinia* stalk rot, brown stripe downy mildew and *Maydis* leaf blight (Basandrai *et al.,* 2000).

Interestingly Ganga 11, PRO 311, PRO 348, Sheha, Gold and Surya 11 are identified varieties which can be deployed in disease prone areas. Most of the stocks are hybrids from private companies, if inbred of these stocks are available further studies can be undertaken on characterization of resistance against these diseases.

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Recommendations of the Symposium on Plant Genetic Resources Management: Advances and Challenges

1-4 August, 2001

The Indian Society of Plant Genetic Resources organised a symposium on 'Plant Genetic Resources Management: Advances and Challenges' from 1-4 August 2001 at National Bureau of Plant Genetic Resources (NBPGR), New Delhi. The symposium provided an opportunity to scientists and other stakeholders associated with various disciplines related to Plant Genetic Resources (PGR) to interact, exchange their views and develop strategies related to conservation and sustainable use of PGR.

The themes were discussed in the different technical sessions with keynote speaker(s) followed by contributory oral and poster presentations. The focus of the symposium was the paradigm shift from genetic resources as "common heritage of (Hu) mankind" to "the sovereign rights of the nations" in the light of the international developments on control and access of PGR, and benefit sharing.

The key recommendations that emerged out during the deliberations of the symposium are as below:

Access to PGR, Phytosanitation and International Developments

- In view of the changing global scenario with regards for access to PGR, there is an urgent need to introduce germplasm from the available sources. Emphasis should be given for trait-specific germplasm and a mechanism should be developed to avoid repeated introductions.
- The phytosanitation aspects of PGR need to be properly addressed. The National Plant Quarantine System needs to be strengthened. There is an urgent need to undertake pest risk analysis as per sanitary and phytosanitary measures of World Trade Organization (WTO) Agreement and identification of pest free areas for large scale seed production for increasing the export potential of our agricultural produce.
- In addition to PGR there is also a need to develop and implement guidelines for safe exchange of beneficial organisms related to agro-biodiversity.
- Domestic quarantine has to be made more effective, and quarantine checks on all imports should be strictly followed.
- The mechanisms and models of benefit sharing need to be developed to ensure the rights of nations and communities on PGR as envisaged in various national and international policies.

Genetic Erosion and Collection Strategies

- There is a need to protect warm-spots, which signify areas having large agro-biodiversity as these have co-evolved with human civilization.
- The fast changing social, cultural, political and economic considerations are leading to rapid erosion of agro-biodiversity in all the regions. There is an urgent need for generating awareness and developing action plans to arrest and restore the lost diversity.
- There is a need to transform the weaknesses of traditional practices into strengths by developing strategies to prevent further loss of agro-biodiversity. Practices such as *jhoom* cultivation should be discouraged and peoples' participatory approach for adoption of practices, such as organic farming should be encouraged.
- The exploration missions should be targeted for the collection of value based/trait specific PGR from diversity rich areas of major diversity zones like desert habitats, wetlands, saline habitats, etc. lest these are lost.
- There is a need to develop human resources in plant taxonomy and biosystematics.
- New tools of geographical information system (GIS) and remote sensing must be utilized to supplement the ground data in the national PGR management programme to exploit agro-biodiversity particularly in difficult/inaccessible areas.

Germplasm Conservation

- There is a need to adopt complementary conservation strategies involving both *in-situ* and *ex-situ* approaches. Due attention is to be given to genetically rich hot spots like tribal belts. Emphasis should be to conserve wild and related species of crop plants that possess many useful genes for biotic and abiotic stresses.
- The National Genebank network should be strengthened and its full potential should be realized.
- There is a need to promote on-farm management and conservation of local genetic diversity. Incentives such as developing niche markets for aromatic rice varieties, organic farming products etc. need to be provided and innovative ideas involving poets and cultural activities etc. should also be explored.
- The vast expanse of PGR requires the development of appropriate methodologies and protocols for promoting conservation of germplasm. The linkage between stakeholders including advanced laboratories, traditional universities, NGOs, etc. need to be strengthened for effective implementation of conservation programmes.
- There is a need to register and conserve value added germplasm such as those generated in the Advance Varietal Trials (II year).

Germplasm Enhancement and Utilization

- There is a need to enhance utilization of the collected and conserved germplasm and to achieve it, evaluation of PGR should receive priority attention. Strong partnership with All-India Co-ordinated Research Projects (AICRP) in crop improvement, State Agricultural Universities and crop-based institutes is necessary to work out a strategic plan for evaluation and genetic enhancement of PGR.
- NBPGR, the nodal institution for PGR management, should arrange a workshop with all Project Coordinators and Project Directors of AICRPs to plan the pre-breeding work.
- The importance of developing core collection particularly in crops having a large number of collections and of native origin should be emphasized. For this purpose, priority may be given to pulses and oilseeds.
- A judicious use of molecular characterization in assessment of diversity needs to be made.

National Policy on Plant Genetic Resources, Action Plan and Implementation Strategies

- National Active Germplasm network should be strengthened and further expanded. Crop based PGR networks for evaluation and enhanced use are required, with concerned AICRPs and crop-based Institutes as major partners in the activities. This national network should have effective linkages with regional and global PGR networks.
- National clonal repositories should be established for horticultural crops and there should be a national coordinator for their proper coordination.
- Collaborative efforts by NBPGR and AICRPs are essential to evaluate germplasm. For this specific budget allocation should be made available to the nodal institution for effective implementation of the programme.
- There is a need for judicious use of biotechnological tools for PGR conservation, characterization and use keeping in view the biosafety aspects for commercial cultivation of transgenics.
- Networks are seen as efficient and cost effective mechanisms of information generation. An encrypted national database linking the various stakeholders engaged in PGR activities needs to be developed on priority and NBPGR should take a lead in this endeavor.
- There is a need to develop suitable mechanisms and procedures for addressing issues like *in-situ*/ on-farm conservation, documentation of indigenous technical knowledge (ITK), benefit sharing, farmers' rights, germplasm sharing with private/ public sectors etc.
- Appropriate policy interventions are required for developing suitable mechanisms for value addition and marketing strategies for on-farm conserved PGR.
- Human Resource Development is very important to compete at international level. Teaching PGR at postgraduate, under graduate and school level

should be taken up. NBPGR could be a facilitator in this activity.

- Mass awareness should be created and for that matter, media should be sensitized.
- In view of the rapid global developments there is an urgent need to put in place the national regulatory mechanism for access, exchange, conservation and utilization of PGR. Further, an Agricultural Attaché in the various Indian embassies or consulates abroad would greatly facilitate the protection of the sovereign rights and national interests *vis-à-vis* PGR related aspects.
- A national symposium should be organized specifically for horticultural crops to analyze the PGR status in horticulture, gaps in collection, characterization, utilization and conservation.
- The scientific community through professional scientific societies like Indian Society of Plant Genetic Resources should contribute in analyzing, assessing and formulating opinion on the implications of various national policies related to PGR management in view of changing international scenario.

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