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Genetic Resources of Tamarind

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The tamarind tree has gained great socio-economic significance in a large part of the globe. It yields a large number of economic products from the fruit pulp and the seed, besides the usage of almost all its plant parts either as timber, fuel, vegetable or medicine. Introduced into the Indian sub-continent during pre-historic days, a wide genetic diversity of tamarind is found in India. The paper provides information on the diversity regions, extent of variability with respect to growth and fruit characters, germplasm holdings, evaluation and selection of genotypes, etc. A scheme of classification of tamarind types based on fruit characters and ideotype description to aim at genetic improvement for commercial exploitation have been suggested.

Key Words: Diversity, Genetic Resource, Germplasm, Tamarind

Tamarind (*Tamarindus indica* Linn.), a truly pantropical tree, is highly drought hardy and can be grown in dryland areas and on degraded, eroded, gravelly, saline and sodic wastelands. Optimum annual rainfall for tamarind is over 750 mm, but it is also found to thrive in regions receiving less than 500 mm rainfall. It can also be grown in localities subject to high winds because of its strong and pliant branches. Thus it is one of the most suitable tree as a windbreak to prevent soil erosion and to protect people, crops and animals in harsh environments.

The tamarind tree has great commercial importance owing to the usefulness of almost all its parts, *i.e.* the leaf, flower, fruit and wood. Its fruit has the greatest value. The fruit contains 43 to 73% edible pulp, 12-40% seed and 11 to 25% shell and fibre. The pulp is very nutritious being rich in calcium, phosphorus, riboflavin, niacin and thiamine (Table 1). Tartaric acid and invert sugars are the major constituents of the pulp. Of the invert sugars, 70% is glucose and 30% is fructose with only a trace of sucrose. A large number of products are prepared from the fruit pulp. Young tamarind seeds contain 10-15% (by weight) amber, sweet-tasting oil (Allen and Allen, 1981). This high quality oil is used in varnishes and paints, for finishing Indian cloth, and as an illuminant. In India and South-east Asia, tamarind seeds are also crushed and boiled to produce a paste that is used as a roofing material. This material is highly resistant to corrosion by salt sprays from sea waters.

Tamarind kernel powder (TKP) contains nearly 60% jellose (Savur and Sreenivasan, 1948) which can be used as a substitute of fruit pectin (Table 1). The TKP is also of great value as a sizing material for cotton and jute yarn. The immature leaves are used to garnish curries and vegetable preparations. The tree is, therefore, of considerable commercial value besides its use as an avenue tree or for rehabilitation of marginal lands.

Diversity Regions

The tamarind is native of tropical Africa and Asia (Bailey, 1949), although the species name *indica* gives an illusion of it being of Indian origin. In fact, Watt (1898) had suggested that tamarind is native to some parts of south India. Tamarind is found in wild form in extensive areas of Africa particularly Ethiopia and Sudan which is believed to be its native home and from where it disseminated throughout the tropics. It reached India and South-east Asia, perhaps during the pre-historic times, where it got naturalized.

Tamarind occurs throughout the tropics and subtropics covering the Caribbean, Central American, South American, European, African, South Central Asian, South-East Asian and Oceania regions. It occurs in wild form all over Central Africa from Senegal in the west through Ghana, Niger, Nigeria, Sudan to Ethiopia in the east and then southwards to Tanzania and Zimbabwe and extending eastward into the Reunion Islands (Fig. 1). It is also found wild in southern India, Sri Lanka in South Asia and in the Philippines, Malaysia, Thailand, Fiji and New Caledonia islands in South-East Asia. Another important diversity region extends from Mexico through central America and the Caribbean region into South American parts of Ecuador, Peru, Colombia, Puerto Rico, Costa Rica, Venezuela and Brazil.

In India, tamarind largely occurs in the peninsular region mainly in the districts of Dharmpuri, Kamrajar and Kanyakumari in Tamil Nadu; in Chintamani and Srinivaspur regions of Karnataka; in Sholapur, Osmanabad, Satara, Sangli, Ahmednagar, Nasik and Aurangabad districts in Maharashtra; and in Bastar in Chhattisgarh (Fig. 2). However, its trees can be found

Table 1. Composition of tamarind pulp, seed, immature leaves and flower

Constituents	Pulp (ripe)	Seed	Young leaves	Flower
Moisture (%)	17.8-69.0	9.4-11.3	70.5-78.0	80.0
Protein (%)	1.3-3.10	13.3-26.9	4.0-5.8	0.45-2.8
Lipid (%)	0.40-0.80	–	–	–
Fat (%)	0.10-1.00	4.5-16.2	1.2-2.1	1.54
Fibre (%)	2.9-5.6	7.4-8.8	1.9-3.0	–
Carbohydrate (%)	41.1-71.8	50.0-61.7	16.0-18.2	1.5
Ash (%)	1.5-4.2	1.6-4.2	1.0-1.5	0.72
Calcium (mg/100 g)	34-170	–	101-250	35.5
Magnesium (mg/100 g)	–	–	71.0	–
Phosphorus (mg/100 g)	34-110	–	140.0	45.6
Iron (mg/100 g)	0.2-10.9	–	2.0-5.2	1.5
Copper (mg/100 g)	–	–	2.0-2.1	–
Chlorine (mg/100 g)	–	–	94.0	–
Sodium (mg/100 g)	24	–	–	8.0
Potassium (mg/100 g)	375	–	–	270.0
Sulphur (mg/100 g)	–	–	63.0	–
Vitamin A	151 IU	–	250 IU	–
Thiamine (mg/100 g)	0.3-0.59	–	0.24	0.072
Riboflavin (mg/100 g)	0.07-0.18	–	0.17	0.148
Niacin (mg/100 g)	0.6-12.0	–	1.5-4.1	1.14
Ascorbic acid (mg/100 g)	0.07-44	–	3.0-6.0	13.8
Tartaric acid (%)	8-28	–	–	–
Total acidity (%)	17.1-18.4	–	–	–
Cellulose (%)	1.8-3.20	–	–	–
Pentose (%)	4.2-4.8	–	–	–
Total sugar (%)	4.4-21.4	–	11.3-25.3	–
TSS (°Brix)	15.5-88.0	–	–	–
Pectin (%)	2.4-4.4	–	–	–
Energy Kcal/100 g	230-272	340.3	75.0	–
Starch (%)	–	33.1-63.0	–	–
In vitro protein digestibility (%)	–	71.6	–	–
Oxalic acid (mg/100 g)	Trace	–	196.0	–

Source: Pratt and Rosario (1913), Padilia and Solivan (1933), Maranon (1935), Galang (1955), Anon (1944), Lewis *et al.* (1954), Mitra and Misra (1967), Intengen (1968), Shanmugavelu and Rangaswami (1969), Anon (1972), Anon (1982), Morton (1987), Keskar *et al.* (1989)

all over the country extending northwards up to the Himalayas and eastwards into West Bengal and Assam plains along the water courses.

Germplasm Collections

The FAO-World Information and Early Warning System on Plant Genetic Resources lists 16 institutions holding 99 germplasm accessions of tamarind. Some of the collections are in Burkina Faso (9 wild/weedy accessions), Costa Rica (1), Ethiopia (5), France (2), Ghana (1), Honduras (1), Mexico (2), Philippines (12), Senegal (2), El Salvador (1), Taiwan (1) and USA (10). In India, there is a wealth of tamarind variability particularly in central and southern regions. However, systematic efforts have not been made so far to collect and evaluate this germplasm. The organizations holding tamarind germplasm in India have been listed in Table 2.

Conservation of elite trees for commercial exploitation has, thus, been done in several countries of the world. Clonally propagated systematic plantations have also been done. Even then, concerted efforts are necessary to conserve its genetic resources. It is equally important that methods and programmes are also developed to systematically evaluate these collections. This should include description using the standard descriptors including the important economic characters besides biochemical characteristics wherever relevant.

Variability in Plant Characters

Tamarind is essentially a cross pollinated crop (Thimmaraju *et al.*, 1977). As a result of cross pollination, seedling plants depict heterozygosity in morphological and physiological traits of the tree (Table 3). The height of tree varies from 25 to 30 m (Chaturvedi *et al.*, 1985) and at breast height maximum diameter from 1 to 4 m (Gamble, 1922). Tree longevity varies from 150 to 200 years (Anon., 1991).

Phenological variations in flowering and fruit maturity have also been reported (Mahadevan, 1991). Similarly, phenotypic variations have been observed in fruit characters such as pod weight, seed and pulp content, colour and taste of pulp, endocarp colour, etc. (Table 4).

Table 2. Tamarind germplasm collections conserved field genebanks in India

Centre	Number
State Agricultural Universities	
Belgaum, Karnataka	40
University of Agriculturel Sciences, Bangalore	19
Aurangabad, Maharashtra	351
Kovilangulam, Kamarajar, Tamil Nadu	26
Periyakulam, Tamil Nadu	85
Rahuri, Ahmednagar, Maharashtra	14
Pune, Maharashtra	118
Parbhani, Maharashtra	3
IGAU, ZARS, Jagdalpur	5
Bastar, Chattisgarh	
Forest Department, Karnataka	
Gottipura, Bangalore	40
Challekere RF, Bellary	50
Bidar	10
Yeregera, Raichur	10
Gungurgatti, Dharwad	70
Other stations in Karnataka	40
Forest Department, Tamil Nadu	
Coimbatore	40
Sesanchavady, Salem	61
Athivur, Erode	5
Varattupallum, Erode	4
Harur, Dharampuri	28
Ramanahalli, Dharampuri	23
Chengam, Tiruvaannamalai	52
Karumbapatti, Salem	77
Varinchipuram, Vellore	38

Table 3. Variability in tree characters in *Tamarindus indica*

Character	Range
Tree height (m)	5-34
Trunk girth (m)	1.5-7.0
Tree spread (m)	2.9-12.6
Tree volume (m^3)	50-1640
Number of leaflets	20-40
Fruit yield/tree(kg)	50-1500
Regularity in bearing (on:off year yields) (kg)	1:1-3 to 16:1

Source: Chaoji (1995), Hooker (1979)

Wide range of variability in morphological and physico-chemical characters of fruit has been observed in Maharashtra (Keskar *et al.*, 1989; Shinde *et al.*, 1995), Karnataka (Samiullah and Sheriff, 1973; Shivanandan, 1980; Challapalli, 1990), Andhra Pradesh (Mastan *et al.*, 1997) and Chhattisgarh (Awasthi and Sharma, 1998). Such variations in tamarind germplasm has been attributed to geographic isolation and gene mutation (Feungchan *et al.*, 1996).

Tamarind Types

Based on fruit characters, attempts have been made to designate different tamarind types. Lewis *et al.* (1954) recognized dark brown, brown, brownish red and light red types. Later they regrouped these into two types,

Table 4. Variability in morphological characters of fruit in *Tamarindus indica*

Characters	Range
Fruit weight (g)	8.9-63.6
Fruit length (cm)	8.2-32.0
Fruit, width (cm)	2.7-5.0
Curvature in pod	Straight, Curved
Bulging in pod	Flat, Bulged, Cylindrical
Pulp content (%)	24-71
Seed number/fruit	3.3-12.0
Seed content (%)	12-48
Rag and shell content (%)	11-42
Pulp colour	Red-Brown-Yellow
Endocarp colour	Extra white, White, Yellow
Seed length (mm)	0.95-1.8
Seed width (mm)	0.60-1.2
Seed weight (g)	2.6-12.5
Fruits (kg)	15-59.0
Seeds (kg)	517-1400

Source: Keskar *et al.* (1989), Chaoji (1995), Mastan *et al.* (1997)

one having rose red pulp and the other common type having light brown pulp. Hernandez-Unzon and Lakshminarayana (1982) also reported two types: one with brown pulp turning dark brown on storage and the other with red pulp. Cowen (1970) reported one tamarind type having brown pulp colour and sour taste and the other with reddish pulp colour and sweet taste.

Tamarind types have also been designated based on fruit shape. Bailey (1947) recognized two types of tamarind, namely, East Indian type having long and narrow fruits containing 6-12 seeds and West Indian type with shorter and broad fruits containing 1 to 14 seeds. In addition, the other important type is Thailand tamarind with shorter pods and sweet pulp. Cowen (1970) has described three types of tamarind having sickle shaped pods, straight long pods and short pods. Paulos (1975) recognized two types of tamarind, one having long and cylindrical pods (*Valakatchi*) and the other producing short cylindrical pods. Shivanandan (1980) recognized four types of tamarind, namely, straight and bulged, straight and flattened, curved and bulged and curved and flattened. Of these, straight and bulged type had longer pods (16.4 cm). Keskar *et al.* (1989) observed three distinct types of tamarind: curved and bulged, straight and flat and straight and bulged. Kennedy *et al.* (1997) classified tamarind fruits into five groups: long and bold fruit, medium fruit, small fruit, curved and irregular fruit and sweet fruit. Thus, the main characters used to classify tamarind types are pulp colour and taste besides endocarp colour, pod length and shape. It is, therefore, suggested that classification of tamarind types may be done on the primary, secondary and tertiary levels, as described subsequently.

(i) Primary characters	*Pulp colour* (red, brown); *Endocarp colour* (white, yellow); *Pulp taste* (sweet, sub acid, acid).
(ii) Secondary characters	*Pod length* (large: > 20 cm; small: < 20 cm); *Pod width* (wide: > 5.0 cm; Narrow: < 5 cm).
(iii) Tertiary character	*Pod shape* (straight and bulged, straight and flattened, curved and bulged, curved and flattened).

Promising Selections

As a result of evaluation of germplasm, trees having high fruit yield and superior quality traits have been identified. Fifty-two high yielding tamarind trees in Chittoor and Anantapur districts were identified by the State Silvicultural Division, Tirupati, Andhra Pradesh, based on morphological and physico-chemical characters of the fruits. Trees in the age group of 18 to 200 years were found to bear flowers and fruits. Highest yield was recorded from a 200-year-old tree in village Begarlapalli. In Chittoor district (village Chengalapuram), the yields were obtained from a tree of 150 years age. Very large size fruits (63.6 g) with light brown pulp and almost white endocarp have been reported from Akkampalli and Mudndi villages of Anantapur district. A more than 200-year-old tree has been reported growing near Urigam, Tamil Nadu, which yields 2 tonnes of fruit/year bearing pods 30 cm in length and 6.25 cm in width.

In three tribal tracts of Bastar (Chhattisgarh), *viz.*, Bastar, Kanker and Dantewada, the fruit yield varied from 40-50 kg/tree in trees of 6-7 years to 150-200 kg/tree in trees of over 20 years. The fruit maturity in different trees varied from early March to late May. Physico-chemical analysis of fruits showed variability in length (5-30 cm), girth (2.0-4.0 cm) and weight (15-60 g) of pod, pulp content (30-70%), pulp:seed ratio (4.0-1.0), pulp colour (light brown, dark brown, reddish brown), endocarp colour (white), acidity (8-12%) and TSS (25-80%). Some promising tamarind selections as a result of evaluation at different institutions are listed below:

PKM 1 : It is a selection made at Horticulture College and Research Institute, Periyakulam. It is an early bearer. Grafts come to flowering three years after planting and give commercial yield from fifth year. Nine-year-old trees gave a mean yield of 263 kg. It is a green tamarind producing yellow pods, having 39% pulp, high acidity (17.1%) and ascorbic acid (3.9 mg/100 g pulp).

Urigam : It is a progeny of more than 200-year-old tree identified near Urigam by the Department of Horticulture, Tamil Nadu, which is reported to yield 2 tonnes of fruits/year. The average length of fruit is 30 cm and width is 6.25 cm. It is a red tamarind.

Pratisthan: The variety was released from Fruit Research Station, Aurangabad. It has 61% pulp, 12% seed, 27% shell and 7-9% acidity. It is a sour-sweet and red tamarind. A 10-year-old tree yields 300 kg fruit. Its pulp can be stored for long period.

No. 263 : The variety has been released from Fruit Research Station, Aurangabad. It is a regular bearing cultivar producing 6-10 quintal fruits/tree. The fruits have pinkish and light yellow pulp, and 18-19% acidity. Fruits are large. On an average 45 fruits weigh to 1 kg.

Yogeshwari : The variety has been released from Taluk Seed Farm, Ambajogai (Beed) in Maharashtra. The fruits are large and have red and sour-sweet pulp with 6-7% acidity.

DTS 1 : It is a selection identified at University of Agricultural Sciences, Dharwad, College of Horticulture, Arabhavi. The pods are straight having semi-curved shape, 23.6 cm length, 3 cm width, 19.5 g weight, 51% pulp and 13.6% acidity. It is a late variety and takes 310 days from fruit set to maturity.

DTS 2 : This is a selection made at University of Agricultural Sciences, Dharwad, College of Horticulture, Arabhavi. The pods are straight having semi-curved shape, 17.6 cm length, 2.6 cm width, 18 g weight, 53% pulp and 12.2% acidity. It is an early variety and the pods mature in 280 days after fruit set.

Sweet tamarind : The origin of sweet tamarind has been attributed to point mutation. It is also assumed that the rare trait of sweetness in tamarind may be governed by recessive genes (Fuengchan *et al.*, 1996). The sweet tamarind is found mostly in South-East Asia and India. One Thailand variety is known as Makham Waan (Morton, 1987). Several sweet fruited trees are found in Cavite, Laguna and Binan regions of Philippines. The pods are 7-10 cm long, 2-3 cm wide, 20-30 g in weight and having 4 to 7 seeds/pod (Villanueva, 1920). The Institute of Plant Breeding, University of the

Philippines, Los Baños has identified promising trees. A variety named Manilla Sweet is reported from Florida.

In India, a red fleshed tamarind having sweet pulp (TSS>85%) has been spotted in village Faraskot, Dantewada, Bastar district of Chhattisgarh (Awasthi and Sharma, 1998).

Genetic Improvement

The objective of improvement strategy should be to select or develop high yielding types producing large and straight pods having extra white endocarp and high content of pulp with high TSS from the two variability groups of tamarind, *i.e.* sweet red and sour yellow-brown. Similarly, trees having dwarf growth habit with loose and well-formed crown, precocious and regular bearing habit need to be identified. The following ideotype description for development of an ideal genotype is suggested:

Ideotype description of tamarind

Character	Ideotype
Root system	Deep
Crown	Loose with profuse branching
Tree canopy	Circular
Tree height	Dwarf
Resistance to stress	Drought and frost resistance
Bearing	Precocious (from 5th year); regular
Pulp colour	Red
Endocarp colour	White
Pod length	>20 cm
Pod width	>5 cm
Pod weight	>20 g
Pod shape	Straight and bulged
Pulp:seed ratio	4:1
Pulp TSS	>80%
Acidity in pulp	Acidic type : 10-15 %; Sweet type : 6-10%

Selection

Presence of a large natural variation both in vegetative and reproductive characters and occurrence of bud spots in tamarind offer ample chances for identifying promising genotypes (Bailey, 1947; Keskar *et al.*, 1989; Challapalli, 1990; Samiullah and Sheriff, 1993; Nagarajan *et al.*, 1999). The desirable ones could be subsequently propagated by vegetative methods. Studies have shown that mid and late flowering types produce higher fruit yields. Some of the fruit characters could be used as markers for high productivity as indicated by the studies of Shivanandan and Raju (1988) and Challapalli *et al.* (1995). The length of fruit was positively correlated with its weight, pulp content and seediness. The fruit thickness was negatively correlated with fibre and seed content.

Hybridization

No attempts have been made to develop improved cultivars by hybridization. However, reproductive biology and breeding system have been studied in five tamarind clones by Nagarajan *et al.* (1999). Controlled pollination studies indicate that tamarind is predominantly an out-crossing species with extremely low level of selfing. Open pollination fruit set is between 1 to 2%. Pollen sterility is very low. Flowers show strong entomophilous adaptations. Apomixis is absent and fruit shows colour dimorphism.

Flowering in tamarind can be early, mid-season or late (Usha and Singh, 1996). The duration of fruiting is the longest in late flowering trees and shortest in early flowering trees. In mid and late flowering trees cross pollination has been observed to be more while the early flowering trees are mostly self-pollinated. In Karnataka, flowering in tamarind occurs between the last week of March and mid June. Anthers dehisce between 9.00 and 11.00 h. In majority of trees (64%), one floral bud was observed to flower at random on every alternate day while in 33% trees there was regular flowering, *i.e.* at least one floral bud opened/ day. A period of 25 days was required for flowering to complete in any infloresence.

The ability of the tamarind tree to adapt to a wide range of agro-ecological conditions and high degree of usefulness of all its plant parts: fruit, seed, leaf and wood, both for domestic utilization as well as in industry merit concerted focus on exploitation of its rich genetic variability by systematic research strategies mainly on (i) Collection, characterization and conservation of genepools, (ii) Identification of provenances with desirable characteristics according to use through characterization and evaluation.

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Genetic Divergence for the Morpho-agronomic Traits in Synthetic Hexaploid Wheats Derived from *Triticum turgidum* [(AABB) x *T. tauschii* (DD)]

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Forty-two synthetic hexaploid wheat (SHW) accessions were studied for their genetic divergence for a set of 10 morpho-agronomic characters using Mahalanobis D^2-statistic. The genotypes were grouped into three clusters with variable number of accessions. On the basis of the data on genetic divergence and cluster means, it is predicted that cluster III and cluster I were important for between cluster and cluster II was important for within cluster improvement. Therefore, this information may be useful to the breeders involved in wheat improvement by using these genotypes in multiple breeding programmes to recover transgressive segregants with desirable combinations of yield components.

Key Words: Cluster, Genetic Divergence, Synthetic Hexaploid Wheats

The germplasm evaluation for maintaining a wide genetic diversity is an urgency for realizing another quantum jump in wheat production. In this regard several workers evaluated germplasms of wheat for yield and its component traits (Joshi and Singh, 1979; Bari *et al.*, 1997; Kant *et al.*, 1999; Sorkhi *et al.*, 1999; Peer *et al.*, 2000). Identification of promising genotypes with good agronomic base and yield traits having resistance/tolerance to biotic/abiotic stresses is the pre-requisite for any plant breeding programme. It is also important that the considerable variability for morpho-agronomic traits must exist in the germplasm for exploitation using recombinant breeding programmes.

Synthetic hexaploid wheats (SHWs) ($2n=6x=42$) derived from the *Triticum turgidum* ($2n=4x=28$) x *T. tauschi* ($2n=2x=14$) developed at CIMMYT, Mexico, constituted relatively untapped germplasm for broadening the genetic base of common hexaploid wheat. Therefore, the present investigation was planned to study genetic divergence in SHWs for different morpho-agronomic traits.

Materials and Methods

The experimental materials consisted of 42 SHW accessions received from CIMMYT, Mexico. The pedigree of SHWs is given in Table 1.

The experiment was conducted in a randomized block design with three replications during the *rabi* season 1998-99 at Experimental Farm, Indian Agricultural Research Institute, New Delhi, India. Each accession was planted in three rows of 3 m length plot and the spacing between the rows was 23 cm and seed to seed distance of 10 cm. The recommended cultural and agronomical practices were followed to raise a good crop. The observations were recorded for 10 yield contributing characters *viz.*, days to anthesis, days to physiological maturity, plant height, culm length, leaf area, spike length, awn length, 1000-grain weight, number of grains/spike and yield/plant. Recording of data on morpho-agronomic characters was done using wheat descriptors of CIMMYT (1985) and IBPGR (1985). Ten plants were randomly selected for recording data from middle row of each test plot. The mean values were subjected to Mahalonobis D^2-statistic to measure genetic divergence as suggested by Rao (1952) and clusters were formed by Tocher's method (Rao, 1952).

Results and Discussion

The analysis of variance exhibited highly significant differences among the SHW accessions for all the 10 characters, indicating the existence of variation and scope for selection of desirable genotypes for use in breeding programmes aimed at enhancing the genetic potential of wheat germplasm.

On the basis of D^2 values, all the 42 accessions were grouped into three clusters (Table 2) with variable number of genotypes indicating the presence of sufficient amount of genetic diversity in the studied material. The maximum number of genotypes were present in cluster I (34 genotypes), while the cluster II accommodated seven genotypes and Syn. 50 was quite distinct from others and formed a separate cluster (cluster III). Cluster I had maximum number of genotypes mostly with same cross/pedigree. Pattern of clustering also indicated that there was no association between eco-geographical distribution of genotypes and genetic divergence as genotypes developed from the different accessions of

Table 1. Cross/pedigrees of synthetic hexaploid wheats

S.No.	Synthetics	Name or Cross/pedigree/accession number
1.	Syn. 2	DOY1 / *Ae. Squarrosa* (188)
2.	Syn. 4	ALTAR 84 / *Ae. Squarrosa* (193)
3.	Syn. 5	ALTAR 84 / *Ae. Squarrosa* (198)
4.	Syn. 9	ALTAR 84 / *Ae. Squarrosa* (211)
5.	Syn. 12	ROK/KML / *Ae. Squarrosa* (214)
6.	Syn. 14	YUK / *Ae. Squarrosa* (217)
7.	Syn. 18	D67.2 / P66.270 // *Ae. Squarrosa* (220)
8.	Syn. 19	DVERD 2 / *Ae. Squarrosa* (221)
9.	Syn. 26	ACO 89 / *Ae. Squarrosa* (309)
10.	Syn. 27	GARZA / BOY // *Ae. Squarrosa* (311)
11.	Syn. 29	68.111 / RGB-U // WARD / 3 / *Ae. Squarrosa* (326)
12.	Syn. 33	YAV3/SCO // JO69 / CRA / 3 / YAV79 / 4 / *Ae. Squarrosa* (398)
13.	Syn. 35	68.11 / RGB-U // WARD / 3 / *Ae. Squarrosa* (511)
14.	Syn. 36	DOY 1 / *Ae. Squarrosa* (515)
15.	Syn. 37	68.111 / RGB-U // WARD / 3 / FGO / 4 / RABI / 5 / *Ae. Squarrosa* (629)
16.	Syn. 39	CROC / *Ae. Squarrosa* (725)
17.	Syn. 40	68.111 / RGB-U // WARDRESEL / 3 / STIL / 4 / *Ae. Squarrosa* (781)
18.	Syn. 41	68.111 / RGB-U // WARD / RESEL / 3 / STIL / 4 / *Ae. Squarrosa* (783)
19.	Syn. 42	YAR / *Ae. Squarrosa* (783)
20.	Syn. 43	YUK / *Ae. Squarrosa* (864)
21.	Syn. 44	68.111 / RGB-U // WARD / 3 / FGO / 4 / RABI / 5 / *Ae. Squarrosa* (878)
22.	Syn. 45	68.111 / RGB-U // WARD / 3 / FGO / 4 / RABI / 5 / *Ae. Squarrosa* (878)
23.	Syn. 46	CROC 1 / *Ae. Squarrosa* (879)
24.	Syn. 47	68.11 / RGB-U // WARD / 3 / FGO / 4 / RABI / 5 / *Ae. Squarrosa* (882)
25.	Syn. 48	SORA / *Ae. Squarrosa* (884)
26.	Syn. 50	CROC 1 / *Ae. Squarrosa* (518)
27.	Syn. 51	PBW 114 / *Ae. Squarrosa*
28.	Syn. 52	ALTAR 84 / *Ae. Squarrosa* (JBANGOR)
29.	Syn. 53	YAV2 / TEZ // *Ae. Squarrosa* (249)
30.	Syn. 55	GAN / *Ae. Squarrosa* (180)
31.	Syn. 56	D67.2 / P66.270 // *Ae. Squarrosa* (257)
32.	Syn. 59	SRN / *Ae. Squarrosa* (358)
33.	Syn. 60	SCOOPI / *Ae. Squarrosa* (358)
34.	Syn. 62	SCA / *Ae. Squarrosa* (518)
35.	Syn. 63	YAR / *Ae. Squarrosa* (518)
36.	Syn. 65	BOTNO / *Ae. Squarrosa* (620)
37.	Syn. 68	D67.2 / P66.270 // *Ae. Squarrosa* (633)
38.	Syn. 74	YAV2 / TEZ // *Ae. Squarrosa* (895)
39.	Syn. 75	ARLIN / *Ae. Squarrosa* (283)
40.	Syn. 86	DOY1 / *Ae. Squarrosa* (372)
41.	Syn. 88	CPI / GEDIZ / 3 / GOO // JO69 / CRA / 4 / *Ae. Squarrosa* (409)
42.	Syn. 90	ALTAR84 / *Ae. Squarrosa* (502)

Table 2. Group constellation of the 42 synthetic wheat genotypes based on Mahalanobis D^2-statistic

Cluster	Number of genotypes	Genotypes
I	34	Syn. 2,56,33,5,47,12,90,39,60,48,51,44,41,36, 14,27,68,35,65,59,86,45,62,88,40,42,63, 26,43,37,75,53,19 and 52
II	7	Syn. 4, 46,74,9,29, 55 and 18
III	1	Syn. 50

Table 3. Average inter and intra cluster distance D^2 values and distance ($\sqrt{D^2}$) for 10 characters

Cluster	I	II	III
I $D^2/\sqrt{D^2}$	346.97 (18.63)	790.99 (28.12)	9632.38 (98.14)
II $D^2/\sqrt{D^2}$		1071.06 (32.73)	8640.89 (92.96)
III $D^2/\sqrt{D^2}$			0.00 (0.00)

T. tauschii selected from diverse locations also clustered together. These findings are on consonance with Bhatt (1970) and Sharma *et al.* (1998) in wheat.

The intra- and inter-cluster divergence among the genotypes was of varying magnitude (Table 3). Cluster II with seven genotypes exhibited maximum intra-cluster distance (18.63) indicating that the genotypes in this cluster are more diverse than the other clusters. This was used to select genetically diverse and agronomically superior genotypes from the 42 genotypes studied. With regards to inter-cluster distance, cluster III showed maximum genetic distance from cluster I than the cluster II. The greater the genetic distance between the clusters, wider is the genetic diversity between genotypes.

The genetic divergence among clusters was well reflected in cluster means (Table 4). Cluster III (Syn. 50) exhibited higher mean values for awn length, number of grains/spike and yield/plant. Genotypes in cluster II performed well for plant height, culm length, leaf area, spike length and 1000-grain weight while cluster I showed the highest mean values for days to anthesis and days to physiological maturity. This indicated that none of the clusters contained genotypes with all the desirable characters, which could be directly selected and utilized in the breeding programmes. Hybridization between the genotypes of different clusters was necessary for the development of desirable genotypes, which accommodates genes from the two parents. The crosses involving cluster III and cluster II may generate a material where negative correlation between the grain number and grain weight is brokendown. Transgressive breeding between the genotypes of different clusters has also been suggested by Singh *et al.* (1996), Deshmukh *et al.* (1999) and Kant *et al.* (1999).

Table 5. Contribution of different characters to genetic divergence

Character	Per cent contribution
Days to anthesis	1.10
Days to physiological maturity	0.60
Plant height	15.22
Culm height	0.80
Leaf area	2.44
Spike length	13.24
Awn length	43.61
1000-grain weight	1.28
Number of grains/spike	18.12
Yield/plant	3.60

(1984) for grains/ear and Singh and Singh (1998) for grains/ear and plant height.

On the basis of divergence for the components of grain yield, it is suggested that good recombinants could be obtained from these SHW accessions. This information may be useful to the breeders for varietal improvement by using this material as new source for genetic diversity for morpho-agronomic characters of wheat.

Table 4. Cluster means of 42 synthetic wheat genotypes for 10 characters

Cluster	Days to anthesis	Days to physiological maturity	Plant height (cm)	Culm length (cm)	Leaf area (sq. cm)	Spike length (cm)	Awn length (cm)	1000-grain weight (g)	No. of grain/ spike	Yield/ plant (g)
I	119.24	147.93	109.73	98.83	8.76	10.98	5.12	38.40	20.35	4.40
II	116.33	144.05	111.89	100.69	10.22	11.20	5.60	40.25	31.95	6.15
III	107.67	137.67	81.87	79.29	6.00	5.91	14.30	38.99	37.19	8.01

Contribution of different characters towards genetic divergence was presented in the Table 5. It can be seen from the table that awn length contributed maximum (43.61%) towards genetic divergence in these SHWs. Characters like, number of grains/spike (18.12%), plant height (15.22%), spike length (13.24%) and grain yield/ plant (3.60%) jointly contributed 50.18% to total genetic divergence. This is in conformity with the observations of Murty and Arunachalam (1966) for plant height in grain crops, Kanwal *et al.* (1983) and Kuruvadi (1988) for plant height and spike length, Das Gupta and Das

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Genetic Variation Among Potato Genotypes for Tuber Protein Subunits

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Tuber protein subunit based genetic variation was analysed among 38 potato genotypes using similarity index value. Results indicated that Kinship did not correspond to similarity in banding patterns of the cultivars. Cultivar combinations *viz.*, Kufri Pukhraj and JX-216, JW-96 and JX-216, MS/91-1325 and JX-216, 85-P-127 and 85-P-670, 85-P-127 and 85-P-11 etc. with low SI values were considered to be divergent parents and recommended for hybrid breeding progarammes.

Plant morphology has been an important criterion for identification, classification and documentation of species and cultivars (Pauksens, 1975). It plays an important role in study of genetics and breeding behaviour of plants. But, since morphology reflects interaction of genotype with its environment, it is inappropriate to compare morphological data for cultivars that have been collected across different years and/or locations. Therefore, descriptors based on proteins (including isozymes) and deoxyribonucleic acid (DNA) are more reliable (Tanksley and Orton, 1983; Ryskov *et al.*, 1988). Isozyme and protein profiles by electrophoresis have been used to characterize potato cultivars (Desborough and Peloquin, 1968; Stegemann and Loeschcke, 1976; Oliver and Martinez-Zapater, 1985) and to investigate species relationships (Hosaka and Matsubayashi, 1983; Oliver and Martinez-Zapater, 1984). Due to the diversity of tuber proteins within the Group *Tuberosum,* protein analysis by electrophoresis is a convenient and effective method of studying the genetic variation. Tubers are suitable for separating proteins, since they represent a stable source of proteins and provide a uniform material for protein extraction (Rajapakse *et al.*, 1991). According to Stegemann *et al.* (1973), mature potato tubers can be used for variety identification by the Tris (hydroxymethyl) aminomethane (Tris) and borate buffer system of polyacrylamide gel electrophoresis. *Tuberosum* is known to have a narrow genetic base (Plaisted, 1972) and a little improvement is observed in tuber yield and its components (Howard, 1963; Mendoza and Haynes, 1974). In present study, an attempt has been made to establish the relationship among *Tuberosum* genotypes and identify the divergent parents through tuber protein profiles.

Materials and Methods

Thirty-eight potato genotypes (Table 1) representing advance generation hybrids and released Indian cultivars were evaluated in a randomized block design with three replications.

About 0.5 g of tuber (80 DAP, 25-30 g weight) from each line was crushed in 500 µl of sample buffer (Laemmli, 1970) without dye, supplemented with 0.1 volumes (50 µl) of 10 mM phenylmethyl sulphonyl fluoride (dissolved in 50% ethanol) at 4°C. The supernatant was separated by centrifugation at 10,000 rpm for 10 min at 4°C. The supernatant was kept for 1 h at room temperature and used directly for sodium dodecyl sulphate-polyacrylamide gel electrophoresis.

The gels were prepared according to the method of Laemmli (1970) and Rajapakse *et al.*, (1991). Protein samples of 25 µl in each genotype was loaded in duplicate along with molecular weight marker protein consisting of phosphorylase b (94 kD), bovine serum albumin (67 kD), egg albumin (43 kD), carbonic anhydrase (30 kD) and ribonuclease a (14.0 kD) subunits. Total protein concentration was estimated for each line by the method of Bradford (1976) using bovine serum albumin (E-Merk-India, Ltd.) as standard. The quantity of protein was adjusted to 10 mg for one lane to obtain a clear separation for coomassie blue staining.

Electrophoresis was done at a constant current of 8 mA per plate for 6-7 h using electrode buffer containing, 0.025 M Tris, 0.192 M glycine and 1 g l^{-1} SDS, with pH 8.4. Gels were stained with 0.2% coomassie brilliant blue R solution (dissolved in ethanol: acetic acid: water = 45: 10: 45) at room temperature for 2 h. The first destaining was done using methanol: acetic acid: water (25: 10: 65) and the second with 7% (v/v) acetic acid, both at room temperature.

The level of similarity among genotypes was determined in terms of similarity index (SI = number of matching bands between two genotypes/total number of bands x 100) by positioning the individual bands in each gel through relative front mobility value

Table 1. List of potato genotypes and their parentage

Genotypes		Parentage
1.	Kufri Pukhraj	Craigs Defiance x JEX/B-687
2.	Kufri Badshah	Kufri Jyoti x Kufri Alankar
3.	Kufri Ashoka	EM/C-1020 x Allerfriitheste Gelbe
4.	Kufri Anand	PJ-376 x PH/F-1430
5.	Kufri Jawahar	Kufri Neelamani x Kufri Jyoti
6.	Kufri Bahar	Kufri Red x Gineke
7.	Kufri Chipsona-1	MEX-750826 x MS/78-79
8.	Kufri Chipsona-2	F-6 x QB/B 92-4
9.	Kufri Jyoti	3069 d(4) x 2814a (1)
10.	Kufri Lalima	Kufri Red x AG 149 (Wis x 37)
11.	JP-100	Kufri Alankar x CP-1406
12.	Kufri Sutlej	Kufri Bahar x Kufri Alankar
13.	JW-23	–
14.	JTH/C-107	Selection from collected material
15.	AB-667	Kufri Jyoti SS-1603
16.	JV-67	JF-4700 x JL-5857
17.	JW-96	Kufri Jyoti x CP-1362
18.	85-P-127	–
19.	MF-1	Local selection
20.	JX-1	Kufri Jyoti x CP-1481
21.	85-P-11	–
22.	85-P-670	Kufri Bahar x PS-4904
23.	85-P-718	Kufri Bahar x PS-4904
24.	JX-23	Kufri Jyoti x CP-1481
25.	JX-371	JE 812 x Kufri Jyoti
26.	JX-576	JE 812 x Kufri Jyoti
27.	JX-235	JE 812 x Kufri Jyoti
28.	JX-216	JE 812 x Kufri Jyoti
29.	JX-115	CP 1346 x MS/78-62
30.	TPS 1/7	–
31.	TPS C-3	JTH/C-107 x EX/A-680-16
32.	JX-44	CP 1546 x SLB/X-23
33.	JX-123	JE812 x Kufri Jyoti
34.	JX-249	JE-812 x Kufri Jyoti
35.	TPS 1/13	MF-1 x TPS-13
36.	MS/92-3128	MS/82-638 x MS/80-758
37.	MS/92-1090	Kufri Jyoti x PH/F-1545
38.	MS/91-1325	Ma/83-27 x CP-1673

(Rf value = distance moved by particular protein band/ total run in a gel). Based on SI values, a dendrogram was constructed using UPGMA (unweighted pair group method using arithmetic average) cluster analysis.

Results and Discussion

Similarity index (SI) indicates the degree of closeness among genotypes (Huang *et al.*, 1997; Shamina *et al.*, 1998). SI values ranged from 22.22% (Kufri Pukhraj and JX-216) to 100% (Kufri Badshah and Kufri Anand, Kufri Badshah and Kufri Ashoka, Kufri Anand and Kufri Ashoka, JX-235 and TPS 1/13 and TPS 1/7 and TPS C-3) (Table 2 & Fig. 2). High SI values indicated close relationship between genotype pairs whereas low values indicated high divergence. Closeness may be due to common parentage or confluence of similar genes from different parents in development of varieties (Bassiri and Adams, 1978; Hosaka *et al.*, 1994). In this investigation, genotype combinations involving common parents did not have identical banding patterns and showed varying degree of SI values. For example, genotypes 85-P-670 and 85-P-718 (Kufri Bahar x PS-4904), JX-1 and JX-23 (Kufri Jyoti x CP – 1481) and JX-123, JX-371, JX-576, JX-216, JX-249, and JX-235 (JE-812 x Kufri Jyoti) exhibited SI values in a range of 31.58% to 94.12%. Similarly, Kufri Badshah, Kufri Jawahar and AB-667, Kufri Lalima and Kufri Bahar, Kufri Sutlej and Kufri Badshah having one common parent exhibited SI values in the range of 69.57% to 90.0%. It was also observed that some genotype combinations like Kufri Badshah and Kufri Ashoka, Kufri Badshah and Kufri Anand,

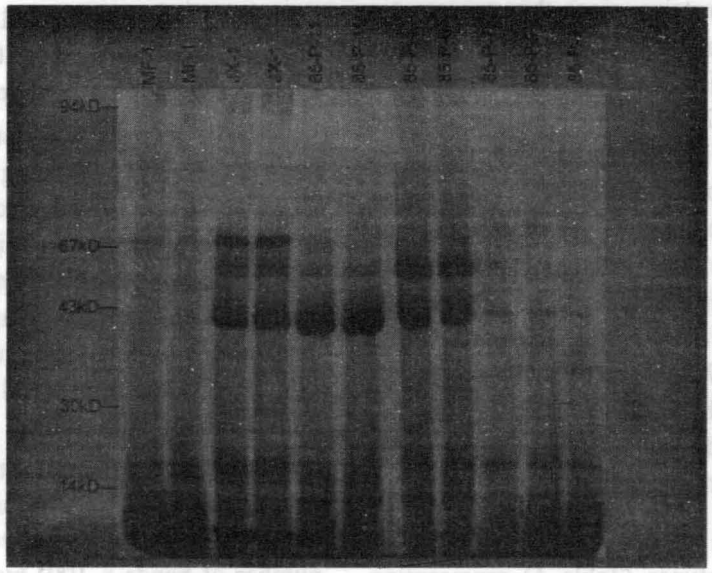

Fig. 1. SDS-PAGE patterns of tuber protein in potato genotypes

Table 2. Similarity index (SI) among potato (*Solamum tuberosum* L.) genotypes

Genotypes*	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1.	-	78.26	78.26	78.26	81.48	72.72	72.0	72.72	63.64	75.00	78.58	70.00	52.18	58.34	63.64	72.00	64.00	44.44	53.84
2.		-	100.00	100.00	83.33	94.74	72.73	94.74	84.21	95.24	80.00	82.35	70.00	66.67	84.21	81.82	72.73	53.33	52.17
3.			-	100.00	83.33	94.74	72.73	94.74	84.21	95.24	80.00	82.35	70.00	66.67	84.21	81.82	72.73	53.33	52.17
4.				-	83.33	94.74	72.73	94.74	84.21	95.24	80.00	82.35	70.00	66.67	84.21	81.82	72.73	53.33	52.17
5.					-	78.26	84.62	78.26	69.57	80.00	89.66	66.67	66.67	72.00	69.57	84.62	76.92	42.11	66.67
6.						-	66.67	88.89	77.78	90.00	75.00	87.50	89.47	70.00	77.78	76.19	66.67	57.14	71.43
7.							-	76.19	85.71	78.26	88.89	52.63	72.73	86.96	76.19	83.33	75.00	58.82	72.00
8.								-	88.89	90.00	75.00	75.00	63.16	70.00	77.78	76.19	66.67	57.14	54.55
9.									-	90.00	75.00	62.50	73.68	80.00	88.89	76.19	66.67	71.43	54.55
10.										-	84.62	77.78	76.19	72.73	90.00	78.26	69.57	62.50	58.33
11.											-	63.64	72.00	76.92	72.00	88.89	81.48	50.00	78.57
12.												-	70.59	55.56	75.00	63.16	52.53	66.67	60.87
13.													-	85.71	84.21	72.73	73.73	66.67	60.87
14.														-	70.00	78.26	78.26	62.50	66.67
15.															-	76.19	66.67	71.43	54.55
16.																-	91.67	47.06	64.00
17.																	-	47.06	64.00
18.																		-	33.33
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*See Table 1

Table2 (contd. row-wise)

Geno-type*	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38
1.	62.08	64.28	73.34	56.00	60.00	58.34	66.66	54.54	22.22	48.00	66.66	66.66	62.08	66.66	47.62	54.54	68.96	60.88	69.57
2.	53.85	72.00	66.67	72.73	70.59	76.19	85.71	73.68	40.00	63.64	85.71	85.71	61.54	58.33	66.67	73.68	61.54	80.00	50.00
3.	53.85	72.00	66.67	72.73	70.59	76.19	85.71	73.68	40.00	63.64	85.71	85.71	61.54	58.33	66.67	73.68	61.54	80.00	50.00
4.	53.85	72.00	66.67	72.73	70.59	76.19	85.71	73.68	40.00	63.64	85.71	85.71	61.54	58.33	66.67	73.68	61.54	80.00	50.00
5.	66.67	82.76	77.42	61.54	57.14	72.00	72.00	60.87	31.58	61.54	72.00	72.00	80.00	71.43	54.55	60.87	73.33	66.67	66.67
6.	48.00	66.67	61.54	66.67	62.50	70.00	80.00	66.67	42.86	66.67	80.00	80.00	56.00	52.17	58.82	66.67	56.00	73.68	42.11
7.	71.43	74.07	68.97	66.67	63.16	78.26	78.26	66.67	47.06	66.67	69.57	69.57	71.43	76.92	70.00	66.67	71.43	63.64	63.64
8.	56.00	66.67	61.54	76.19	60.00	70.00	70.00	66.67	42.86	57.14	80.00	80.00	56.00	52.17	70.59	66.67	56.00	73.68	42.11
9.	56.00	58.33	53.85	76.19	75.00	80.00	90.00	77.78	57.14	66.67	80.00	80.00	56.00	60.87	82.35	77.78	56.00	73.68	42.11
10.	59.27	69.23	64.29	78.26	66.67	81.82	90.91	80.00	50.00	69.57	90.92	90.91	66.67	64.00	73.68	80.00	66.67	85.71	47.62
11.	77.42	86.67	81.25	74.07	54.55	76.92	76.92	64.00	40.00	74.07	76.92	76.92	83.87	82.76	60.87	64.00	83.87	72.00	64.00
12.	76.92	54.55	50.00	52.63	71.43	66.67	66.67	62.50	33.33	52.63	77.78	77.78	52.17	57.14	53.33	62.50	52.17	70.59	47.06
13.	61.54	64.00	59.26	63.64	58.82	85.71	76.19	73.68	53.33	72.73	76.19	76.19	61.54	66.67	66.67	73.68	61.54	70.00	50.00
14.	66.67	69.23	64.29	69.57	55.56	72.73	72.73	60.00	50.00	60.87	63.64	63.64	59.26	64.00	63.16	60.00	59.26	57.14	47.62
15.	56.00	58.33	53.85	66.67	75.00	90.00	90.00	88.89	57.14	76.19	90.00	90.00	64.00	69.57	82.35	88.89	64.00	84.21	52.63
16.	64.29	81.48	75.86	66.67	63.16	78.26	78.26	66.67	35.39	75.00	69.57	69.57	71.43	76.92	60.00	66.67	71.43	63.64	63.64
17.	64.29	81.48	75.86	66.67	52.63	69.57	69.57	57.14	23.53	66.67	60.87	60.87	71.43	69.23	50.00	57.14	78.57	54.55	63.64
18.	38.10	30.00	27.27	47.06	66.67	62.50	62.50	57.14	40.00	47.06	62.50	62.50	47.62	52.63	61.54	57.14	38.10	53.33	40.00
19.	89.66	85.71	80.00	80.00	50.00	66.67	58.33	63.64	55.56	72.00	66.67	66.67	75.86	74.07	66.67	63.64	82.76	69.57	60.87
20.	-	83.87	90.91	78.57	52.17	66.67	59.26	64.00	47.62	64.29	66.67	66.67	7.00	73.33	66.67	64.00	93.75	69.23	69.23
21		-	93.75	81.48	54.55	61.54	69.23	80.00	40.00	66.67	69.23	69.23	75.42	75.86	60.87	66.67	83.87	72.00	72.00
22.			-	75.86	50.00	57.14	64.29	61.54	36.36	62.07	64.29	64.29	72.73	70.97	56.00	61.54	90.91	66.67	74.07
23				-	63.16	69.57	78.26	76.19	58.82	66.67	78.26	78.26	64.29	61.54	80.00	76.19	71.43	81.82	45.46
24.					-	77.78	77.78	75.00	50.00	70.59	77.78	77.78	50.17	66.67	80.00	75.00	52.17	70.59	58.82
25.						-	90.91	90.00	6.250	86.96	90.91	90.91	74.07	80.00	84.21	90.00	70.07	85.71	66.67
26.							-	90.00	62.50	78.26	90.91	90.91	66.67	72.00	84.21	90.00	66.67	85.71	57.14
27.								-	71.43	76.19	90.00	90.00	64.00	69.57	94.12	100.00	72.00	94.74	63.16
28.									-	58.82	62.50	62.50	38.10	31.58	76.92	71.43	46.62	66.67	26.67
29.										-	78.26	78.26	71.43	76.92	70.00	76.19	71.43	72.43	54.55
30.											-	100.00	74.07	72.00	84.21	90.00	74.07	95.24	57.14
31.												-	74.07	72.00	84.21	90.00	74.07	95.24	57.14
32.													-	86.67	66.67	64.00	81.25	69.23	69.23
33.														-	63.64	69.57	80.00	66.67	75.00
34.															-	94.12	75.00	88.89	55.56
35.																-	72.00	94.74	63.16
36.																	-	76.92	76.92
37.																		-	60.0

* See Table 1

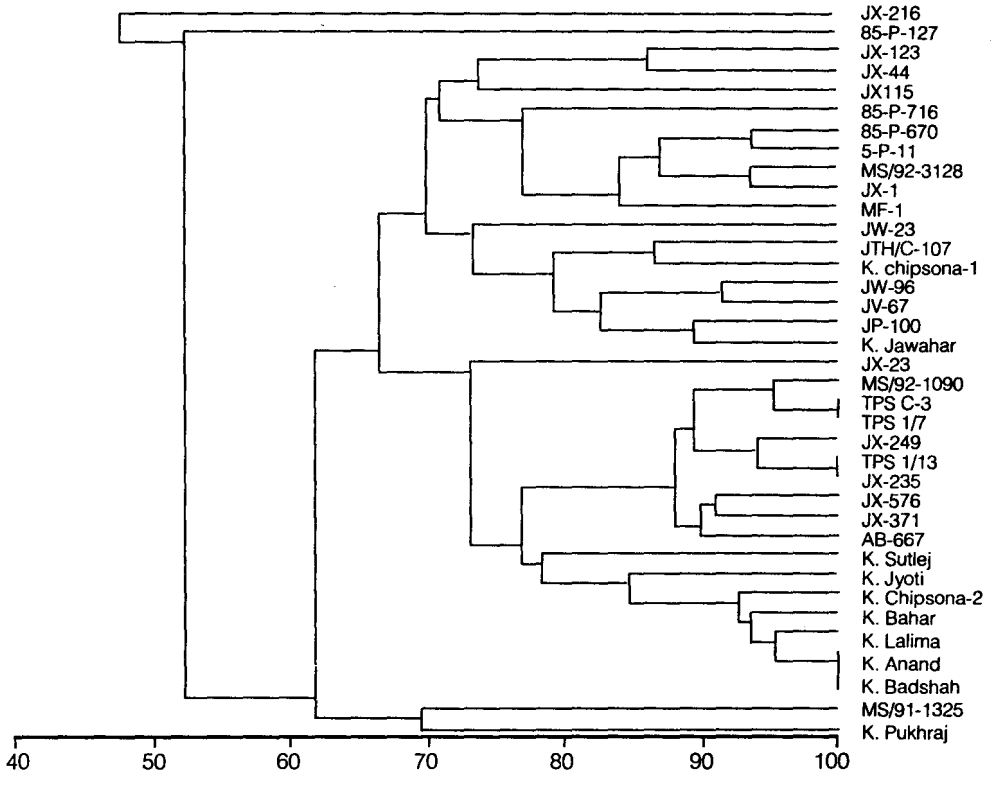

Fig. 2. Dendrogram of 38 potato (Solanum tuberosum) genotypes

Kufri Ashoka and Kufri Anand, JX-235 and TPS 1/13 and TPS 1/7 and TPS C-3 exhibiting SI value of 100% were not related by pedigree. Demeke *et al.* (1996) also studied genetic diversity of 28 North American potato cultivars and observed that cultivars with close kinship were as genetically diverse as those with no immediate relationship. The kinship could not be reflected in the similarity in banding patterns, due to highly heterozygous nature of the tetraploid genome (Cubillos and Plaisted, 1976; Tarn and Tai, 1977; Mendiburu *et al.*, 1974; Mendoza and Haynes, 1974) resulting in segregating F_1s.

Genetic divergence measured on the basis of environmentally and developmentally stable characters like tuber proteins can be reliable and reproducible (Hosaka and Hanneman, 1991; Rajapakse *et al.*, 1991). Therefore, the combinations *viz.*, Kufri Pujrak x JX-216, JX-216 x JW-96, JX-216 x MS/91-1325, 85-P-127 x 85-P-670, JX-216 x Kufri Jawahar, 85-P-127 x 85-p-11, JX-216 x Kufri Sutlej, 85-P-127 x MF-1, JX-216 x JV-67, JX-216 x 85-P-670, 85-P-127 x JX-1, JX-P-127 x JP-100, JX-216 x Kufri Anand, JX-216 x Kufri Ashoka, JX-216 x Kufri Badshah, JX-216 x 85-P-127, JX-216 x 85-P-11, 85-P-127, MS/91-1325 and Kufri Sutlej x MF-1 with low similarity index values are recommended for future hybrid breeding programmes in potato.

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Interspecific Hybrids Involving Genetic Male Sterile Line of *Gossypium arboreum* and *Gossypium stocksii*

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An interspecific hybrid between *Gossypium arboreum* x *G. stocksii was* obtained by pollinating previous day bagged flowers of *G. arboreum* genetic male sterile line MPKV GMS with pollen from wild *G. stocksii*. A single boll was obtained after 768 pollinations, containing 9 seeds out of which only two germinated and proved hybrid. The hybridity was conferred on the basis of cytomorphological observations made in the hybrid plants in comparison with their parents. The hybrid was intermediate in growth habit, height, leaf shape, petal colour, while anther colour was different from both the parents. The hybrid plant produced few flowers after 240 days, which were sterile. The chromosome behaviour during meiosis in both the parent was normal, however, in F_1 hybrid the average chromosome association were found to be unequal. The separation of chromosome and chromatid during anaphase-I and II respectively, leading to formation of 3 to 7 microspores pollen mother cell and pollen grains with high size variation and sterility was observed. Efforts are under way to induced chromosome doubling in this hybrid to restore fertility and exploit this cross combination for transferring drought resistance from *G. stocksii* to *G. arboreum*.

Key Words: ***Gossypium, Gossypium arboreum, G. stocksii,* Inter-specific Hybrid.**

Gossypium contains about 50 diploid and tetraploid species. The diploid species ($2n = 26$) fall into different cytotypes designed as A to K genome (Fryxell, 1979; Endrizzi *et al.*, 1985; Gorham and Young, 1996). The species of both diploid and tetraploid provide the most intriguing but difficult sources of genetic variability for cotton variety improvement. Difficulties in the use of species arise from chromosome structural differences and in differences in chromosome complements between the wild diploids and the tetraploids (Niles, 1980). Fertility relationship among species is highly variable, and only about two thirds of the interspecific hybrids studied produce fertile F_1s (Anonymous, 1968 a). Even though interspecific hybridization presents considerable problems, its use offers intriguing possibilities. The exotic species have provided useful variability for improvement of fibre properties, cold tolerance, disease resistance and insect resistance (Fryxell, 1976). Nuclear complements of two upland cottons were combined with cytoplasm of seven other *Gossypium* species; these provide a valuable and unique germplasm source for cotton improvement (Meyer, 1973). Hybridization between species is resorted for securing genes or gene combinations that are not available within the limits of a species (Sikka and Joshi, 1960). In addition, it may be possible to obtain increase or improvement in certain characters through transgressive breeding (Stephens, 1944) since genes favourable for intensification of a particular character may occupy independent loci in the parental species and may also act independent of one another (Richmond, 1950). There is a wide scope for incorporating desired characteristics from cultivated or wild forms into the species of commerce.

Narayanan *et al.*, (1984) discussed the role of wild species in importing technological properties of fibre and verification and resistance. Since interspecific hybridization provides a means for transferring new and useful genes from wild into cultivate cotton, the improvement of fibre quality, particularly tensile strength which is receiving considerable attention in interspecific programme (Kamra, 1980).

The wild Arabian *G. stocksii* species reported to be drought resistant (Abraham, 1940). Crosses between *G. arboreum* and *G. stocksii* reported to produce viable seed but sterile hybrids (Sikka and Joshi, 1960). Crosses between *G. arboreum* var. *nankins*, *sanguinium*, *G. arboreum* and *G. herbaceum* and *G. stockii* were attempted earlier (Skovsted, 1937; Webber, 1939; Abraham, 1940; Beasley, 1942). Since more than 95% cotton is grown on rainfed situation and also soils of submersible lands, hence, it is worth to evolve varieties having built-in inherent cotton varieties tolerant to drought situations in the areas of the assured as well as moderate to low rainfall situation. Since, it is already indicated that broadening of the base of breeding material involving wild species such as *G. stocksii* are supposed to have the drought resistance in crosses with cultivated cotton, hence, present investigations were attempted.

Materials and Methods

Pollen at anthesis from *G. stocksii* plants were collected and dusted on previously bagged flowers of *G. arboreum* MPKV GMS line. There were single boll and nine seeds after 768 pollinations out of which only two seeds were germinated. Parents and F_1 hybrids were raised and studied with reference to characters of genetical importance (Table 1).

The various morphological characters were studied in these *G. arboreum, G stocksii* and their F_1 hybrid (Table 1). The length of flower bud of various meiotic stages was determined by studying meiosis in fertile counterpart. For cytological analysis, young flower buds of F_1 hybrid and their respective parents were fixed in Carnoy's fluid (6:3:1) and squashed mounts. Pollen sterility was tested with differential stain (Alexander, 1969). Cytological analysis was made from temporary preparations. The pollen germination tests were carried out as per Iyengar (1939). Microphotographs were taken on coloured film with the help of Rico 35mm Camera mounted on Trinocular Leica Microscope.

Table 1. Morphological characteristics of the parents and inter-specific cross (*G. arboreum* MPKV GMS x *G. stocksii*)

Character	MPKV GMS	*G. stocksii*	F_1 (GMS x *G. stocksii*)
Plant height (cm)	155.0	28.5	72.0
Monopodia (No.)	0-1	6	3
Sympodia (No.)	24	3	8
Length of monopodia (cm)	114	59.3	50.4
Length of sympodia (cm)	24	21.4	34.6
Leaf shape	5 long, narrow lobe, deeply palmate	3-5 lobes, rounded and deeply constricted at base	5 long, narrow lobes
Leaf length (cm)	4.6	2.7	4.5
Leaf width (cm)	5.4	3.7	6.0
Leaf thickness (mm)	0.62	0.42	0.39
Leaf surface	Smooth	Glabrous	Glabrous
Leaf venation	Reticulate and palmate divergent	Reticulate	Reticulate and palmate divergent
Leaf nectari	Present	Present	Present
Leaf petiole length (cm)	3.1	2.5	4.0
Leaf petiole thickness (cm)	1.9	1.24	1.09
Lobe length (cm)	3.1	1.8	3.4
Lobe width (cm)	1.2	1.0	1.4
Lobe sinus (cm)	1.8	1.6	1.48
Flower			
Peduncle length (cm)	1.8 Medium	0.5 Short	1.3 medium
Petal colour	Dark yellow	Pale yellow with spot	Yellow with spot
Petal claw	Short	Short	Short
Petal length (cm)	3.4	2.8	2.8
Petal width (cm)	2.7	1.9	2.3
Petal spot	Dark red	Red	Red
Length of petal spot (cm)	1.9	0.8	0.76
Width of petal spot (cm)	1.7	0.5	0.66
Calyx length (cm)	0.9	0.7	0.63
Bracteole (No.)	3, broad	3, small	3, small
Length of bract (cm)	2.3	1.9	2.8
Width of bract (cm)	2.1	1.1	1.9
Teeth (No.)	3-5 teeth, serrated at apex, tapering end	8 long teeth, radiating	8-9 long teeth, radiated
Anther colour	White	Creamy	Yellow
Anther (No.)	68 Sterile	74	77
Style length (cm)	1.6	1.7	1.4
No. of ovules	25	18	24
Boll/capsule			
Boll shape	Elongated and medium, tapering	Small, round	No bollsetting
Boll surface	Sparsely pitted	Prominently gland	-
Boll weight (g)	2.1	0.16	-
No. of locules	4	3-4	-
Locule length (cm)	2.7	1.3	-
Locule width (cm)	1.3	1.0	-
Seeds/locule	8	8	-
Seed index	7.4	2.18	-
Lint index	3.9	0.61	-

Results

The comparison of different morphological characters of parents with F_1 hybrid is presented in Table 1 (Plate 1). From the data it appeared that the F_1 was intermediate in height (72 cm), (3) monopodia, (8) sympodia, while it showed higher number of monopodia and less number of sympodia in both the parents. Further the length of sympodia (34.6 cm) and monopodia (50.4 cm) was more as compared to both the parents.

Leaf lobes of *G. arboreum* (Plate I, Fig. 7) were found dominant. The leaves of the hybrids (Plate I, Fig. 6) were higher in length and breadth than *G. stocksii* (Plate I, Fig. 8). Whole leaves were intermediate in these crosses. Flower of the hybrids (Plate I, Fig. 9a) were bigger than both male and female (Plate I, Fig. 9a and b). Petal colour and spot were found to be intermediate in F_1 (Plate I, Fig. 10) as compared to its both parents (Plate I, Fig. 11 and 12). Anther of the hybrids was yellow, which was different from both the parents. Since hybrid plant was completely sterile, the boll and seed characters could not be compared. *G. stocksii,* produced prolific bolls, containing seeds with brown fuzz (Plate I, Fig. 13).

Chromosome pairing behaviour have been showed in both parents at diakinensis and metaphase stages (Table 2). As reported by Abraham (1940) the formation of 13 perfect bivalents and differential contraction of chromosomes was noticed at deplotene in both the species (Plate II, Fig. 1,2,5 and 6). Some bivalents shortened and thickened more rapidly than others. The first and second meiotic divisions have been found to be quite normal giving rise to normal tetrad and pollen grains (Table 3 and 5) (Plate II, Fig. 3,4,7 and 8).

While in F_1 hybrid the number of bivalents in PMCs was seen to vary from four to nine (Plate II, Fig. 9). The rest of chromosomes remained unpaired as univalent. On examination of large number of PMCs in any case configurations higher than bivalents could be seen. On an average 11.2 I + 7.4 II were seen at metaphase-I, the bivalents and univalent were seen scattered about at random in the cytoplasm. Such irregular arrangement was due to the fact that all the chromosomes have not reached the equatorial pole and arranged themselves in the normal compact manner (Plate II, Fig. 10-12). Although, mass of the bivalents arranged themselves at the equatorial plate, very few of them were seen away from the plate, scattered about in the cytoplasm along with the univalants. At anaphase-I in addition to bipolar separation (Plate II, Fig. 12) (occasionally with laggards); tripolor separation in F_1 was also observed (Table 4) (Plate II, Fig. 11) which led to formation of abnormal sporads (Plate II, Fig. 13) and sterile pollen grains (Table 5), (Plate II, Fig. 14).

As usual in many sterile interspecific hybrids at metaphase, the bivalents and the univalent were seen scattered at random in the cytoplasm. This irregular arrangement was due to the fact that all the chromosomes have not reached the equatorial plate and arranged themselves in the normal compact manner.

Discussion

It is evident from the observations made that sterility in this hybrid is mainly due to incomplete pairing of chromosomes at meiosis, as was observed by Skovsted (1935, 1937).

Such failure of pairing is generally caused by lack of homology of various degrees between the chromosomes of the two species involved. Absence of homology in the present instances may be attributed to loss of homology of the chromosomes of the two species as a result of geographical isolation for long periods and

Table 2. Chromosome behaviour during meiosis of *G. arboreum MPKV GMS, G. stocksii* and hybrid

Gossypium spp./hybrids Meiotic stage	Chromosome associations I	II	PMCs observed
***G. arboreum MPKV GMS* (2*n*=2*x*=26)**			
Diakinensis	0.0	13.0	12
Metaphase-I	0.0	13.0	10
***G. stocksii* (2*n*=2*x*=26)**			
Diakinensis	0.0	13.0	18
Metaphase-I	0.0	13.0	19
***G. arboreum MPKV GMS* x *G. stocksii* (2*n*=2*x*=26)**			
Diakinensis	11.6	7.2	22
Metaphase-I	11.2	7.4	18

Table 3. Bipolar separation of chromosomes observed at anaphase-I during meiosis in the *G. arboreum MPKV GMS, G. stocksii* and hybrid

Chromosome distribution at each pole 17-9	16-10	15-11	14-12	13-13	PMCs (no.) observed
***G. arboreum MPKV GMS* (2*n*=2*x*=26)**					
–	–	–	–	5	5
***G. stocksii* (2*n*=2*x*=26)**					
–	–	–	–	9	9
***G. arboreum MPKV GMS x G. stocksii* (2*n*=2*x*=26)**					
1	3	5	4	0	13

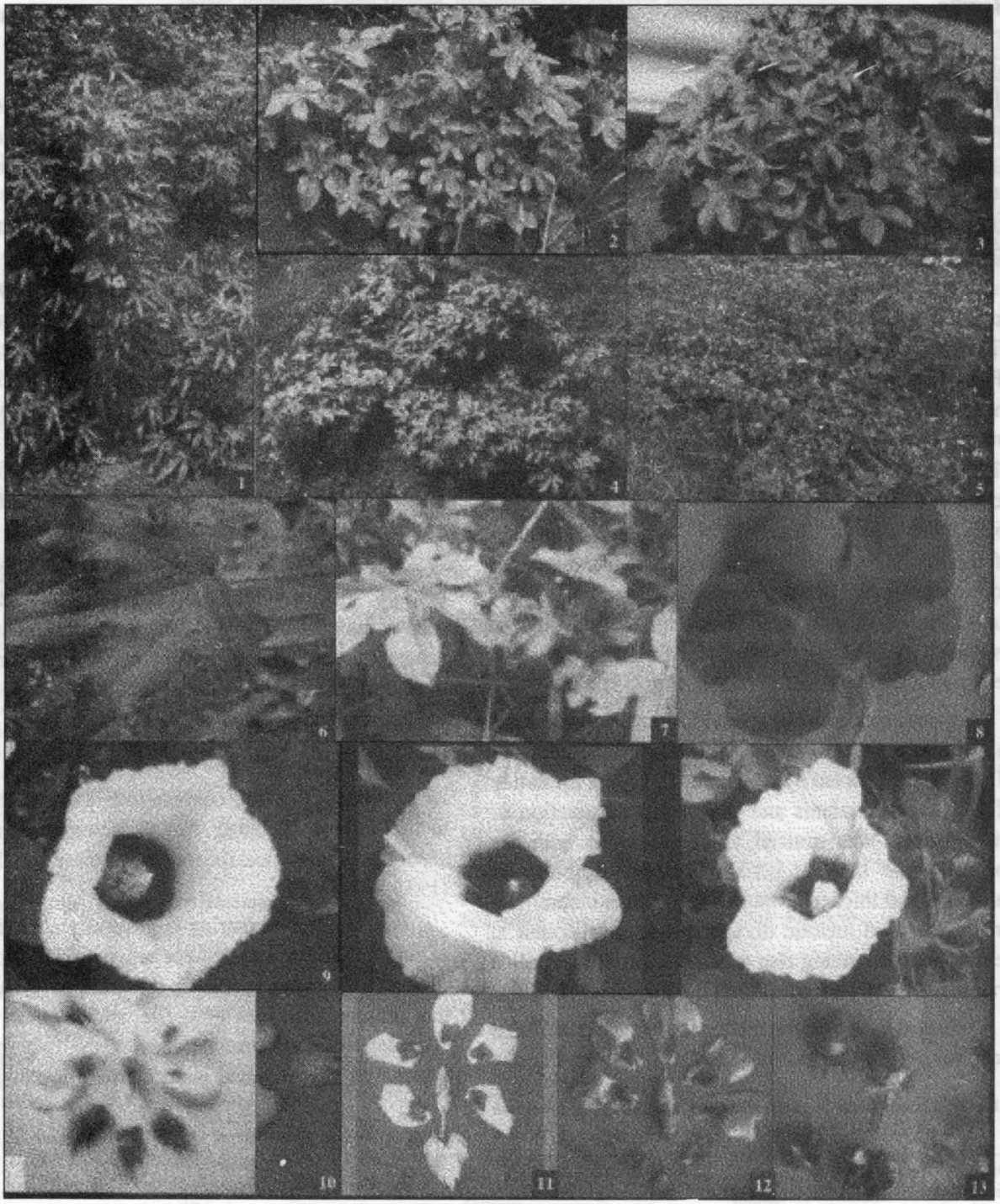

Plate I

Fig. 1. Adult plant at flower initiation stage of G. arboreum MPKC GMS
Fig. 2-4. Adult plant before flowering of F_1 hybrid
Fig. 5. Adult plant at wild G. stocksii
Fig. 6-8. Leaf shape and size of G. arboreum MPKV GMS F_1 hybrid and G. stocksii, respectively
Fig. 9a,b,c. Flower colour, shape and size of G. arboreum MPKV GMS. F_1 hybrid and G. stocksii, respectively
Fig. 10,11,12. Petal colour petal spot bractiole size, shape in F_1 hybrid G. arboreum and G. stocksii, respectively
Fig. 13. Green boll, open capsules and seed with fur of G. stocksii

Table 4. Tripolar separation of chromosomes observed at anaphase-I during meiosis of hybrid between *G. arboreum MPKV GMS, G. stocksii*

Chromosome distribution at each pole during anaphase-I of meiosis			PMCs (no.) observed
6-9-11	5-10-11	4-12-10	24
4	13	7	

Table 5. Pollen size fertility and germination *G. arboreum MPKV GMS, G. stocksii* and hybrid

Gossypium species, ploidy level chromosome number (2*n*)	Pollen		
	Size (microns)	Fertility %	Germination %
G. arboreum MPKV GMS (2*n*=2*x*=26)	95.25	96.15	89.36
G. stocksii (2*n*=2*x*=26)	87.54	86.45	82.66
*G. arboreum MPKV GMS*x *G. stocksii* (2*n*=2*x*=26)	56.89	2.51	0.00

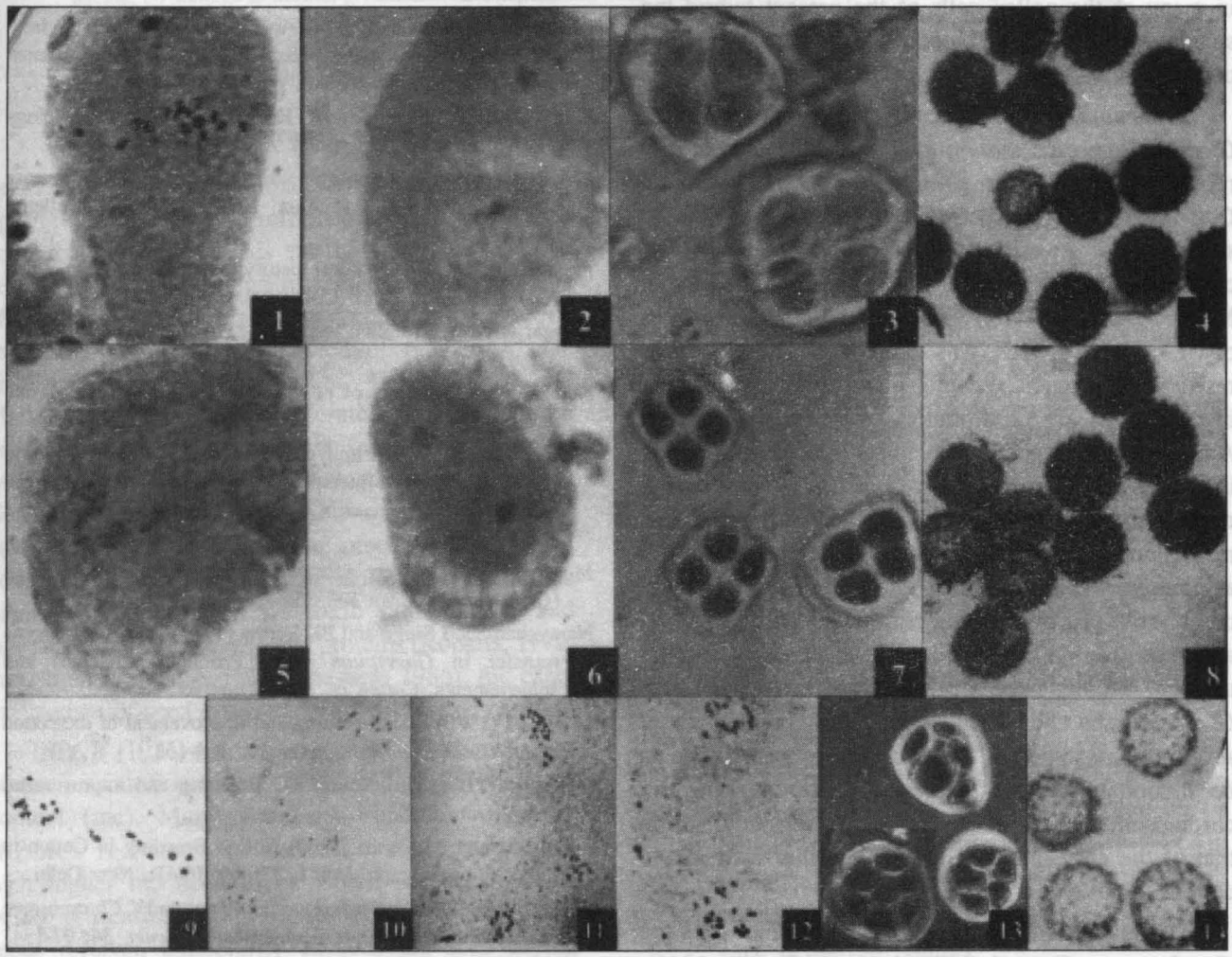

Plate II

Meiosis of pollen development of G. arboreum, Fig. 1-4.

1. *Metaphase-I with 13^{II} (1250 X)*
2. *Normal anaphase (950 X)*
3. *Normal tetrad (750 X)*
4. *Normal fertile pollens (550 X)*

G. stocksii Fig. 5-8.

5. *Metaphase-I with 13^{II} (1350 X)*
6. *Normal Ist telophase (850 X)*
7. *Normal tetrad (450 X)*
8. *Normal fertile pollens (550 X)*

F_1 hybrid (G. arboreum x G. stocksii) Fig. 9-14.

9. *Abnormal metaphase showing $10^{I} + 5^{II}$ (950 X)*
10. *Abnormal anaphase showing unequal separation with laggards (1050 X)*
11. *Tripolar separation of chromosome at anaphase-I (1050 X)*
12. *Bipolar separation with unequal chromosomes (1150 X)*
13. *Abnormal sporads containing five, six and seven spores (450 X)*
14. *Sterile pollen grains (550 X)*

their consequent independent evolution (Skovsted 1935, 1937). The degree of incompatibility brought about in the genomes of the two species by such divergent evolutions was vividly shown by the abnormal meiotic behaviour of the chromosome in the hybrid.

Therefore, if follow the variations in the irregularities of the spindle may depend also on the varying number of paired chromosomes present. It has been shown that in many of the pollen cells of the present hybrid the spindle was straight and bipolar like the normal spindles of the parents.

Abraham (1940) obtained hybrid seedlings of cross *G. arboretum* race *indium x G. stocksii* Davis (1964) reported normal pollen germination of *G. stocksii* on *G. arboretum* stigma. Peter (1971) observed 20% seed setting and germination of cross seeds in the crosses *G. arboretum x G. stocksii* F_{15} obtained by of Mahboob Ali *et al.* (1964) were dwarf indicating dwarfness of *G. stocksii* which was dominant. Hybrids were resistant to drought. Results obtained during present investigations are confirmatory with earlier workers. Abraham (1940) reported incomplete chromosome pairing in a hybrid of *G. arboreum* x *G. stocksii.* The bivalent ranged from five to nine with an average of 7.13. The mean number of chiasma/bivalent at deplotene was 1.3 as compared to about 1.7 in its parent. This reduction of chiasma per bivalent of chromosomes during first anaphase was observed, might be because of tripolar and bent spindled were occurred. On all crosses between *G. stocksii* and Old World cottons, not more than about seven chromosomes of the two species were found to be homologous. This suggested that remaining six chromosomes of *G. stocksii* have different origin from that of the corresponding set in the other New World cottons reported.

Partially fertile synthetic allotetraploid between *G. arboreum x G. stocksii* (Stephens and Cassidy 1946); similar fertile amphidiploid (Brown 1948) were reported. Efforts are underway to induce chromosome doubling in this hybrid with a view to restore fertility and transfer of the drought resistance of *G. stocksii* to tetraploid *G. hirsutum* and *G. barbadense* cottons.

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Deterioration of Lentil Seeds: Studies on Germination and Vigour in Relation to Membrane Leakiness and Lipid Peroxidation

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Accelerated ageing of seeds of lentil led to a significant decline in seed viability and seedling vigour. The same is true for controlled aged seeds (14% moisture content) stored at ambient and ±25°C temperatures. Under controlled ageing, no damage to normal germination and vigour was observed in seeds stored up to 90 days at ± 4°C, 60 days at –10°C and 30 days at –20°C temperatures. Increased electrical conductance, inorganic phosphate content, UV absorbancy of leachate, and lipid peroxidation accompanied seed deterioration which can be used as markers. These changes associated with ageing, are interpreted as results due to membrane deterioration.

Key Words: Accelerated Ageing, *Lens culinaris*, Lentil, Seed Sterage

Seeds lose vigour and ultimately their viability during ageing. Under low temperature and moisture conditions, orthodox seeds can be stored for a long period. Accelerated ageing of seeds over several days of exposure to high temperature and humidity has been recognized as a reliable method of predicting seed viability (Delouche and Baskin, 1973; Powell and Mathews, 1977). Such accelerated aged seeds are known to germinate and grow into seedlings comparable with naturally aged seeds (Bhattacharya *et al.*, 1985; Ganguli and Sen-Mandi, 1990). Although many hypotheses have been proposed for the mechanism of seed deterioration, such as lipid peroxidation and membrane damage, accumulation of toxic compounds, and degradation of nucleic acid and proteins (Roberts, 1972; Parrish and Leopold, 1978; Priestley, 1986), the exact mechanism of seed deterioration still remains obscure.

IBPGR (1976) has recommended the conservation of the orthodox seeds at –18°C with 3-7% moisture content (mc). Many genebanks operate following IBPGR's recommendations while sometimes seeds with higher mc need to be stored for short period before processing into genebanks when the amount of seeds received temporarily exceeds the seed drying capacity of a genebank.

The present investigation was undertaken to study some of the growth and biochemical characteristics of lentil seeds subjected to accelerated ageing as well as controlled ageing. Another objective of this study was to determine the optimum conditions for the short-term storage of lentil seeds with higher moisture contents.

Materials and Methods

Freshly harvested seeds of lentil (*Lens culinaris* Medic.; cv L-4147) was obtained from Division of Genetics, Indian Agricultural Research Institute, New Delhi. Initial mc of seeds was 7±0.5% as estimated by high-constant-temperature oven method (ISTA, 1985).

Accelerated Ageing

Seeds were spread uniformly on a wire mesh placed in an air-tight glass desiccator containing saturated solution of sodium chloride at the bottom to maintain 75-78% relative humidity. The desiccator was kept at 35±2°C (ambient temperature) in an incubator. Seeds were drawn for germination and biochemical tests after 7 days of ageing.

Controlled Ageing

A seed lot was conditioned to 14% mc by adding the required quantity of water using the formula:

$$W_F = W_I \frac{(100 - I_M)}{(100 - F_M)}$$ where

W_F = Final weight that will be attained by seeds after adding water

W_I = Initial weight of seeds

I_M = Initial mc of seeds

F_M = Final mc to which seeds were conditioned (*i.e.* 14% in present study)

Seeds added with required amount of water were sealed in Laminated Aluminium Foil (LAF) pouches and incubated at +10°C for 4 days to equilibrate the seeds to 14% mc which was further verified by high-constant-temperature oven method (ISTA, 1985). Seeds with 14% mc were divided into five lots and sealed hermetically in LAF packets (size: 10 cm x 10 cm) to maintain the same mc. These seed packets were stored constantly at ambient, +25°C, + 4°C, –10°C, and –20°C temperatures. Seeds were sampled at every 1 month interval for germination and biochemical estimations.

Germination and Seedling Vigour

To study seed germination and seedling vigour, three sets of 150 seeds each were placed between germination towel papers at 20±2°C in a seed germinator for 7 days. Each set consisting of three replications of 50 seeds each, was used to study seed germination, seedling vigour (shoot and root length) (ISTA, 1985), and to calculate mean germination time (MGT) by counting the germinating seeds everyday for 5 days (Ellis and Roberts, 1981).

Leachate Analyses

Twenty-five seeds were soaked in 25 ml deionised water for 24 h at 20±2°C. The leachate was collected and the conductance was measured using a digital conductivity meter (Control Dynamics). UV absorbancy of leachate was measured at 264 nm using a spectrophotometer (Backman DU 7400). The inorganic phosphate content (Pi) in the leachate was estimated by the method of Fiske and Subba Row (1925).

Lipid Peroxidation

It was estimated in whole seeds by following the method described by Heath and Packer (1968).

Results

Accelerated Ageing

The results showed the significant decline in seed germination of lentil after 7 days of accelerated ageing at 75-78% RH (=13.5% mc) at 35°C. Also, data on MGT revealed the relevant changes indicating seed deterioration. In accelerated aged seeds, a significant loss in seedling vigour – both in root and shoot was observed (Table 1). The conductance of leachate measured almost twice as that of control seeds (Fig. 1a), whereas Pi content in the leachate was *ca.* four-fold (1830 µg/g fw against 470 µg/g fw in the control) (Fig. 1b). Also, UV absorbancy of leachate at 264 nm (Fig. 1c) and lipid peroxidation values (Fig. 1d) showed a significant increase in the accelerated aged seeds.

Controlled Ageing

Storage behaviour of controlled aged seeds was different under various temperature regimes. Seed germination decreased significantly at ambient temperature after 30 days of storage period. However, at other four temperature regimes tested, no marked decline in seed germination was observed during 30 days of storage. With the increase of storage period, seed germination and seedling vigour decreased significantly at ambient and +25°C temperatures in correspondence with significant increase in MGT (Table 1), conductance, Pi content, UV absorbancy of leachate, and lipid peroxidation (Fig. 1 a-d). Seeds stored at ±4°C up to 90 days and –10°C, up to 60 days did not deteriorate markedly and maintained full complement of viability and vigour as is evident by the trend in other biochemical parameters studied. However, there was a non-significant decrease in the root length and increase in the conductance value as well as UV absorbancy of the samples stored at –10°C after 90 days of storage. At –20°C temperature, no indication of seed deterioration was observed up to 30 days of storage (Table 1, Fig. 1 a-d).

Discussion

Accelerated ageing of lentil seeds resulted in a decline in germination and seedling vigour. These observations are in accordance with a number of reports on legume and other crops – soybean (Byrd and Delouche, 1971; Priestley and Leopold, 1979), pigeonpea (Kalpana and Madhava Rao, 1994; 1995) and *Dalbergia* (Thapliyal and Connor, 1997). Also, the other parameters on membrane leakiness studied are indicative of seed deterioration.

The increased leakage of solutes with both accelerated aged (at 35°C) and controlled aged seeds (at ambient and +25°C temperatures), suggests an increase in membrane permeability. In the present study, the increase in leakage of solutes with progressive ageing indicates that the membrane damage in the aged seeds were beyond repair and thereby increased permeability remained a feature associated with ageing of lentil seeds. Leakage of solutes has been reported to be a good index of seed vigour by several workers who also concluded that loss of integrity of plasma membrane in deteriorated seeds led to greater leaching of solutes into the imbibing medium (Parrish and Leopold, 1978; Kakefuda and Duke, 1982; Simon, 1984; Palanisamy and Karivartharaju, 1991; Chhetri *et al.*, 1993; Shen and Oden, 2000). In the present study, we demonstrate that lipid peroxidation is associated with deterioration of accelerated and controlled aged seeds of lentil. Investigations documented in literature do not rule out that lipid peroxidation is a cause of seed deterioration under various storage conditions. Lipids within the membrane are likely sites of ageing damage and lipoxigenase mediated peroxidase reactions are the probable chemical mechanisms for seed ageing (Koostra and Harrington, 1969; Wilson and McDonald, 1986). Gradual and progressive decline in

Table 1. Effect of storage conditions on germination, mean germination time (MGT) and seedling vigour of lentil

Storage condition	Days	Germination (%)	MGT (Days)	Vigour Shoot (cm)	Vigour Root (cm)
Control	0	100	1.18	11.48	8.31
Accelerated Ageing	7	72	1.54	7.83	4.68
Controlled Ageing					
Temperature ambient	30	92	1.33	8.45	5.19
	60	64	2.06	5.13	3.16
	90	26	2.42	1.97	1.11
+25°C	30	95	1.14	10.69	7.08
	60	81	1.34	7.72	6.28
	90	67	1.99	8.56	5.34
+4°C	30	96	1.08	11.66	8.54
	60	95	1.03	11.82	8.36
	90	98	1.14	11.09	8.07
-10°C	30	96	1.05	11.43	8.03
	60	96	1.16	10.90	7.46
	90	96	1.28	11.85	7.28
-20°C	30	99	1.06	11.61	7.65
	60	99	1.01	11.21	7.24
	90	92	1.29	11.29	7.02
LSD > 0.01P		7	0.26	1.36	0.85

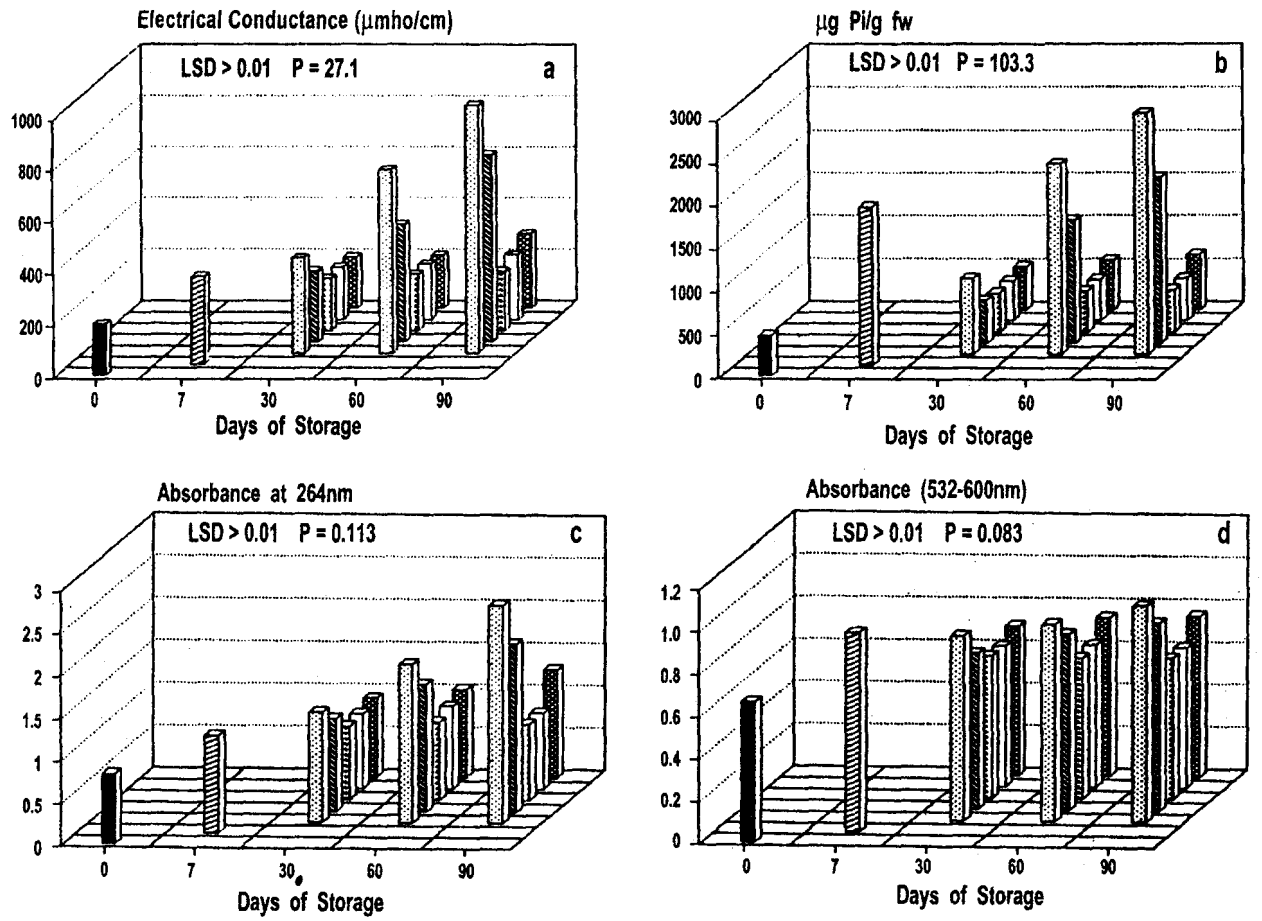

Fig. 1(a-d). Changes in electrical conductance (a), inorganic phosphate content (b), UV absorbance (C) and lipid peroxidation (d) at different storage regimes. Bars represent the storage treatments: control (■), accelerated ageing for 7 days (▨), accelerated ageing for 30, 60, 80, 90 days (▩) + 25°C (▤), + 4°C (▤), -10°C (□), –20°C (▩).

seed germination during longer exposure to sub-zero temperatures with high mc (14%) confirms the results obtained in lettuce (*Lactuca sativa*) stored at –20°C with high mc (12%) in which germination decreased with increased storage period (Kraak and Vos, 1987). It is presumed that damage to the seed viability and vigour at sub-zero temperature with 14% mc results from the freezable water in tissues which contributes to formation of ice crystals gradually, probably in intercellular space within the seeds (Levitt, 1980; Roberts and Ellis, 1989). It is suggested that seeds at around 14-15% mc and below it can be safely stored at –20°C (Roberts, 1972; Harrington, 1973). Our results showed that with higher mc (14%), lentil seeds can be stored safely but temporarily at +4°C at least up to 90 days and at sub-zero temperatures *i.e.* –10°C up to 60 days and –20°C up to 30 days before drying the seeds for long-term conservation in the genebank. Beyond this period, sub-zero temperatures proved to be detrimental to lentil seeds with 14% mc. Our present findings are consistent under accelerated and controlled ageing conditions, and clearly indicate that membrane deterioration including lipid peroxidation is closely linked with ageing of lentil seeds. The various parameters studied may be used as markers for seed viability and vigour.

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Characterization and Evaluation of Sweet Potato Genetic Resources of West Bengal

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Seventy genotypes of sweet potato were collected from various sources and evaluated for morphological, agronomical and quality characters in Augmented Design during *Rabi* season of 2000-2001 under sub-humid condition of West Bengal. The descriptive terminology recommended by International Plant Genetic Resources Institute was adopted in the present study. Wide range of variations were recorded for most of the traits. Frequency percentage of genotypes for variability in each character was calculated. Majority of the genotypes had white/cream flesh whilst five had orange/pale orange colour. A close relationship between orange flesh and high carotenoid pigments as well as white flesh and high dry matter content of tuber were observed. However, none of the biochemical constituents showed any relationship with plant morphologic characters. Some of the genotypes were identified as potential genotypes for commercial production and processing.

Key Words: Characterization, Diversity, Genetic Resources, Quality, Sweet Potato

Sweet potato has the potential to contribute in agriculture because of its calorie yield, nutritive value, adaptability and asexual mode of reproduction. Genetic variation and conservation of diversity within a crop species are the basis for all varietal improvement programmes. An efficient plant breeding programme required a ready access to the useful and representative genetic resources with a clear cut definition on the identity of a variety, its relationship with other varieties in a particular collection and the amount of variation existing in that germplasm. Therefore, evaluation of the existing germplasm is needed since the cultivars are showing high level of genetic variability in leaf shape, vine and emerging leaf colour, tuber yield, root shape, skin and flesh colour of tubers, maturity period, biochemical constituents etc. An attempt has been made in the present paper to evaluate the existing germplasm of sweet potato in West Bengal for identification of genotypes with desirable plant characteristics and their use in further crop improvement programme.

Materials and Methods

Seventy genotypes of sweet potato collected from various sources were planted in an Augmented Design during *Rabi* season in 2000-2001 at Horticultural Research Station, Mondouri, Bidhan Chandra Krishi Viswavidyalaya, Nadia, West Bengal, India (23.5° N Latitude; 80° E Longitude; Altitude of 9.75 m). The soil type was sandy loam in texture having pH 6.1. Each genotype was planted in three rows of 2 m each bed at a distance of 60 cm from row to row and 20 cm within the row. Recommended cultural practices were followed as scheduled for its cultivation. Five competitive plants from each genotype were tagged and data were recorded. The accessions were characterized for different morphological traits as per descriptors recommended by Huaman (1999). Agronomic parameters like length, girth, number and weight of tuber/plant were measured from marketable tubers of 120 days maturity. Dry matter of tube was determined by drying known weight of fresh samples till constant weight was achieved at 70°C. Pooled samples from five tubers of 4-month-old of each accession were used for the analysis of biochemical constituents. Starch and total sugar [(fresh weight basis (FWB)] of tubers were analysed by rapid titrimetric method as described by Moorthy and Padmaja (2000). Ascorbic acid as well as total carotenoids as expressed by β-carotene content of tuber were determined by the method of Ranganna (1977) and crude fibre was estimated by following the procedure of A.O.A.C. (1975). The frequency percentage of genotypes for each morphological, agronomical and qualitative trait was analysed.

Results and Discussion

The germplasm showed a wide range of variations for different agro-botanical and biochemical characteristics. Diversity for some of the plant morphological characters and their frequency percentage are presented

in Table 1. Root morphological characters of different germplasms are presented in Table 2. The tuber shape of the genotypes varied from round to long, irregular or curved and having some defects. The tuber arrangements of most of the germplasms were disperse except two where close clustering habit was observed. Majority of the genotypes had white/cream flesh whilst five had orange/pale orange colour.

Wide variations were observed in different agronomic traits *viz.*, length of tuber (8.1-17.5 cm), girth of tuber (2.2-7.3 cm), number of tuber/plant (2.5-8), weight of tuber/plant (62-340 g) etc. which are presented in Table 3. The evaluated germplasm were grouped into three categories (high, medium and low) based on their qualitative characteristics (Table 4). A wide diversity was observed in different biochemical constituents *viz.*, starch (7-22.50% FWB), total sugar (1.2-4.5% FWB), ascorbic acid (8-42 mg/100g), β-carotene (0.5-8 mg/100g), crude fibre (0.5-0.9% DWB) etc. The dry-matter content of tuber varied between 22% and 35%. In general, the genotype having white coloured flesh exhibited higher amount of dry matter. This finding corroborated the earlier findings of Hamilton *et al.* (1986) that higher dry matter was correlated with light flesh colour. Similarly, correlation between orange/dark cream flesh colour and high carotenoid pigments was observed and reported by several workers (Hernandez, 1963; Garcia *et al.*, 1970). A more or less similar variation for ascorbic acid and crude fibre content were observed as recorded by Kays (1992) and Babu *et al.* (1990), respectively. However, none of the biochemical constituents could be correlated with plant morphological characters of sweet potato. So, selection based on biochemical traits would be effective for identification of genotypes for commercial production and processing. The promising lines identified for different traits are detailed in Table 5.

From the above discussion, it is inferred that the collected germplasms showed a significant variation in almost all the characters studied. Some of the accessions/indigenous cultivars (BCSP-5, BCSP-10, OP-57, RS-5, H-635, 90/704, CO-3) having high starch coupled with low sugars and crude fibre could be recommended for industrial uses for the preparation of noodles and flour. Similarly, genotypes (Kamala Sundari, 90/101, H-85/16, 90/566) recorded high β-carotene, low starch and high moisture were identified for preparations like desserts and juices etc. On the other hand, genotypes

Table 1. Diversity for different plant morphological traits of sweet potato

Character	No. of accessions	Frequency (%)
Plant type		
Erect (< 75 cm)	24	34.28
Semi-compact (75-150 cm)	41	58.57
Spreading (151-250 cm)	05	7.14
Internode length		
Very short (< 3 cm)	15	21.22
Short (3-5 cm)	44	62.85
Intermediate (6-9 cm)	10	14.28
Very long (> 12 cm)	01	1.42
Colour of vine		
Green	31	44.28
Green with few purple spots	17	24.28
Green with many purple spots	08	11.42
Mostly purple	09	12.85
Totally purple	05	7.14
Vine tip pubescence		
None	52	74.28
Sparse	13	18.57
Moderate	03	4.28
Heavy	02	2.85
General leaf outline		
Triangular	20	28.57
Hastate	18	25.71
Lobed	30	42.85
Almost divided	02	2.85
Shape of central leaf		
Teeth	04	5.71
Triangular	08	11.42
Semi circular	02	2.85
Semi elliptic	25	35.71
Elliptic	24	34.28
Lanceolate	04	5.71
Oblanceolate	01	1.42
Kinear	02	2.85
Number of leaf lobes		
01	08	11.42
03	25	35.71
05	37	52.85
Abaxial leaf vein pigmentation		
Yellow	06	8.57
Green	19	27.14
Purple spot at base of main rib	19	27.14
Purple spot in several veins	01	1.42
Main rib partially purple	03	4.28
Main rib totally purple	03	4.28
All veins partially purple	05	7.14
All veins totally purple	14	20.00
Mature leaf colour		
Yellow green	29	41.42
Green	33	47.14
Green with purple edge	03	4.28
Green with purple veins on upper surface	01	1.42
Slightly purple	01	1.42
Mostly purple	03	4.28
Petiole length		
Very short (< 10 cm)	43	61.42
Short (11-20 cm)	24	34.28
Intermediate (21-30 cm)	03	4.28
Petiole pigmentation		
Green	25	35.71
Green with purple near leaf	16	22.85
Green with purple at both ends	19	27.14
Green with purple spot throughout petiole	04	5.71
Green with purple stripes	04	5.71
Totally or mostly purple	02	2.85

Table 2. Diversity for different root morphological characters of sweet potato

Character	No. of accessions	Frequency (%)
Root skin colour		
White	02	2.85
Cream	09	12.85
Yellow	01	1.42
Orange	01	1.42
Brownish orange	02	2.85
Purple red	39	55.71
Dark purple	16	22.85
Flesh colour		
White	35	50.00
Cream	24	34.28
Pale yellow	06	8.57
Pale orange	03	4.28
Dark orange	01	1.42
Intermediate orange	02	2.85
Root shape		
Round	03	4.28
Round elliptic	07	10.00
Elliptic	23	32.85
Obovate	01	1.42
Ovate	09	12.85
Oblong	01	1.42
Long elliptic	24	34.28
Long irregular/curved	02	2.85
Root defects		
Shallow horizontal constrictions	30	42.85
Deep horizontal constrictions	10	14.28
Shallow longitudinal grooves	10	14.28
Deep longitudinal grooves	11	15.71
Deep constrictions and deep grooves	08	11.42
Veins	01	1.42
Root arrangement		
Closed cluster	02	2.85
Open cluster	10	14.18
Disperse	43	61.42
Very disperse	15	21.42

Table 3. Diversity for different agronomic characters of sweet potato

Character	No. of accessions	Frequency (%)
Length of tuber		
Long (> 12 cm)	36	51.43
Short (< 12 cm)	34	48.57
Girth of tuber		
High (> 6 cm)	18	25.71
Low (< 6 cm)	52	74.29
Number of tuber/plant		
High (> 4)	10	14.29
Low (< 4)	60	85.71
Tuber weight/plant		
High (> 250 g)	15	21.43
Low (< 250 g)	55	78.57

Table 4. Diversity for different qualitative traits of sweet potato

Character	No. of accessions	Frequency (%)
Starch (%) FWB		
High (18-22.5)	20	28.57
Medium (13-17.9)	38	54.29
Low (7-12.9)	12	17.14
Total sugar (%) FWB		
High (3.1-4.5)	12	17.14
Medium (2.1-3)	50	71.43
Low (1-2)	08	11.43
β-carotene (mg/100g)		
High (5-8)	05	7.14
Medium (2.5-4.9)	30	42.86
Low (0.5-2.4)	35	50.00
Ascorbic acid (mg/100g)		
High (30-42)	12	17.14
Medium (15-29.9)	33	61.43
Low (8-14.9)	25	21.43
Crude fibre (%) DWB		
High (0.76-0.90)	12	17.14
Medium (0.66-0.75)	38	54.29
Low (0.50-0.65)	20	28.57
Dry-matter of tuber (%)		
High (> 30%)	08	11.43
Medium (25-29.9%)	28	40.00
Low (22-24.9%)	34	48.57

Table 5. Promising lines identified in sweet potato

Character	Accessions/indigenous cultivars
Erect plant habit	90/101, 90/704. 90/566, Pol-4-4-5-, OP-57, IGSP-6, IGSP-7
Longer petiole	WBSP-4, RNSP-1
Totally pigmented vine	H-85/16, S-30, X-180-2, Tripty, WBSP-4
Longer tuber	H-620, H-85/16, -635, X-5, IB-81, OP-219, OP-217, BCSP-10, BCSP-4, IGSP-9, IGSP-8, NDSP-9, IBM-96-229, WBSP-4
Higher girth of tuber	X-100-2, 90/101, X-38, H-85/16, BCSP-6, BCSP-9, BCSP-10, Sree Bhadra, S-1121, Tripty, Kamala Sundari, WBSP-4, IGSP-8
Higher weight of tuber/plant	BCSP-10, S-1221, Tripty, Kamala Sundari, WBSP-4, IGSP-8, BCSP-5, BCSP-7, 90/101, 90/704
Orange fleshed tuber	Kamala Sundari, H-42, 90/101, H-85/16, 90/566
High starch content	H-635, S-783, BCSP-10, X-5, 90/704, H-268, RS-5
High sugar content	H-268, BCSP-3, Sree Vardhini, BCSP-2, 90/101, Kamala Sundari, Tripty, S-1221
Low sugar content	BCSP-5, OP-21, 84-X-1, CO-3, H-635, BCSP-10, IBM-95-229
High β-carotene content	Kamala Sundari, H-85/16, H-42, 90/101, 90/566, S-1221, C—3, Tripty, 90/704, H-268, X-110-2
High ascorbic acid content	9-/704, Tripty, X-110-2, H-85/16, BCSP-5, S-1221, CO-3, H-268, Kamala Sundari, 90/101
Low crude fibre content	90/704, Rs-5, H-85/16, BCSP-10, OP-57, 90/101, Kamala Sundari, H-635, BCSP-5, CO-3
High dry matter content	S-72, OP-57, H-635, H-268, X-5, RS-5, BCSP-5, BCSP-10, OP-21

(90/704m S-1221, Kamala Sundari, H-268, 90/101, X-110-2, Tripty) having high sugars, ascorbic acid, carotene content coupled with high yield are most suited for commercial production for consumption purpose on account of their high nutritive value.

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Evaluation of Exotic Lines of Maize for Forage Traits

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One hundred and thirty-seven lines of maize were evaluated against African Tall and J 1006 at Indian Grassland and Fodder Research Institute, Jhansi, in an unreplicated design for various forage traits. All the lines exhibited lesser green fodder yield as compared to African Tall. African Tall recorded green yield/3 plants as 3.8 kg whereas maximum yields *i.e.* 2.62 kg was recorded in Hyd 9997-1580. African tall recorded high DMY (1.2 kg) as compared to maximum yield recorded in germplasm line Hyd 99-129 (0.544 kg). Lines such as Hyd 997-1544, -1551, -1552, -1577, and -1666 showed at par or slightly better (%) dry matter as compared to African Tall. Except dry matter per cent and the days to 50% flowering, the various morphological traits under study showed positive correlation with green fodder yield. A total of 50% flowering among the germplasm lines was attained as early as within 48 days of sowing. African tall and J1006 were quite late and showed 50% flowering after 70 to 73 days of sowing. Per day per plant green as well as dry matter productivity of African Tall was very high. Certain germplasm lines with comparatively high per day productivity, green and dry matter productivity can be further exploited in breeding programmes in order to breed early flowering varieties with high biomass productivity. The values of skewness were found to be very low for leaf width, number of nodes, green fodder yield and per day productivity indicated a marginal deviation of modal value from the mean. The values of kurtosis for all the traits were in low range sketching platycurtic curve indicating high range of variability in the population. The quality parameters estimated on selected lines revealed that the crude protein (CP) ranged from 9.3% to 10.64% at 50% flowering stage. Natural detergent fibre content ranged from 67.32% to 72.13, acid detergent fibre ranged from 38.91% to 42.57%, lignin content and ash content ranged from 6.98% to 9.67% and 9.63% to 12.08 respectively.

Key Words: Forage Traits, Maize, Morphology, Nutritional Evaluation, *Zea mays*

Maize is a crop which is grown in almost all parts of the country irrespective of latitude, longitude and altitude. In India it occupies nearly 9 m ha land area with an average productivity of 3035 t/ha (Hazra, 1995) The crop has also been exploited to the maximum by scientists for its improvement utilizing cytogenetical, breeding and biotechnological methods. The crop has attracted the attention primarily as grain crop in spite of the fact that for centuries the crop has also been used by farmers as fodder crop. The mode of utilization as fodder may vary from its use as green fodder, hay (*kadavi*) or silage. Due to less attention to improve maize for fodder purpose, presently there are very few varieties in the market since long. The breeding objectives defined by Mishra (1988) indicated for improvement in terms of dry matter content, early maturing, resistance for lodging, and the nutritional value of the crop as fodder. Hence, the present investigation was undertaken to evaluate some exotic lines of maize received from CIMMYT with respect to extent of variability and nature of association among forage yield and related traits.

Materials and Methods

One hundred thirty seven maize lines (Table 1) were grown at Central Research Farm of Indian Grassland and Fooder Research Institute (IGFRI), Jhansi, in an unreplicated plot. Each entry was grown in one row plot of 4 m length keeping 50 cm distance between the rows and 15 cm between the plants within a row. The two checks *i.e.* African Tall and J 1006 were put after every 10 rows. The data recorded on these checks was averaged individually and then compared with different genotypes. The crop was raised adopting standard package and practice under rainfed condition. Data was recorded on three randomly selected plants at 50% flowering stage. Nutritional parameters such as crude protein content (CP), neutral detergent fibre (NDF), acid detergent fibre (ADF), inorganic matter (ash) and lignin were measured on percentage of dry matter. The representative samples of whole plant were analyzed in duplicate for selected proximate constituents (AOAC, 1980) and fibre content (Goering and Van Soest, 1970).

Results and Discussion

African tall is a fodder maize variety with its known high biomass yield potential but the variety is long duration which restricts its acceptability among farmers. In the present investigation the germplasm lines of maize were evaluated for yield and other forage traits against the two fodder type of varieties. The study revealed that all the lines showed lesser green fodder yield as compared to African Tall (Table 2). African Tall recorded

Table 1. List of maize germplasm evaluated

Accession	Pedigree	Origin Mexacc	Accession	Pedigree	Origin Mexacc
Hyd 997-1514	O2POOL 27 C8	6083	Hyd 997-1686	CUBA T-15	6255
Hyd 997-1515	O2POOL 28 C8	6084	Hyd 997-1687	CUBA T-79	6256
Hyd 997-1517	O2POOL 32 C16	6086	Hyd 997-1688	CUBA T-82	6257
Hyd 997-1518	O2POOL 33 C23	6087	Hyd 997-1689	CUBA T-87	6258
Hyd 997-1519	O2POOL 34 C24	6088	Hyd 997-1697	V-33	6266
Hyd 997-1520	POBLAC 61 C1	6089	Hyd 997-1698	MONARC	6267
Hyd 997-1521	POBLAC 63 C2	6090	Hyd 997-1700	OAXA 821	6269
Hyd 997-1522	POBLAC 65 C6	6091	Hyd 997-1701	OAXA 814	6270
Hyd 997-1523	POBLAC 66 C0	6092	Hyd 997-1704	OAXA 711	6273
Hyd 997-1524	POBLAC 67 C1	6093	Hyd 997-1707	COMPUE BLANCO	6276
Hyd 997-1525	POBLAC 68 C0	6094	Hyd 997-1715	CHIH 43	6284
Hyd 997-1526	POBLAC 69 C4	6095	Hyd 997-1716	CHIH 4	6285
Hyd 997-1527	POBLAC 70 C0	6096	Hyd 997-1718	OAXA SEQUIA	6287
Hyd 997-1533	GUAT 209	6102	Hyd 997-1719	GUAD 15	6288
Hyd 997-1543	SNLP 104	6112	Hyd 997-1721	GUAD 6	6290
Hyd 997-1553	BRAZ 859	6122	Hyd 997-1722	RDOM 300	6291
Hyd 997-1566	BRAZ 1006	6135	Hyd 997-1724	GUAD GP 1	6293
Hyd 997-1568	BRAZ 1114	6135	Hyd 997-1725	PUER 5	6294
Hyd 997-1570	BRAZ 1151	6139	Hyd 997-1730	CUBA 94	6299
Hyd 997-1571	BRAZ 1177	6140	Hyd 997-1731	PUER GP 6	6300
Hyd 997-1573	BRAZ 1644	6142	Hyd 997-1732	SVIN GP2	6301
Hyd 997-1574	BRAZ 1720	6241	Hyd 997-1743	CUBA 134	6312
Hyd 997-1580	BRAZ 2121	6149	Hyd 997-1744	HAIT GP3	6313
Hyd 997-1581	BRAZ 2146	6150	Hyd 997-1750	CUBA 113	6319
Hyd 997-1582	BRAZ 2148	6151	Hyd 997-1755	PUER GP4	6324
Hyd 997-1583	BRAZ 2305	6152	Hyd 997-1758	CUBA 126	6327
Hyd 997-1591	OAXA 246	6160	Hyd 997-1762	TRIN GP1	6331
Hyd 997-1595	URUG 215	6164	Hyd 997-1784	GUAD GP2	6353
Hyd 997-1596	URUG 59	6165	Hyd 997-1786	CUBA 85	6355
Hyd 997-1597	URUG 80	6166	Hyd 997-1790	CUBA 83	6359
Hyd 997-1598	URUG 138	6167	Hyd 997-1793	CUBA 82	6362
Hyd 997-1603	JALI 281	6172	Hyd 997-1799	CUBA 130	6368
Hyd 997-1604	NAYA 154	6173	Hyd 997-1501	BRAZ 2461	6070
Hyd 997-1605	NAYA 166	6174	Hyd 997-1507	ARZM 01113	6076
Hyd 997-1609	BRAZ 2234	6178	Hyd 997-1508	ARZM 01114	6077
Hyd 997-1620	BRAZ 1711	6189	Hyd 997-1509	SINA 25	6078
Hyd 997-1626	SUWAN TUXP	6195	Hyd 997-1510	MART 10	6079
Hyd 997-1627	CMS 06	6196	Hyd 997-1512	BRAZ 1116	6081
Hyd 997-1629	COPM MANAUS	6198	Hyd 997-1513	SONO 144	6082
Hyd 997-1634	BRAZ SEO28	6203	Hyd 997-1517	O2POOL 32 C16	6086
Hyd 997-1635	BRAZ SEO32	6204	Hyd 997-1528	SNLP 105	6097
Hyd 997-1641	CHZM 04030	6210	Hyd 997-1529	SNLP GP 15	6098
Hyd 997-1642	CHZM 05015	6211	Hyd 997-1530	VERA 213	6099
Hyd 997-1647	SNMART 126	6216	Hyd 997-1531	JALI GP 5	6100
Hyd 997-1648	ARZM 13026	6217	Hyd 997-1532	VERA 190	6101
Hyd 997-1649	ARZM 16021	6218	Hyd 997-1540	GUAD GP 5	6109
Hyd 997-1650	ARZM 16026	6219	Hyd 997-1542	GUAD 9	6111
Hyd 997-1651	ARZM 16035	6220	Hyd 997-1544	SNLP 99	6113
Hyd 997-1652	ARZM 17026	6221	Hyd 997-1545	SNLP 136	6114
Hyd 997-1653	ARZM 17056	6222	Hyd 997-1547	RIGS GP5	6116
Hyd 997-1657	CUBA T-4	6226	Hyd 997-1548	VERA 147	6117
Hyd 997-1658	CUBA T-7	6227	Hyd 997-1551	VERA 207	6120
Hyd 997-1659	CUBA T-12	6228	Hyd 997-1552	VERA 217	6121
Hyd 997-1662	CUBA T-30	6231	Hyd 997-1554	BRAZ 881	6123
Hyd 997-1664	CUBA T-1-41	6233	Hyd 997-1556	BRAZ 928	6125
Hyd 997-1665	CUBA T-1-44	6234	Hyd 997-1557	BRAZ 931	6126
Hyd 997-1666	CUBA T-1-48	6235	Hyd 997-1559	BRAZ 972	6128
Hyd 997-1668	CUBA T-52	6237	Hyd 997-1560	BRAZ 981	6129
Hyd 997-1669	CUBA 1-56	6238	Hyd 997-1561	BRAZ 988	6130
Hyd 997-1670	CUBA 1-60	6239	Hyd 997-1562	BRAZ 993	6131
Hyd 997-1672	CUBA 1-63	6241	Hyd 997-1563	BRAZ 1019	6132
Hyd 997-1673	CUBA 1-67	6242	Hyd 997-1565	BRAZ 917	6134
Hyd 997-1674	CUBA 1-71	6243	Hyd 997-1567	BRAZ 1058	6136
Hyd 997-1675	VENE BG002	6244	Hyd 997-1569	BRAZ 1133	6138
Hyd 997-1676	VENE 07403	6245	Hyd 997-1572	BRAZ 1192	6141
Hyd 997-1679	VENE 07809	6248	Hyd 997-1577	BRAZ 1847	6146
Hyd 997-1681	CUBA 1-61	6250	Hyd 997-1699	OAXA 803	6268
Hyd 997-1682	CUBA 1-69	6251	African Tall		
Hyd 997-1684	CUBA T-78	6253	J 1006		
Hyd 997-1685	CUBA T-83	6254			

Table 2. Yield and yield attributes in exotic gemplasm lines of maize

Accession	Plant height (cm)	Leaf width (cm)	Leaf length (cm)	Stem dia. (cm) (cm)	Number of nodes	GFY (kg) (3 plants)	Dry wt (kg) (3 plants)	DM%	Days to 50% flower	Per day GFY (g)/ plant	Per day DMY (g)/ plant
Hyd 997-1514	149.3	5.5	50.8	1.4	10.0	0.855	0.122	14.27	48.00	5.94	0.85
Hyd 997-1515	166.0	5.5	61.5	1.4	9.7	1.060	0.136	12.83	50.00	7.07	0.91
Hyd 997-1517	182.0	7.6	6.10	1.6	10.7	1.100	0.136	12.36	51.00	7.19	0.89
Hyd 997-1518	174.7	6.1	70.4	1.8	10.7	1.010	0.122	12.08	51.00	6.60	0.80
Hyd 997-1519	188.3	7.7	66.4	1.8	11.0	1.425	0.222	15.58	50.00	9.50	1.48
Hyd 997-1520	149.3	8.2	63.0	1.7	10.3	1.200	9.248	20.67	9.00	6.78	1.40
Hyd 997-1521	226.7	9.0	62.5	2.2	16.5	1.810	0.351	19.39	57.00	10.58	2.05
Hyd 997-1522	279.0	6.2	52.5	1.7	14.7	1.700	0.279	16.41	52.00	10.90	1.79
Hyd 997-1523	201.7	8.8	64.1	2.1	12.5	1.900	0.294	15.47	51.00	12.42	1.92
Hyd 997-1524	190.0	7.3	66.9	1.7	12.0	1.200	0.178	14.83	50.00	8.00	1.19
Hyd 997-1525	198.3	7.3	61.7	1.6	10.0	1.050	0.159	15.14	52.00	6.73	1.02
Hyd 997-1526	185.7	8.2	70.7	1.8	9.7	1.420	0.180	12.68	51.00	9.28	1.18
Hyd 997-1527	200.3	8.2	68.5	1.9	12.0	1.865	0.297	15.92	50.00	12.43	1.98
Hyd 997-1533	216.3	7.6	61.0	1.7	12.7	1.525	0.252	16.52	52.00	9.78	1.62
Hyd 997-1543	247.3	7.6	67.0	1.6	15.3	1.580	0.297	18.80	56.00	9.40	1.77
Hyd 997-1553	234.0	6.3	66.6	1.6	11.7	1.320	0.234	17.73	50.00	8.80	1.56
Hyd 997-1566	178.3	9.1	81.8	2.0	12.3	1.500	0.237	15.80	57.00	8.77	1.39
Hyd 997-1568	208.3	8.1	75.4	1.9	13.3	1.950	0.341	17.49	56.00	11.61	2.03
Hyd 997-1570	222.5	8.6	68.0	2.0	12.0	1.480	0.268	18.11	57.00	8.65	1.57
Hyd 997-1571	192.5	9.8	75.1	1.9	12.5	1.020	0.259	25.39	61.00	5.57	1.42
Hyd 997-1573	247.7	9.4	65.8	1.6	13.7	1.600	0.297	18.56	56.00	9.52	1.77
Hyd 997-1574	229.7	8.7	80.8	2.0	13.0	1.800	0.291	16.17	54.00	11.11	1.80
Hyd 997-1580	227.0	8.7	8.0	2.5	14.0	2.620	0.415	15.84	55.00	15.88	2.52
Hyd 997-1581	220.0	7.7	73.0	2.2	13.5	1.520	0.280	18.42	54.00	9.38	1.73
Hyd 997-1582	148.7	6.6	73.0	1.5	12.0	0.850	0.213	25.06	59.00	4.80	1.20
Hyd 997-1583	195.3	8.1	78.0	1.9	13.0	1.480	0.377	25.47	59.00	8.36	2.13
Hyd 997-1591	214.7	8.6	73.3	1.7	12.7	1.520	0.328	21.58	57.00	8.89	1.92
Hyd 997-1595	187.3	8.6	70.7	1.7	10.0	1.265	0.163	12.89	50.00	8.43	1.09
Hyd 997-1596	176.3	7.5	53.0	1.8	10.7	1.250	0.185	14.80	53.00	7.86	1.16
Hyd 997-1597	220.3	7.2	68.8	1.8	11.0	1.445	0.238	16.47	50.00	9.63	1.59
Hyd 997-1598	221.0	7.0	62.4	1.8	11.7	1.700	0.241	14.18	51.00	11.11	1.58
Hyd 997-1603	252.3	8.4	66.5	1.8	12.0	1.870	0.310	16.58	56.00	11.13	1.85
Hyd 997-1604	241.2	8.1	77.6	1.8	15.3	1.710	0.354	20.70	59.00	9.66	2.00
Hyd 997-1605	233.0	7.2	65.7	1.8	14.3	1.310	0.273	20.84	57.00	7.66	1.60
Hyd 997-1609	216.7	9.3	81.7	1.9	14.0	1.850	0.324	17.51	54.00	11.42	2.00
Hyd 997-1620	192.0	8.0	75.3	2.4	14.0	1.230	0.267	21.71	59.00	6.95	1.51
Hyd 997-1626	228.0	8.6	70.6	1.7	11.3	1.430	0.243	16.99	54.00	8.83	1.50
Hyd 997-1627	225.0	8.9	67.7	2.0	14.0	2.400	0.479	19.96	54.00	14.81	2.96
Hyd 997-1629	230.3	8.3	73.7	1.8	11.7	1.880	0.292	15.53	51.00	12.29	1.91
Hyd 997-1634	180.3	8.5	72.4	2.1	15.3	2.380	0.446	18.74	56.00	14.17	2.65
Hyd 997-1635	197.7	7.4	67.7	1.9	13.0	1.250	0.285	22.80	57.00	7.31	1.67
Hyd 997-1641	133.0	6.5	58.4	1.3	9.0	0.470	0.093	19.79	59.00	2.66	0.53
Hyd 997-1642	138.5	6.7	71.0	1.7	9.0	0.440	0.098	22.27	59.00	2.49	0.55
Hyd 997-1647	187.7	9.2	89.8	2.1	1.37	2.030	0.512	25.22	61.00	11.09	2.80
Hyd 997-1648	201.7	7.2	70.7	2.0	11.0	1.360	0.259	19.04	57.00	7.95	1.51
Hyd 997-1649	177.0	7.9	62.9	1.8	9.7	0.930	0.174	18.71	54.00	5.74	10.7
Hyd 997-1650	126.0	6.8	59.5	1.5	9.0	0.350	0.068	19.43	59.00	1.98	0.38
Hyd 997-1651	170.3	7.1	66.1	1.8	9.0	1.330	0.135	10.15	51.00	8.69	0.88
Hyd 997-1652	180.7	7.4	73.5	2.1	9.7	1.260	–	–	55.00	7.64	–
Hyd 997-1653	183.0	6.5	49.2	1.6	12.0	1.450	0.146	10.07	51.00	9.48	0.95
Hyd 997-1657	221.3	8.8	74.3	1.7	12.7	1.250	0.238	–	56.00	7.44	–
Hyd 997-1658	229.5	9.4	68.0	2.1	13.5	1.180	0.255	21.61	57.00	6.90	1.49
Hyd 997-1659	194.0	9.0	74.7	1.7	1.25	0.800	0.176	22.00	61.00	4.37	0.96
Hyd 997-1662	234.3	9.6	75.5	1.9	13.3	1.950	0.368	18.87	57.00	11.40	2.15
Hyd 997-1664	245.7	9.3	70.8	1.7	14.0	2.030	0.349	17.19	54.00	12.53	2.15
Hyd 997-1665	216.3	9.6	75.2	2.1	14.0	2.420	0.422	17.44	55.00	14.67	2.56
Hyd 997-1666	196.0	9.6	69.1	2.2	12.0	1.120	0.331	29.55	57.00	6.55	1.94
Hyd 997-1669	232.0	7.6	56.0	1.7	13.3	1.030	0.202	19.61	54.00	6.36	1.25
Hyd 997-1670	272.2	6.7	58.4	1.5	14.7	1.250	0.268	21.44	54.00	7.72	1.65
Hyd 997-1672	262.7	6.6	57.3	1.6	14.7	1.340	0.255	19.03	54.00	8.27	1.57
Hyd 997-1673	224.0	9.2	73.3	1.8	13.3	1.690	0.323	19.11	54.00	10.43	1.99

Contd.

Accession	Plant height (cm)	Leaf width (cm)	Leaf length (cm)	Stem dia. (cm) (cm)	Number of nodes	GFY (kg) (3 plants)	Dry wt (kg) (3 plants)	DM%	Days to 50% flower	Per day GFY (g)/ plant	Per day DMY (g)/ plant
Hyd 997-1674	230.7	8.0	76.5	2.0	13.7	1.480	0.292	19.73	56.00	8.81	1.74
Hyd 997-1675	198.0	8.0	61.7	1.6	10.7	1.080	0.190	17.59	52.00	6.92	1.22
Hyd 997-1676	159.7	7.4	67.4	1.7	12.3	1.160	0.245	21.12	59.00	6.55	1.38
Hyd 997-1679	168.3	7.1	79.4	1.7	12.7	1.120	0.305	27.23	59.00	6.33	1.72
Hyd 997-1681	203.0	8.8	76.9	2.0	12.0	0.930	0.182	19.57	57.00	5.44	1.06
Hyd 997-1682	171.5	6.9	65.0	1.9	11.0	0.560	0.110	19.64	57.00	3.27	0.64
Hyd 997-1684	208.3	8.1	74.8	1.7	11.7	1.640	0.204	12.44	51.00	10.72	1.33
Hyd 997-1685	239.0	7.5	77.7	1.8	15.3	1.480	0.200	13.51	6.100	8.09	1.09
Hyd 997-1686	271.7	7.0	65.7	1.9	14.3	1.810	0.376	20.77	54.00	11.17	2.32
Hyd 997-1687	232.7	8.2	65.4	1.9	15.3	1.710	0.319	18.65	54.00	10.56	1.97
Hyd 997-1688	247.3	8.5	72.7	2.1	14.0	2.000	0.444	22.20	57.00	11.70	2.60
Hyd 997-1689	227.0	8.6	71.3	2.0	15.0	1.850	0.293	15.84	55.00	11.21	1.78
Hyd 997-1697	157.3	5.9	59.7	1.4	9.0	0.835	0.092	11.02	48.00	5.80	0.64
Hyd 997-1698	185.7	7.7	56.4	1.9	10.3	1.420	0.145	10.21	48.00	9.86	1.01
Hyd 997-1700	195.0	9.4	88.0	2.0	14.0	1.150	0.245	21.30	59.00	6.50	1.38
Hyd 997-1701	175.5	7.3	68.0	1.9	12.0	0.780	0.199	25.51	59.00	4.41	1.12
Hyd 997-1704	207.7	8.3	67.8	1.8	10.3	1.580	0.198	12.53	51.00	10.33	1.29
Hyd 997-1707	175.7	7.4	61.1	1.9	9.0	1.080	0.103	9.54	51.00	7.06	0.67
Hyd 997-1715	168.0	7.6	61.1	1.6	10.3	0.800	0.137	17.13	45.00	4.94	0.85
Hyd 997-1716	135.3	6.9	54.0	1.5	12.0	0.500	0.085	17.00	56.00	2.98	0.51
Hyd 997-1718	167.3	7.2	66.5	1.6	11.3	0.850	0.149	17.53	56.00	5.06	0.89
Hyd 997-1719	153.7	5.6	65.4	1.6	10.0	0.870	0.120	13.79	51.00	5.69	0.78
Hyd 997-1721	216.3	7.0	64.9	1.7	11.7	1.660	0.238	14.34	51.00	10.85	1.56
Hyd 997-1722	211.0	7.0	61.8	1.8	11.3	1.580	0.188	11.90	51.00	10.33	1.23
Hyd 997-1724	205.0	8.1	73.5	1.7	12.3	1.680	0.270	16.07	51.00	10.98	1.76
Hyd 997-1725	214.0	7.3	59.9	1.5	12.3	1.260	0.232	18.41	54.00	7.78	1.43
Hyd 997-1730	222.0	6.9	60.7	1.6	12.0	1.320	0.245	18.56	56.00	7.86	1.46
Hyd 997-1731	253.7	7.1	81.7	1.9	14.3	1.970	0.387	19.64	56.00	11.73	2.30
Hyd 997-1732	205.7	8.8	64.3	1.4	12.3	1.630	–	–	56.00	9.70	–
Hyd 997-1743	223.7	8.0	65.0	1.6	12.3	1.240	0.265	21.37	57.00	7.25	1.55
Hyd 997-1744	255.3	7.2	74.3	1.9	13.7	1.630	0.316	19.39	56.00	9.70	1.88
Hyd 997-1750	261.5	10.2	66.5	2.3	16.5	2.010	0.379	18.86	56.00	11.96	2.26
Hyd 997-1755	220.3	7.1	66.3	1.7	14.3	2.00	0.368	18.40	54.00	12.35	2.27
Hyd 997-1758	285.7	7.2	58.3	1.6	1.80	0.327	54.00	11.11	2.02	–	–
Hyd 997-1762	261.7	9.2	67.6	2.2	15.0	2.225	0.476	21.39	59.00	12.57	2.69
Hyd 997-1784	219.3	6.0	53.3	1.5	13.3	1.080	0.190	18.43	54.00	6.67	1.23
Hyd 997-1786	226.0	5.7	64.0	1.6	14.0	1.490	0.265	17.79	55.00	9.03	1.61
Hyd 997-1790	249.3	7.5	63.3	1.7	14.0	1.570	0.294	18.73	52.00	10.06	1.88
Hyd 997-1793	230.0	7.1	60.9	2.0	14.7	1.790	0.343	19.16	55.00	10.85	2.08
Hyd 997-1799	222.3	7.6	67.3	1.9	13.0	1.510	0.326	21.59	56.00	8.99	1.94
Hyd 997-1501	111.5	7.5	68.0	1.8	11.0	0.455	0.316	21.72	65.00	7.46	1.62
Hyd 997-1507	184.5	9.9	70.8	2.0	14.0	1.200	0.286	23.83	61.00	6.56	1.56
Hyd 997-1508	159.3	7.3	75.7	2.0	12.0	1.720	0.225	13.08	51.00	11.24	1.47
Hyd 997-1509	187.0	6.4	65.2	1.7	12.3	0.980	0.193	19.69	57.00	5.73	1.13
Hyd 997-1510	200.0	6.1	48.6	1.6	13.0	1.800	0.183	10.17	51.00	11.76	1.20
Hyd 997-1512	183.3	7.5	60.9	1.7	14.3	1.800	0.268	14.89	61.00	9.84	1.46
Hyd 997-1513	207.7	6.4	67.0	1.6	11.7	1.300	0.180	13.85	55.00	7.88	1.09
Hyd 997-1517	262.7	7.3	69.3	1.7	13.0	1.480	0.199	13.45	54.00	9.14	1.23
Hyd 997-1528	263.3	7.7	73.3	1.7	15.3	1.460	0.337	23.08	56.00	8.69	2.01
Hyd 997-1529	227.0	9.2	86.4	2.0	13.3	2.370	0.544	22.95	59.00	13.39	3.07
Hyd 997-1530	236.7	8.1	75.0	2.3	16.0	2.390	0.520	21.76	59.00	13.50	2.94
Hyd 997-1531	174.0	7.7	80.7	1.6	11.7	1.250	–	–	56.00	7.44	–
Hyd 997-1532	220.0	10.4	80.2	2.3	13.5	1.360	0.326	23.97	58.00	7.82	1.87
Hyd 997-1540	202.3	7.4	60.6	1.6	13.7	1.325	0.276	20.83	58.00	7.61	1.59
Hyd 997-1542	195.2	7.7	65.7	1.7	11.0	1.150	0.187	16.26	52.00	7.37	1.20
Hyd 997-1544	244.0	8.6	76.3	1.8	13.3	1.645	0.481	29.24	59.00	9.29	2.72
Hyd 997-1545	237.2	7.9	84.8	1.7	14.3	1.360	0.336	24.71	62.00	7.31	1.81
Hyd 997-1547	219.3	7.0	77.9	1.9	13.7	1.430	0.299	20.91	58.00	8.22	1.72
Hyd 997-1548	192.3	7.3	8.00	1.8	15.0	1.370	0.356	25.99	66.00	6.92	1.80
Hyd 997-1551	191.7	8.3	76.0	1.7	13.7	1.290	0.428	33.18	66.00	4.80	1.43
Hyd 997-1552	191.7	8.3	76.0	1.7	13.7	1.290	0.428	33.18	66.00	6.52	2.16
Hyd 997-1554	198.0	8.3	69.3	1.7	14.3	1.270	0.289	22.76	59.00	7.18	1.63

Contd.

Accession	Plant height (cm)	Leaf width (cm)	Leaf length (cm)	Stem dia. (cm) (cm)	Number of nodes	GFY (kg) (3 plants)	Dry wt (kg) (3 plants)	DM%	Days to 50% flower	Per day GFY (g)/ plant	Per day DMY (g)/ plant
Hyd 997-1556	191.0	8.4	88.3	2.0	11.3	1.380	0.345	25.00	62.00	7.42	1.85
Hyd 997-1557	147.5	8.2	64.8	1.7	9.5	0.875	0.104	11.89	58.00	5.03	0.60
Hyd 997-1559	96.5	7.5	62.7	1.4	11.7	0.890	0.172	19.33	56.00	5.30	1.02
Hyd 997-1560	157.5	7.3	7.15	1.8	13.0	0.700	0.164	21.30	66.00	3.89	0.83
Hyd 997-1561	221.7	9.0	69.6	2.1	12.0	1.750	0.287	16.40	54.00	10.80	1.77
Hyd 997-1562	215.0	7.7	67.4	2.1	13.5	1.400	0.206	14.71	58.00	8.05	1.18
Hyd 997-1563	217.0	6.7	63.9	1.8	13.7	1.330	0.233	16.77	56.00	7.92	1.33
Hyd 997-1565	160.7	8.9	85.1	1.9	12.0	1.330	0.249	18.73	58.00	7.64	1.43
Hyd 997-1567	213.3	7.5	79.5	1.7	14.7	1.530	0.397	25.95	61.00	8.36	2.17
Hyd 997-1569	188.7	7.1	62.2	1.7	11.3	1.900	0.208	10.95	55.00	11.52	1.26
Hyd 997-1572	179.3	7.7	81.3	2.1	12.3	1.330	0.261	19.62	58.00	7.64	1.50
Hyd 997-1577	202.7	9.1	85.2	2.0	13.3	1.610	0.488	30.31	61.00	8.80	2.67
Hyd 997-1699	229.3	6.7	69.7	1.7	12.0	1.130	0.213	18.85	54.00	6.98	1.31
African Tall	262.5	9.8	86.7	2.6	15.5	3.8	1.2	30.47	73.00	17.51	5.34
J 1006	221.5	9.8	67.8	2.4	15.0	2.1	0.6	27.83	70.00	9.76	2.72

green yield/3 plants as 3.8 kg whereas amongst the germplasm maximum yield *i.e.* 2.62 kg was recorded in Hyd 997-1580. This accession attained 50% flowering nearly 18 days in advance. Some other lines which showed GFY/3 plants above 2 kg were Hyd 997-1627, -1647, -1664, -1634, -1665, -1688, -1750, -1755, -1762, -1529 and –1530. As regards dry fodder yield, African tall recorded quite high DMY (1.2 kg) as compared to maximum yield recorded in germplasm line Hyd 997-1529 (0.544 kg). In terms of dry matter content also only few lines such as Hyd 997-1544, -1551, -1552, -1577, and -1666 showed at par or slightly better percent dry matter as compared to African Tall. It was observed that the lines with high dry matter content were also late flowering and out of these five lines identified for high or at par dry matter content two lines *i.e.* Hyd 997-1577 and -1544 were comparatively better in dry fodder yield also. Gupta *et al.* (1984) have recommended that fodder varieties should be early growth type and late flowering type as has been observed that late flowering types are better in quality. Bunting (1973) has indicated that there are genotypic differences in rate and duration of dry matter accumulation in maize which also depends on the canopy structure and barrenness. He emphasized that for selecting suitable canopy selection should be made for leaf size and shape.

Except dry matter per cent and the days to 50% flowering, the various morphological traits under study showed positive correlation with green fodder yield (Table 3). In view of this finding certain germplasm lines were identified for further exploitation in breeding programme. These lines showed superiority over the check variety African Tall e.g. Hyd 997-1670, -1686, -1758, -1528 were taller, Hyd 997-1750, -1507, -1532, -1571 possessed broader leaves; Hyd 997-1647, -1700 possessed longer leaves; Hyd 997-1530, -1750, -1521 possessed higher number of nodes per plant. Paramathma and Balasubramanian (1986) have also reported that stem girth, plant height and leaf width are important traits for improving fodder yield. Similarly Patel and Shelke (1984) reported that leaf area, internode number and stem girth have significant positive effect towards fodder yield in maize.

Fifty per cent flowering among the germplam lines was attained as early as within 48 days of sowing and that in some lines it was late. A few lines flowered 66 days after sowing. Both the checks African tall and J1006 were quite late and showed 50% flowering after 70 t0 73 days of sowing. Still, per day per plant productivity in terms of green as well as dry matter of African Tall was also very high. On account of this finding it seems that population improvement programme in African Tall could be an important breeding strategy. Only a few lines were close to per day productivity of African Tall. Thus, as such these lines can not compete with African Tall. However, the lines amongst the germplasm lines with comparatively high per day productivity, green and dry matter productivity can be further exploited in breeding programmes in order to breed early flowering varieties with high biomass productivity. It is possible that the lines so developed may show somewhat less green fodder yield but may outyield the African Tall in terms of per day productivity. Thus, introducing early flowering character in African tall may prove beneficial as the same is expected to increase its acceptability among farmers. Gupta *et al.* (1984) have recommended that fodder varieties should be early growth type and late flowering type as it has

Table 3. Range, mean and other statistical parameters of yield and yield attributes in 137 exotic germplam lines of maize

	Plant height (cm)	Leaf width (cm)	Leaf Length (cm)	Stem Diameter (cm)	Number of nodes	GFY (kg) (3 plants)	Dry wt (kg) (3 plants)	DM%	Days to 50% flowering	Per day green fodder productivity/ plant (g)	per day dry matter productivity/ plant (g)
Min	96.3	5.5	48.6	1.3	9.0	0.350	0.068	9.537	48	1.98	0.38
Max	285.7	10.5	89.8	2.5	16.5	2.62	0.544	33.18	66	15.88	3.07
Average	205.6	7.8	69.2	1.81	12.66	1.455	0.264	19,217	55.7	8.55	1.57
Kurtosis	0.146	-0.338	-0.083	0.163	-0.543	0.230	0.1196	0.361	0.167	-0.014	0.001
Skewness	-0.305	0.119	0.113	0.442	-0.136	0.136	0.4810	0.423	0.422	0.050	0.358
SD	35.211	1.026	8.365	0.220	1.765	0.432	0.100	4.599	3.916	2.682	0.559
Correlation coefficient with GFY	0.599	0.413	0.263	0.547	0.572		0.774	-0.199	-0.133		

been observed that late flowering types are better in quality. Thus, these lines can be used as donor for these traits and can be combined with African Tall in its improvement programme.

The value of skewness were found to be very low for leaf width and number of nodes, green fodder yield and per day productivity which indicated a marginal deviation of modal value from the mean (Table 3). The values of kurtosis for all the traits were in low range sketching platycurtic curve which indicated high range of variability in the population. The low values of kurtosis for all the traits together with low values of skewness for most of the traits also showed better distribution of individuals yielding in a greater variance.

The quality parameters estimated on selected lines revealed that the crude protein (CP) percent ranged from 9.13% to 10.64% at 50% flowering stage. NDF content ranged from 67.32% to 72.13%, ADF ranged from 38.91% to 42.57% (Table 4). Lignin content and Ash content ranged from 6.98% to 9.67% and 9.63% to 12.08 respectively. *Ganga Safed* variety has 10.0% CP at 50% flowering stage (Pachauri *et al.*, 1988) whereas 5.35% CP was observed in seven germplasm lines of maize (Singh and Katiyar, 1999a). In another set of ten germplasm lines 10.17 to 12.92% CP in leaf and 3.49 to 12.92% CP in stem fraction was reported (Singh and Katiyar, 1999b). Thus, in the present set of germplasm lines there was not much variation for quality traits.

Table 4. Forage quality parameters of exotic germplasm lines of maize

Accessions	CP%	NDF	ADF	Lignin	Ash
Hyd 997-1520	10.52	70.85	41.47	9.65	9.93
Hyd 997-1521	10.26	69.82	41.27	7.53	11.03
Hyd 997-1522	10.39	67.89	39.93	9.54	11.31
Hyd 997-1523	9.88	68.81	40.68	6.98	10.96
Hyd 997-1533	10.13	69.39	40.5	7.39	10.63
Hyd 997-1543	9.88	68.93	41.38	8.06	11.09
Hyd 997-1553	9.39	69.68	39.31	7.59	10.06
Hyd 997-1566	9.01	71.82	41.44	8.72	10.21
Hyd 997-1568	10.13	70.62	39.48	7.89	12.08
Hyd 997-1573	10.13	67.37	41.38	8.59	10.26
Hyd 997-1574	9.51	70.83	40.82	8.54	10.98
Hyd 997-1580	9.13	72.13	41.62	8.92	11.06
Hyd 997-1603	9.88	67.37	39.99	8.12	11.03
Hyd 997-1604	9.13	70.87	39.39	8.06	9.63
Hyd 997-1605	10.13	70.27	40.98	7.56	10.02
Hyd 997-1647	9.39	70.35	40.95	8.21	9.68
Hyd 997-1648	10.26	71.18	41.35	8.29	10.63
Hyd 997-1657	9.76	69.88	40.05	7.91	12.03
Hyd 997-1658	10.13	69.31	39.85	7.59	11.08
Hyd 997-1670	9.76	68.38	39.35	7.81	10.23
Hyd 997-1672	9.88	70.18	40.87	9.08	10.58
Hyd 997-1685	9.51	69.05	41.68	8.65	10.24
Hyd 997-1697	9.69	71.3	40.92	7.85	9.86
Hyd 997-1704	9.13	70.95	40.81	8.08	12.04
Hyd 997-1732	10.13	70.01	41.05	8.65	11.21
Hyd 997-1758	10.64	68.93	41.38	9.95	11.24
Hyd 997-1762	9.69	68.83	41.66	8.92	11.02
Hyd 997-1786	9.13	66.68	41.06	7.93	10.52
Hyd 997-1790	9.88	69.05	39.73	7.62	9.63
Hyd 997-1501	10.39	69.32	39.92	9.67	10.27
Hyd 997-1512	9.89	70.08	40.38	9.31	10.24
Hyd 997-1530	9.89	67.32	30.01	7.89	11.06
Hyd 997-1531	9.64	69.05	39.67	8.96	11.85
Hyd 997-1544	9.74	66.98	38.92	8.07	12.05
Hyd 997-1545	9.55	68.21	39.08	7.79	11.52
Hyd 997-1548	9.55	67.38	41.07	7.98	11.96
Hyd 997-1554	9.89	68.65	41.39	8.95	12.05
Hyd 997-1557	9.39	68.23	42.57	8.02	11.08
African Tall	9.39	64.14	33.18	8.59	10.97
J 1006	9.45	63.15	38.45	8.76	10.52

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Morphological Characterization of Tea Flower in Some Tea Genetic Resources

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The present investigation attempts to characterize 20 tea genetic resources which were growing in the Experimental Garden for Plantation Crops, Assam Agricultural University, Jorhat, on the basis of 10 flower characters. Three basic kinds of tea *viz.* China, Assam and intermediate Cambod types were considered as standards in the present study. Apart from using dimensional methods, morphological descriptor was used for characterization of floral morphology as per the recommendations of International Plant Genetic Resources Institute (IPGRI), Rome, Italy. The germplasm AS6, AS7, AS8, AS9, AS10, AS14, AS15 and AS16 resembled the Cambod type and exhibited better floral morphology, whereas AS1, AS2, AS4, AS11, AS12 and AS18 were similar to the Assam type and AS5, AS13, AS17, AS19 and AS20 were closer to the China type.

Key Words: *Camellia*, Descriptors, Germplasm, Morphological Characters, Taxonomy, Tea

Commercial tea plantations are extremely heterogeneous. They exhibit considerable variability in morphological characters due to natural hybridization over a prolonged period among the three principal tea producing taxa, *Camellia sinensis* (L.) O. Kuntze (China type), *C. assamica* (Masters) Wight (Assam type) and *C. assamica* ssp. *lasiocalyx* (Planchan ex. Watt.) Wight (Cambod type) and hybrids thereof or between them and other non-tea producing species of *Camellia* (Wight and Barua, 1957). The genetic diversity of tea plant is narrowing down due to massive uprooting of seed grown sections which were replanted with a few popular vegetative clones. Collection and conservation of genetic resources is gaining importance all over the world with the objectives of utilizing their genetic resources in the ongoing as well as future plant improvement work. In the process of collecting tea genetic resources for future improvement work, it is important to understand the genetic organization of the tea plant and the combination of genes in those hybrids which comprises the tea germplasm (Chen and Liao, 1987).

The floral morphology may be one of the best ways to understand the genetic combination of the tea plant and will help in the various improvement work for yield, quality and other desirable characters. Floral morphology provides a reliable diagnostic criteria for differentiating various taxa and their classification into discrete groups. Floral organs which have considerable importance are flower diameter, sepal number, corolla colour, petal number, filament length, anther length, stigma, stigma position, style and splitting of style. Unlike previous workers Wight (1962) relied mostly on the characteristics of style in differentiating between species and sub-species. Banerjee (1992) stated that the characteristics of taxonomical importance include variation in the number of styles and the degree of their fusion, disposition of stylar arm and globular or pubescent ovary. Banerjee (1992) further reported that Linnaeus recognized two species of tea, *Thea bohea* and *T. viridis* which were reported solely on the basis of number of petals, the former had six and the later nine.

Materials and Methods

Twenty different tea genetic resources (coded AS 1 to AS 20) growing in the Experimental Garden for Plantation Crops, Assam Agricultural University, Jorhat, were considered as the experimental material for studying floral morphology. Observations were made on 10 flower characters in peak flowering season *i.e.* December to January of the season, 2001-2002. For all the flower characters average of 10 flowers was taken. Flower diameter, sepal number, petal number, filament length and anther length were measured by using dimensional method. Corolla colour, stigma, stigma position, style and splitting of style were measured as per the recommendation of International Plant Genetic Resources Institute (IPGRI), Rome, Italy, descriptor and weightage used for numerical taxonomy are presented in Table 1. The three basic types of tea indigenous to the geographical region of South East Asia *viz.*, China, Assam and intermediate Cambod type were considered as standards in the present study.

Results and Discussion

Mean performance of the flower characters studied and weightage used for numerical taxonomy are presented in Table 2.

Table 1. Plant morphological descriptors of *Camellia* spp. used for diversity analysis for flower characters

Characters	Weightage
Flower diameter	Measured in cm
Sepal number	Measured in number
Corolla colour	1 White
	2 Cream
	3 White with red purple tinge
	4 Purple to purple violet
Petal number	Measured in numbers
Filament length	Measured in cm
Anther length	Measured in mm
Stigma l	Linear
	2 Apical
Stigma position	1 Extrose
	2 Introse
	3 Coplanar
Style l	Ascending
	2 Geniculate
	3 Terminal
Splitting of style	1 Geniculate (free for greater part of their length)
	2 Ascending (free for about half of their length)
	3 Terminal (united for greater part of the length)

The high flower diameter values was recorded in AS8 (5.5 cm), AS6 (5.4 cm), AS7 (5.4 cm) and AS15 (5.3 cm) while smallest flowers (3.3 cm) were observed in AS12 and AS13. The germplasm AS3 and AS12 had 2 sepals while most of the other germplasm had 5 sepals. Corolla colour was found to be white in all except AS11, AS15 and AS17 which exhibited white corolla with red purple tinge. In general, petal numbers were found to vary between 6 to 7 with an exception of 4 number of petals in germplasm AS7 and AS9. Filament length was found to be maximum (1.5 cm) in germplasm AS9 and AS 16 and the lowest was observed in AS13 (0.2 cm). The maximum anther length (2.1 cm) was found in AS6 and AS7. Table 2 also revealed that the germplasm AS1, AS2, AS11, AS16 and AS18 exhibited linear stigma whereas rest of the germplasm exhibited apical stigma. The germplasm AS5, AS9, AS10, AS11, AS12, AS13, AS17, AS19 and AS20 exhibited extrose type of stigma, AS1, AS3, AS4, AS14 and AS18 exhibited introse type of stigma and AS2, AS6, AS7, AS8, AS15 and AS16 exhibited coplanar stigma position. Geniculate type of splitting of style was found in germplasm AS3, AS5, AS13, AS19 and AS20, while germplasm AS6, AS7, AS8, AS9, AS15 and AS17 showed ascending type of splitting of style and germplasm. AS1, AS2, AS4, AS10, AS11, AS12, AS14, AS16 and AS18 had style having terminal splitting.

From the experimental findings it was observed that germplasm AS6, AS7, AS8, AS9, AS14, AS15 and AS16 have larger flower diameter, longer filament length and

Table 2. Mean performance of 10 flower characters and weightage on reproductive parts of flowers of different germplasm of tea on the basis of IPGRI descriptor

Germplasm	Flower diameter (cm)	No. of sepals	Corolla colour	No. of petals	Filament length (mm)	Anther length (mm)	Stigma	Stigma position	Style	Splitting of style
AS1	4.1	5	2	7	0.8	1.1	1	2	1	3
AS2	4.2	5	2	7	1.4	1.2	1	3	1	3
AS3	4.1	2	2	6	1.0	1.0	2	2	2	1
AS4	4.2	5	2	7	0.7	1.0	2	2	1	3
AS5	3.4	5	2	6	0.3	1.0	2	1	2	1
AS6	5.4	3	1	6	0.8	2.1	2	3	3	2
AS7	5.4	3	1	4	1.0	2.1	2	3	3	2
AS8	5.5	3	1	6	1.0	2.0	2	3	3	2
AS9	4.3	3	2	4	1.5	1.0	2	1	2	2
AS10	4.3	3	2	6	1.1	1.0	2	1	2	3
AS11	4.0	3	3	6	1.0	1.1	1	1	1	3
AS12	3.3	2	2	7	0.6	1.1	2	1	1	3
AS13	3.3	5	2	6	0.2	1.0	2	1	2	1
AS14	3.9	3	2	6	1.3	1.0	2	2	3	3
AS15	5.3	3	1	7	1.4	2.0	2	3	3	2
AS16	4.1	3	2	6	1.5	1.0	1	3	1	3
AS17	3.8	5	3	6	0.6	1.0	2	1	2	2
AS18	4.3	4	2	7	0.7	1.2	1	2	1	3
AS19	3.7	5	2	6	0.4	1.0	2	1	2	1
AS20	3.5	5	2	6	0.4	1.0	2	1	2	1
Assam	3.9	5	2	7	0.7	1.0	1	2	1	3
China	3.8	5	2	6	0.3	1.0	2	1	2	1
Cambod	6.0	3	1	6	1.0	2.0	2	3	3	2

Table 3. Comparison of tea germplasm with the three standard types for 10 flower characters

Germplasm	Flower diameter (cm)	No. of sepals	Corolla colour	No. of petals (mm)	Filament length (mm)	Anther length	Stigma	Stigma position	Style	Splitting of style	No. of characters resembling			Germplasm closer to standard
											Assam (A)	China (Ch)	Cambod (Ca)	
AS1	A/Ch	A/Ch	A/Ch	A	A	A/Ch	A	A	A	A	6	–	–	Assam
AS2	A/Ch	A/Ch	A/Ch	A	Ca	A/Ch	A	Ca	A	A	4	–	2	Assan
AS3	A/Ch	Ca	A/Ch	Ch/Ca	Ca	A/Ch	Ch/Ca	A	Ch	Ch	1	2	2	China/ Cambod
AS4	Ca	A/Ch	A/Ch	A	A	A/Ch	A/Ch	A	A	A	5	–	1	Assam
AS5	A/Ch	A/Ch	A/Ch	Ch/Ca	Ch	A/Ch	Ch/Ca	Ch	Ch	Ch	–	4	–	China
AS6	A/Ch	Ca	Ca	Ch/Ca	A	Ca	Ch/Ca	Ca	Ca	Ca	1	–	6	Cambod
AS7	Ca	Ca	Ca	–	Ca	Ca	Ch/Ca	Ca	Ca	Ca	–	–	8	Cambod
AS8	Ca	Ca	Ca	Ch/Ca	Ca	Ca	Ch/Ca	Ca	Ca	Ca	–	–	8	Cambod
AS9	Ca	Ca	A/Ch	–	Ca	A/Ch	Ch/Ca	Ch	Ch	Ca	–	2	4	Cambod
AS10	Ca	Ca	A/Ch	Ch/Ca	Ca	A/Ch	Ch/Ca	Ch	Ch	A	1	2	3	Cambod
AS11	A/Ch	Ca	–	Ch/Ca	Ca	A/Ch	A	Ch	A	A	3	1	2	Assam
AS12	A/Ch	Ca	A/Ch	A	A	A/Ch	Ch/Ca	Ch	A	A	4	1	1	Assam
AS13	A/Ch	A/Ch	A/Ch	Ch/Ca	Ch	A/Ch	Ch/Ca	Ch	Ch	Ch	–	4	–	China
AS14	Ca	Ca	A/Ch	Ch/Ca	Ca	A/Ch	Ch/Ca	A	Ca	A	2	–	4	Cambod
AS15	Ca	Ca	–	A	Ca	Ca	Ch/Ca	Ca	Ca	Ca	1	–	7	Cambod
AS16	Ca	Ca	A/Ch	Ch/Ca	Ca	A/Ch	A	Ca	A	A	3	–	4	Cambod
AS17	A/Ch	A/Ch	–	Ah/Ca	A	A/Ch	Ch/Ca	Ch	Ch	Ca	1	2	1	China
AS18	A/Ch	A/Ch	A/Ch	A	A	A/Ch	A	A	A	A	6	–	–	Assam
AS19	A/Ch	A/Ch	A/Ch	Ch/Ca	Ch	A/Ch	Ch/Ca	Ch	Ch	Ch	–	4	–	China
AS20	A/Ch	A/Ch	A/Ch	Ch/Ca	Ch	A/Ch	Ch/Ca	Ch	Ch	Ch	–	4	–	China

anther length. It was also found that the sampled germplasm can be grouped into three distinct groups on the basis of stigma position *i.e.* extrose type, introse type and coplanar type which is an important character for breeding work. The style of the flower is also important character which can be used for categorization of different tea species into three basic types of tea. The genetic materials were grouped into three groups– geniculate type, terminal type and ascending type on the basis of splitting of style which also helped to group the germpalsm into the three standard types.

For breeding work, plants with larger and improved reproductive organs are considered better which are exhibited by germplasm AS6, AS7, AS8, AS9, AS14, AS15 and AS16 compared to rest of the germplasm. Again when 20 germplasm are compared with the three standard types, it was observed that AS6, AS7, AS8, AS9, AS14, AS15 and AS16 were found to be similar with standard Cambod type, AS1, AS2, AS4, AS11, AS12, AS18 are found to be similar with standard Assam type and AS5, AS13, AS17, AS19, AS20 are found to be similar with standard China type (Table 3).

It can be concluded that the genetic resources nearer to Cambod type have larger flower structure compared to the two extreme types. Natural out-crossing among various species of *Camellia* might have resulted in better form of *Camellia* species with improved reproductive organs in the course of its evolution. Such germplasm, thus, be considered for further breeding programme and for future conservation.

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Morphological, Chemical and Genetic Variability in Neem Accessions

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Fifty-eight accessions of neem collected from two agro-ecological regions of North-western plains of India covering the states of Punjab, Haryana and Rajasthan wer. characterized at morphological, chemical and molecular level to ascertain the variability. For statistical treatment, the regions were sub-divided into sub-zones (categories) with the sub-zone 5 further sub-divided into two. Seed characters for morphological, oil, azadirachtin, salannin and nimbin for chemical and six AFLP primer combinations for molecular evaluation were considered. Variability was observed for all the morphological and chemical characters amongst the samples. Among the categories, significant chemical variability existed for azadirachtin-A but the morphological variability was non-significant. At molecular level the genetic similarity (Jaccard's coefficient) varied from 0.07 to 0.759. UPGMA cluster analysis grouped the accessions into five, four and three clusters, respectively based on genetic, morphological and chemical analyses. The dendrograms based on these three parameters revealed no uniformity in their grouping pattern. A high correlation between the cophenetic and dissimilarity matrices has been observed, the correlation being the highest for genetic (r = 0.969) followed by morphological (r = 0.835) and chemical (r = 0.727) matrices. Mantel's test revealed a low correlation among the three parameters.

Key words: *Azadirachta indica*, Chemical Components, Genetic Markers, Morphological Characters, Neem

Neem (*Azadirachta indica* A. Juss) is a multipurpose tree species that grows naturally in the Indian sub-continent. Of late, the tree has caught worldwide attention because of its spectacular therapeutic and bioactive properties (National Research Council, 1992; Tiwari, 1992; Schmutterer, 1995; Randhawa and Parmar, 1996;). It has a cultural heritage in India and its medicinal properties are enshrined in the ancient scriptures. A wide variation in survival, growth, morphological and physiological characters (Rajawat *et al.*, 1994; Kundu and Tigerstedt, 1997; Kundu *et al.*, 1998); physio-chemical, chemical and bioactivity parameters (Ermel *et al.*, 1987; Rengasamy *et al.*, 1993; Rengasamy and Parmar, 1995; Parmar, 1995; Kumar and Parmar 1996, 1997) and the genetic variability based on the isozyme (Kundu, 1999) and AFLP markers (Singh *et al.*, 1999) has been reported. The various studies reported variability in a narrow respect. No effort has been made to study comprehensively the morphological, chemical and genetic variability on the same population.

This paper reports variability amongst 58 accessions of neem from North-western India based on morphological and chemical characters and genetic (AFLP) markers. An attempt has been made to study the correlation amongst the different parameters by comparing their distance matrix employing Mantel test.

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Material and Methods

Neem Seeds

Fifty-eight seed samples of open-pollinated trees were collected from three states of North-western India, namely, Punjab, Haryana and Rajasthan, representing two agro-ecological regions (Fig. 1, Sehgal *et al.*, 1992) and 12 agro-climatic sub-zones (Ghosh, 1991). Details about the test accessions are given in Table 1. For genetic analysis the seeds were grown in a greenhouse of National Bureau of Plant Genetic Resources (NBPGR), New Delhi. The samples falling in a sub-zone were put in one category except P_5, which has been divided into P_5 and $P_{5.1}$ based on aridity and rainfall in this sub-zone. Thus, a total of 13 categories formed were used for statistical analysis.

Seed Morphometric Analysis

Average seed length (mm), diameter (mm) and diameter/length (D/L) ratio were recorded based on 10 measurements each. For weight (g), hundred seeds/ accession were taken.

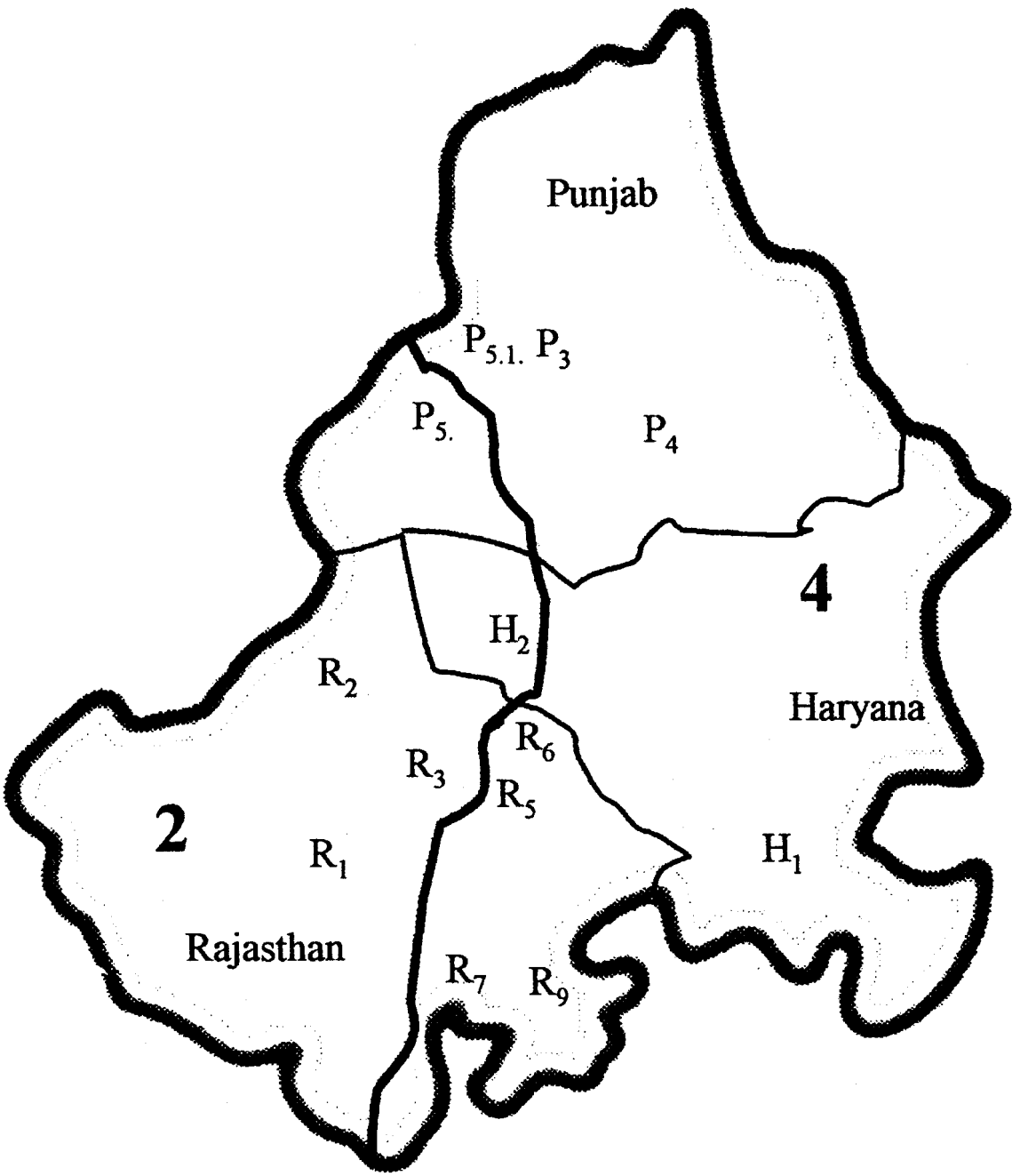

Fig. 1. Agro-climatic regions of India from where neem (Azadirachta indica A. Juss.) *samples were collected*

Chemical Parameters

Oil yield

Dry, cleaned seeds were decorticated manually to obtain kernels, which were crushed in a Waring blender. A known quantity of the crush was extracted in n-hexane (60-80 °C) in a Soxhlet extractor for 8 h (at this stage a drop of n-hexane extract when evaporated on a filter paper left no residual oily spot). n-Hexane was removed in a rotavapor under reduced pressure at 60°C to yield oil.

Table 1. Details of neem accessions used for study

Tree no.	Region	Sub-zone	Category	Tehsil, District	State
N_1	2	R_1	1	CAZRI, Jodhpur	RJ
N_2	2	R_1	1	JD-20, Jodhpur	RJ
N_3	2	R_1	1	JD-21, Jodhpur	RJ
N_4	2	R_1	1	Bhopalgarh, Jodhpur	RJ
N_5	2	R_1	1	Bhopalgarh, Jodhpur	RJ
N_6	2	R_1	1	CSWRI, Bikaner	RJ
N_7	2	R_1	1	CSWRI, Bikaner	RJ
N_8	2	R_1	1	RAU, Bikaner	RJ
N_9	2	R_1	1	RAU, Bikaner	RJ
N_{10}	2	R_2	2	Pilibanga, Bikaner	RJ
N_{11}	2	R_2	2	Ganganagar, Ganganagar	RJ
N_{12}	2	R_2	2	Ganganagar, Ganganagar	RJ
N_{13}	2	R_3	3	Khimsar, Nagor	RJ
N_{14}	2	R_3	3	Nagor, Nagor	RJ
N_{15}	2	P_5	4	Malot, Muktsar	PB
N_{16}	2	P_5	4	Malot, Muktsar	PB
N_{17}	2	P_5	4	Gidarbha, Muktsar	PB
N_{18}	2	P_5	4	Bhatinda, Bhatinda	PB
N_{19}	2	P_5	4	Bhatinda, Bhatinda	PB
N_{20}	2	P_5	4	Bhatinda, Bhatinda	PB
N_{21}	2	H_2	5	Barwala, Hisar	HR
N_{22}	2	H_2	5	CCSHAU, Hisar	HR
N_{23}	2	H_2	5	Hisar, Hisar	HR
N_{24}	2	H_2	5	Hisar, Hisar	HR
N_{25}	2	H_2	5	Mundal, Bhiwani	HR
N_{26}	2	H_2	5	Mundal, Bhiwani	HR
N_{27}	2	H_2	5	Bawal, Rewari	HR
N_{28}	2	H_2	5	Bawal, Rewari	HR
N_{29}	2	H_2	5	Bawal, Rewari	HR
N_{30}	2	H_2	5	Bawal, Rewari	HR
N_{31}	4	R_5	6	Kotputli, Jaipur	RJ
N_{32}	4	R_5	6	Amer, Jaipur	RJ
N_{33}	4	R_6	7	Bahror, Alwar	RJ
N_{34}	4	R_7	8	Jahajpur, Bhilwara	RJ
N_{35}	4	R_7	8	Jahajpur, Bhilwara	RJ
N_{47}	4	R_7	8	Chittorgarh, Chittorgarh	RJ
N_{48}	4	R_7	8	Begu, Chittorgarh	RJ
N_{49}	4	R_7	8	Begu, Chittorgarh	RJ
N_{50}	4	R_7	8	Chittorgarh, Chittorgarh	RJ
N_{36}	4	P_4	9	Barnala, Sangrur	PB
N_{37}	4	$P_{5.1}$	10	Abohar, Ferozpur	PB
N_{38}	4	$P_{5.1}$	10	Abohar, Ferozpur	PB
N_{39}	4	$P_{5.1}$	10	Abohar, Ferozpur	PB
N_{40}	4	H_1	11	Rohtak, Rohtak	HR
N_{41}	4	H_1	11	Pehwa, Rohtak	HR
N_{42}	4	H_1	11	Pehwa, Rohtak	HR
N_{43}	4	H_1	11	Kaithal, Kaithal	HR
N_{44}	4	H_1	11	Kaithal, Kaithal	HR
N_{45}	4	H_1	11	Narwana, Jind	HR
N_{46}	4	H_1	11	Rohtak, Rohtak	HR
N_{51}	4	R_9	12	Hindoli, Bundi	HR
N_{52}	4	R_9	12	Bundi, Bundi	RJ
N_{53}	4	R_9	12	Ladpura, Kota	RJ
N_{54}	4	P_3	13	Jagroan, Ludiana	PB
N_{55}	4	P_3	13	PAU, Ludhiana	PB
N_{56}	4	P_3	13	Khanna, Ludhiana	PB
N_{57}	4	P_3	13	Amoth, Fatejgarh Sahib	PB
N_{58}	4	P_3	13	Rajpura, Rajpura	PB

RJ = Rajasthan, PB = Punjab, HR = Haryana
PAU = Punjab Agricultural University, RAU = Rajasthan Agricultural University
CCSHAU = Chaudhary Charan Singh Haryana Agricultural University, JD = Jodhpur
CAZRI = Central Arid Zone Research Institute
CSWRI = Central Soil and Water Conservation Research Institute
$P_{5.1}$ = Classified based on aridity and rainfall of the sub-zone.

Azadirachtin, salannin and nimbin content

Five gram lots of each of the crushed samples (3 replicates each) were immersed in 10 ml methanol and agitated in an ultrasonic bath for 5 min. The contents were filtered through a G2 Buchner funnel. The residue was re-extracted twice, each time with 7 ml methanol and filtered. The filtrates were combined and volume made to 25 ml. Two ml of this solution was cleaned up by passing through Lichrolut filter cartridge containing RP-18 material and analyzed for azadirachtin, salannin and nimbin contents employing Shimadzu HPLC system fitted with LC9A pumps in binary mode, a Rheodyne 7161 injector with a 20 ml loop and a SPDM6A photodiode array detector. Samples were resolved isocratically on a 15 cm x 6 mm i.d. Shimpack CLC phenyl stainless steel column using methanol-water (70:30) mobile phase at 1.0 ml min^{-1}. Absorbance was measured at 214 and 250 nm at sensitivity of 0.05 AUFS. Each chromatogram was run up to 20 min. The data were acquired on a PCS-DG India Ltd. Work station and quantification was done in the post-analysis session at 214 nm. Under these conditions, azadirachtin, nimbin and salannin showed retention times of 7.13, 13.43 and 15.36 min, respectively.

Genetic Analysis

DNA extraction

Total genomic DNA was isolated from the leaves of 8-week-old seedlings by the method of Dellaporta *et al.* (1983). DNA was quantified using DyNA Quant Fluorometer (Hoefer) and samples were diluted to a final concentration of 100 ng/ml.

AFLP analysis

AFLP™ Plant Mapping Kit (Perkin Elmer Biosystems Inc., USA) was used for DNA restriction, ligation, pre-selective and selective amplification. The amplification reactions were carried out on Perkin-Elmer DNA thermal cycler 9600. The selective amplification reactions were denatured with ABI GENESCAN 500 ROX internal standard for 3 min. at 93°C and chilled quickly by placing on ice before loading. The primer combinations used during selective amplification are given in Table 3. DNA samples were capillary electrophoresed at constant voltage (14.9 KV) and current (12.9 mA) at a temperature of 60°C on an automated DNA sequencer (PE Applied Biosystems model ABI Prism 310) equipped with Genescan software. Analysis of data was done with Genescan analysis software.

Data Analyses

Seed morphometric and chemical data

The data were analyzed for the differences amongst the categories by analysis of variance (ANOVA) using PROC GLM procedure of the SAS statistical software package (SAS Institute Inc., Cary, NC, USA). When differences were significant the means were separated by Duncan's Multiple Range Test (P = 0.06). Contrast analysis was also carried out to test the equality of region means and categories within the regions. For this CONTRAST statement, PROC GLM of SAS was used. Morphological and chemical data were also subjected to interval analysis using NTSYS Software (version 1.70). Distance coefficients were used to generate the dendrogram employing UPGMA (Unweighted pair grouping method of average, Sneath and Sokal, 1973). In addition, principal co-ordinate analysis was performed.

Genetic data

Binary data obtained in the form of peaks during analyses were converted to numerical values using Genotyper (version 2.5). AFLP bands ranging in size from 50 to 500 bp (with minimum peak height 100) were scored for presence (1) and absence (0) across the neem accessions of each primer combination. The pair-wise genetic similarity among the samples was estimated according to the Jaccard's coefficient. The statistical analysis was carried using NTSYS software (version 1.70). The similarity values were converted to distance (D) by subtracting each value from unity. A dendrogram was constructed by employing UPGMA in order to group genotypes into discrete clusters. In addition, principal co-ordinate analysis was performed. Resolving power for each primer has been calculated. According to Prevost and Wilkinson (1999) resolving power (Rp) of a primer is: Rp = Ib, where Ib (band informativeness) takes value for each primer and has been calculated as $1-|2'(0.5-p)|$, p being the proportion of the 58 accessions containing the bands.

SPSS software package was used for the squared Euclidean distance analysis (as this was the only distance criteria which was common for both qualitative and quantitative data) for all three parameters and the average linkage (between samples) was used for the construction of dendrogram on uniform scale.

Matrix comparison

The Mantel matrix correspondence test (Mantel, 1967) was used to compare the cophenetic matrices with similarity matrices to define the degree of congruence as well as to compare similarity and cophenetic matrix among the three parameters to establish the level of association between them.

Results

Seed Morphometric Parameters

All the characters, namely, seed length (9.8-16.5 mm), seed diameter (4.9-7.8 mm), D/L ratio (0.38-0.63) and 10-seed weight (9.8-26.21g) showed variation. Weighted mean and standard deviation for each character from the two regions are reported in Table 2. Contrast analysis revealed that there was no significant difference between the regions for all the seed parameters. However, seed diameter showed variation among the categories of the region 4 at 6% level of significance (Table 3). No significant difference has been found when comparison was done at the level of categories (Table 2).

Chemical Parameters

Contrast analysis revealed significant differences between the regions for oil yield. However, differences were non-significant for other characters (Table 3). The categories of region 4 were found to be significantly different with respect to oil yield and azadirachtin (Table 3). At category level (Table 2), the azadirachtin varied significantly (P = 0.06) from 0.21-0.57. For azadirachtin P_3 sub-region (Punjab) showed the maximum variation followed by H_1 sub-region (Haryana). The oil, salannin and nimbin contents varied non-significantly for all 13 categories. Oil yield varied from 27.16-56.11, salannin 0.03-1.09 and nimbin 0.13-1.19% (w/w).

Fingerprint Profile

The 58 accessions of neem using six selective AFLP primer combinations (Table 4) generated a total of 567 amplicons with an average of 94.5 amplicons/primer. All the primers were polymorphic and generated accession specific bands. The primer combinations MseI-CTG/EcoRI-ACT, MseI-CTG/EcoRI-ACC, MseI-CTG/EcoRI-ACG were more informative as these generated more than hundred bands. Each combination MseI-CTG/EcoRI-ACT showed the highest (35.38) and MseI-CTT/EcoRI-AAC, the least (2.76) resolving power (Table 4). Data

Table 2. Region- and category- wise means of morphological and chemical data on the neem accessions

Region	Category	No. g samples	Seed length (mm)	Seed diameter (mm)	D/L ratio	100-seed weight	Oil yield (% w/w)	Azadirachtin (%0	Salannin (% w/w)	Nimbin (% w/w)
2	1	9	13.26	6.46	0.49	17.96	42.61	$0.472^{b,c}$	0.313	0.551
	2	3	14.20	6.20	0.43	17.17	45.15	$0.453^{b,c}$	0.383	0.547
	3	2	12.10	6.45	0.53	15.46	47.92	$0.450^{b,a,c}$	0.445	0.470
	4	6	12.32	6.57	0.54	16.51	44.43	$0.393^{b,c}$	0.370	0.407
	5	10	13.26	6.56	0.49	17.31	43.03	$0.494^{b,c}$	0.288	0.535
Weighted Mean		30	13.09	6.49	0.50	17.21	43.81	0.460	0.332	0.511
SD ±			1.52	0.49	0.06	3.41	4.60	0.09	0.18	0.27
4	6	2	13.30	6.05	0.45	13.86	49.58	$0.260^{b,c}$	0.305	0.385
	7	1	11.70	4.90	0.41	9.80	38.66	0.210^{c}	0.230	0.380
	8	6	13.13	6.70	0.51	16.76	42.25	$0.331^{b,a,c}$	0.413	0.450
	9	1	13.40	6.90	0.51	20.50	27.16	0.520^{a}	0.760	0.530
	10	3	12.97	6.66	0.52	16.95	45.17	$0.443^{b,a}$	0.613	0.633
	11	7	13.81	6.77	0.49	18.07	44.27	$0.527^{b,c}$	0.329	0.459
	12	3	13.60	6.40	0.47	17.87	40.80	$0.360^{b,c}$	0.326	0.327
	13	5	14.72	6.74	0.46	15.57	43.62	$0.578^{b,a,c}$	0.566	0.842
Weighted Mean		28	13.59	6.59	0.48	16.69	43.01	0.437	0.430	0.556
SD ±			1.26	0.59	0.05	4.41	5.75	0.19	0.22	0.23
			NS	NS	NS	NS	NS	S	NS	NS

Means with the same superscript letters are not significantly different at P = 0.06 using DMRT (Duncan's Multiple Range Test)
NS = Nonsignificant S = Significant

Table 3. Significance level of equality of region means, category means within region

Contrast	Seed	Seed length (mm)	D/L ratio diameter	100 seed weight (g)	Oil yield (% w/w)	Azadirachtin (% w/w)	Salannin (% w/w)	Nimbin (% w/w)
Region	0.51	0.74	0.29	0.59	0.04*	0.27	0.19	0.66
Categories (region 2)	0.29	0.85	0.11	0.93	0.65	0.69	0.78	0.83
Categories (region 4)	0.47	0.05*	0.48	0.53	0.03*	0.01*	0.09	0.18

*Significant at P = 0.06

were used to make pair-wise comparison of the lines based on shared and unique amplification products to generate similarity matrix using the NTSYS-PC statistical package (Version 1.70) The value of similarity for all the 58 lines ranged from 0.07 to 0.759. The two neem samples N_1 and N_{50}, collected from Jodhpur (sub-zone R_1, Rajasthan) and Chittorgarh (sub-zone R_7, Rajasthan), respectively, displayed greater genetic similarity with a similarity coefficient of 0.759.

Cluster and Principal Coordinate Analysis

Morphological clusters

Cluster analysis of the morphological data yielded a phenogram (Fig. 2), which grouped the 58 accessions into four clusters. N_{58} was distinct from all other samples. The principal coordinate analysis revealed that the first three coordinates explained 88.24, 10.55 and 1.79% of total variation.

Chemical clusters

Cluster analysis of the chemical data gave the resultant phenogram (Fig. 3), which grouped the 58 accessions into three clusters. The principal coordinate analysis revealed that the first three coordinates explained 80.75, 18.92 and 0.92% of total variation.

Genetic clusters

Cluster analysis of the genetic data yielded phenogram (Fig. 4), which grouped the 58 accessions broadly into five major clusters based on similarity coefficient. Except clusters 1 and 2, the other clusters are represented by two samples each. Clusters 1 and 2 are represented by samples from all the three states. Therefore, no geographical isolation has been observed. Cluster 1 was further sub- divided into four sub-clusters (a-d). Cluster 1d as represented by the samples of category 11 and 13 has the highest azadirachtin variability. In cluster 5, two samples collected from Begu (Rajasthan) are grouping together and are very distinct from the other samples. In principal coordinate analysis the first three principal coordinates explained 55.98% of the total variation. In this analysis, all the analysed samples were separated which is coherent with the phenogram generated by UPGMA cluster analysis.

Squared Euclidean Distance Analysis was also performed using average linkage between groups. Six clusters were prepared based on the hierarchical analysis. In morphological dendrogram (dendrogram not presented here), N_{42} and N_{47} were distinct from rest of the samples and in chemical analysis N_2 and N_{37} were distinct from the rest. Dendrogram based on binary data showed that N_{46} and N_{55} are distinct from the rest of the accessions. Hence, no uniformity was observed between the dendrograms.

Table 4. Selective AFLP primer combinations along with total number of bands amplified and resolving power (Rp)

Mse I primers/ EcoRI primers	Total no. bands amplified	Resolving power (R_p)
MseI-CTG/EcoRI-ACT	120	35.38
MseI-CTG/EcoRI-ACC	123	33.83
MseI-CTG/EcoRI-ACG	109	18.69
MseI-CTT/EcoRI-ACA	90	9.20
MseI-CTT/EcoRI-AAC	55	2.76
MseI-CTT/EcoRI-AGG	70	8.41

Comparison of cluster and matrices

Comparison of the three dendrograms for the grouping pattern revealed no uniformity. But high correlation between the cophenetic and dissimilarity matrices for each of the three parameters was observed and this correlation was the highest for genetic matrix (r = 0.969) followed by morphological matrix (r = 0.835) and chemical matrix (r = 0.727). The correlation between the dissimilarity matrices of the three parameters was also tested using the Mantel's test. A low correlation was observed between the marker systems studied. A relatively high correlation (r = 0.16) was observed between morphological and genetic matrices, whereas chemical and morphological matrices were weakly

Fig. 2. Dendrogram generated by UPGMA based on morphological characters of 58 accessions of neem (Azadirachta indica)

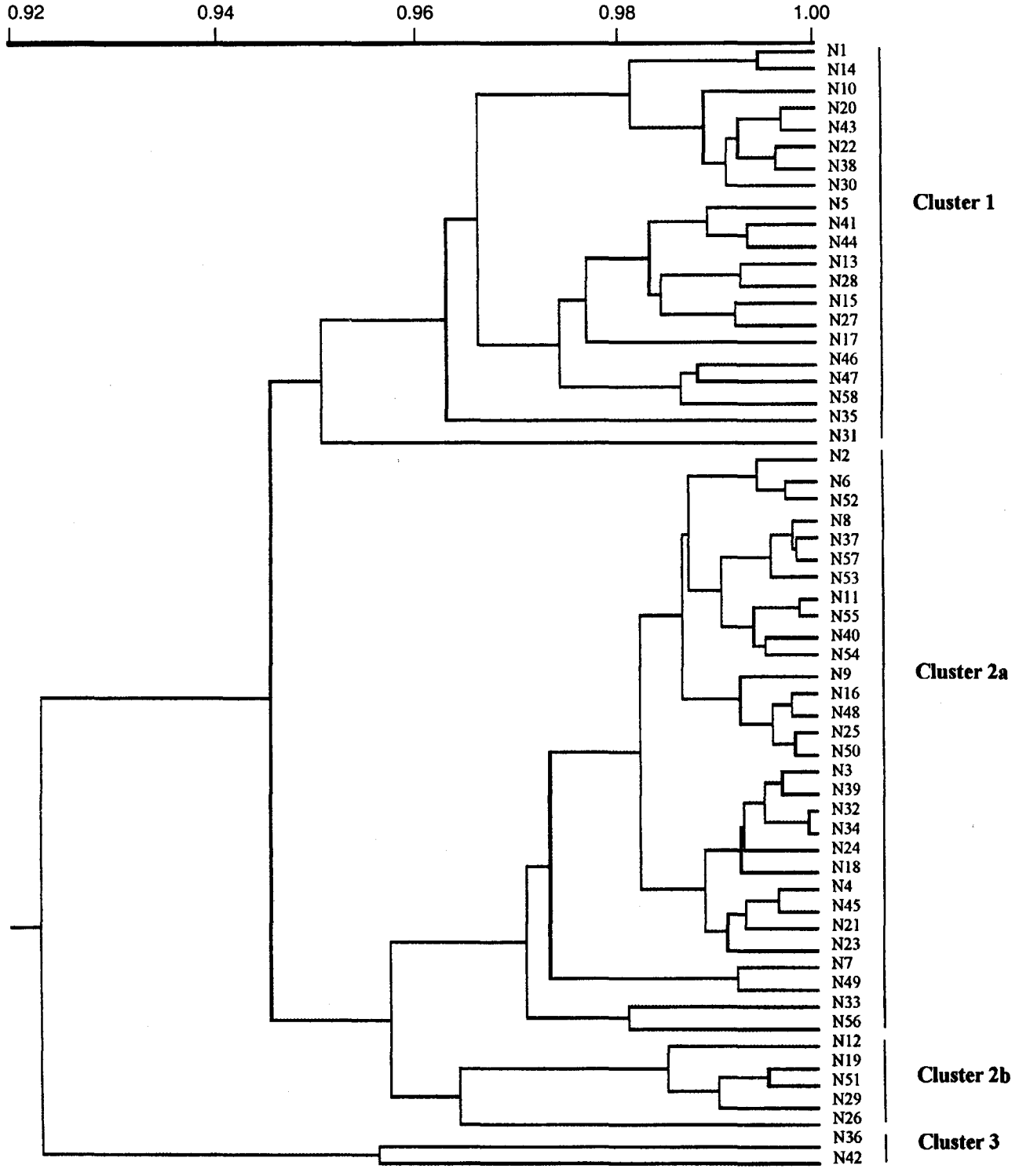

Fig. 3. Dendrogram generated by UPGMA based on chemical characters of 58 accessions of neem (Azadirachta indica)

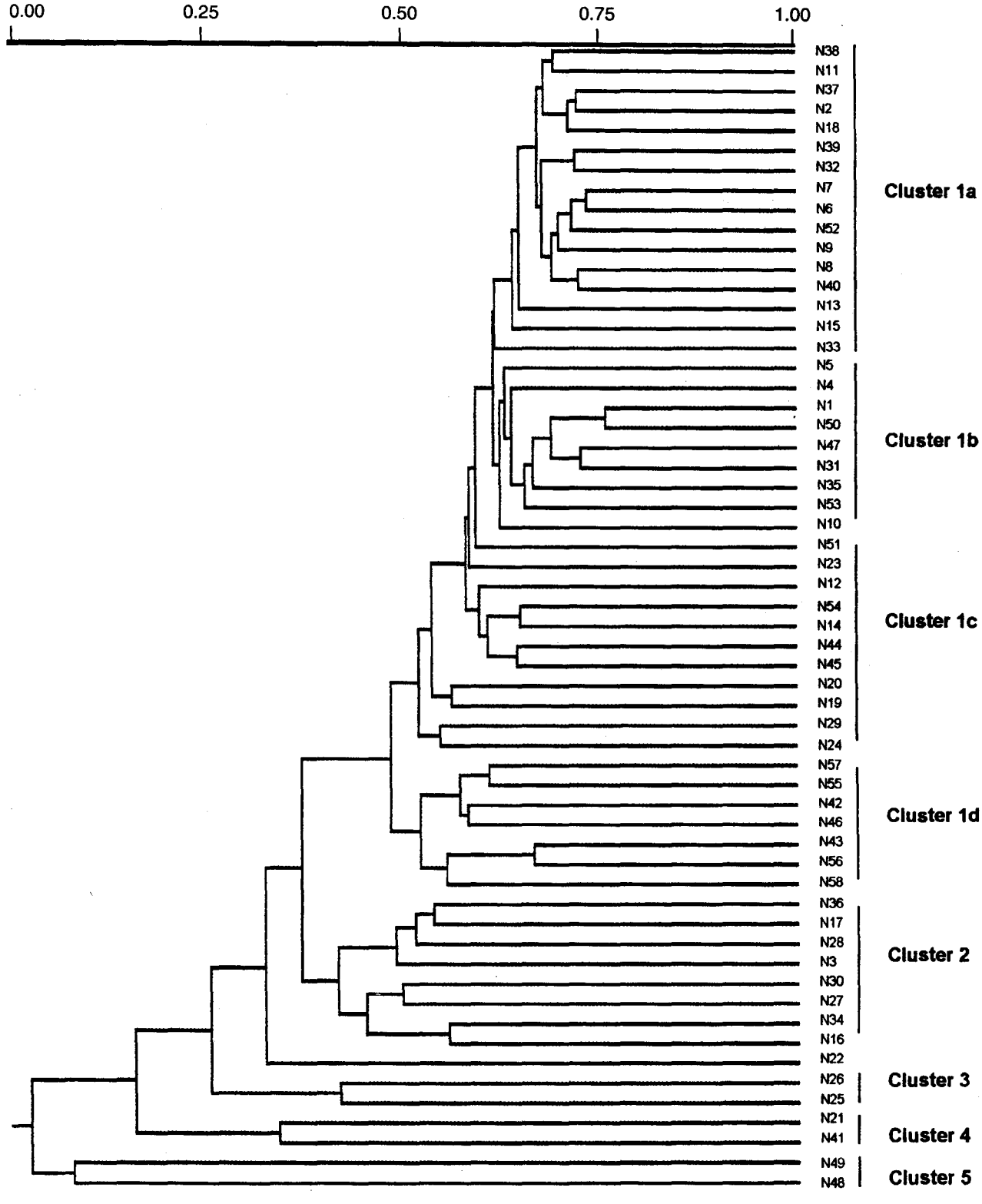

Fig. 4. Dendrogram generated by UPGMA based on Jaccard's coefficients of AFLP markers for 58 accessions of neem (Azadirachta indica)

correlated (0.0068). However, when cophenetic matrices of these marker systems were compared with each other, the correlation values were almost similar ranging from 0.0027 to 0.012.

Discussion

Objective of this study was to estimate the diversity existing in neem in the North-western region of India, and to establish the relationship between morphological, chemical and genetic data to enable selection of some elite lines to bring about an over all improvement in neem for enhanced output of oil, azadirachtin, nimbin and salannin. A high degree of genetic polymorphism and variation in the amount of azadirachtin was detected in all the categories of neem accessions selected for the study. No seed morphometric variation was detected at category level. However, when significance level of equality of region mean was tested, seed diameter showed variation for the region 4. Kundu (1999) reported significant variation in morphological data based on a study of four different neem populations collected from different countries. In the present study, no significant variation in morphology was observed, probably because the population represented a limited North-western part of India. Azadirachtin content showed significant variation for the sub-zone P_5 (Punjab) followed by H_1 (Haryana). This clearly shows that within a population, much variation existed for azadirachtin. Amplified fragment length polymorphism (AFLP) (Vos *et al.*, 1995) has been widely used for differentiating between closely related cultivars in different crop species and to detect genetic variability in the germplasm of a crop species. The technique permits analysis of large number of loci in a single experiment and detects more polymorphism as compared to RFLP and RAPD methods (Powell *et al.*, 1996). The present genetic diversity estimated by AFLP is very close to that reported by Kundu (1999) based on isozyme analysis. Among the primer combinations used in the present study, three out of six primer combinations produced more than one hundred bands (Table 4). Such a large number of polymorphic fragments generated with specific primer pairs has also been reported in biomass willows (Barker *et al.*, 1999) and daylily (Tomkins *et al.*, 2001). Ellis *et al.* (1997) suggested that most informative primer combinations have the greatest coverage across the genome. The three primer combinations have apparently covered widely the genome and can be useful markers for fingerprinting work (Table 4). However, the principal component analysis has shown that the first three components could explain only 55.98% of the variability. Therefore, to cover the genome more extensively, there is need to study the variability with more numbers of AFLP primers as well as different types of marker systems such as simple sequence repeats. A linear correlation was found between resolving power and ability of primer to distinguish the accessions of neem. Thus, primer combination Mse I CTG/EcoR I ACT (Rp = 35.83) and Mse I CTG/ EcoR I ACC (Rp = 33.38) were able to distinguish all the 58 accessions. The result of cluster analysis of seed morphometric, chemical and genetic data presented different pictures. A low correlation between different parameters was observed on the basis of comparison of cophenetic and similarity matrices using Mantel's matrix correspondence test. The poor correlation between genetic similarity value based on AFLP markers and morphological characters may be caused by marker sampling error and biased representation of genome differences revealed by AFLPs (Schut *et al.*, 1997). Little or no consistency between morphological and genetic distances should not be considered a limitation of this system. Morphologically similar genotype may not be genotypically similar, as different genepool can be manipulated to create similar phenotypes. Close association, on the other hand, between morphological and genetic relationships would indicate a very restricted commercial genepool. Similarly, weak correlation between chemical and genetic matrices can be explained, because for a chemical synthesis usually a pathway consisting of several enzymes (more than one gene) plays their role. A weak correlation between morphological and chemical data suggests that seed morphometry has no relation with azadirachtin content. The low correlation between the genetic parameter with chemical or morphology is expected because all the loci, which are actually responsible for chemical and morphological gene expression, are not being covered by the genetic markers. And marker used here is mostly repeated sequence. To establish better correlation, there is need to use different DNA marker systems such as those based on ESTs, so that maximum number of functional loci may be covered and better relation among the three parameters will be established to enable supporting the future neem tree improvement programme.

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Genetic Divergence in Sunflower (*Helianthus annuus* L.)

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Thirty-nine genotypes of sunflower were evaluated for their genetic divergence by D^2 analysis for a set of 14 divergent characters. The D_2 analysis revealed that genotypes exhibited considerable diversity and were grouped into nine clusters. Twenty-seven genotypes representing different eco-geographical regions were grouped into cluster I indicating that genetic divergence and geographical divergence were not related. The characters, oil content, total number of seeds/head and total dry matter/plant, contributed maximum towards genetic divergence in D_2 analysis. Based on Tocher's clustering pattern the genotypes with accession numbers 1144, 780, 1164, 1217 and 1220 were suggested for inclusion into hybridization for obtaining desirable recombinants.

Key Words: Clustering, D^2 analysis, Genetic Divergence, *Helianthus annuus* L., Sunflower

Sunflower is an important non-traditional oilseed crop. Extension of sunflower crop to different areas, seasons and situations has necessitated diversification of varietal/ hybrid base in the country. Genetic divergence among parents is essential since a crossing programme involving genetically diverse parents is likely to produce high heterotic effects and also more variability could be expected in segregating generations. Mahalonobis D^2 Statistic has been employed widely to resolve genetic divergence at inter-varietal and sub-species level in classifying the crop, therefore, an attempt was made in sunflower to study genetic divergence.

Materials and Methods

Thirty-nine genotypes of sunflower (Table 1) with different origins were raised in a randomized block design replicated thice, during *rabi* 1997-98 at college farm, SV Agricultural College, Triupathi. In each replication each genotype was sown in a row of 4 m length with a spacing of 60 x 30 cm. Recommended agronomic practices were followed during the entire growth period under protective irrigation. In each replication five competitive plants were tagged and observations were recorded for 14 characters, namely, days to flowering, days to maturity, plant height (cm), number of leaves, stem diameter (cm), head diameter (cm), leaf area index, total number of seeds/head, seed filling (%), 100-seed weight (g), oil content (%), total dry matter (g), Harvest index (%) and seed yield/plant (g). The data were subjected to analysis of variance followed by multivariate analysis (Mahalanobis, 1930). The genotypes were further grouped into different clusters based on Tocher's method (Rao, 1952)

Results and Discussion

The analysis of variance revealed significant differences among genotypes for all the 14 characters studied. The analysis of variance of dispersion of 39 genotypes was significant indicating the significant pooled effect among all the characters studied between different genotypes.

The 39 genotypes were grouped into 9 clusters using Tocher's method (Table 1). Cluster 1 consisted of maximum number of 27 genotypes representing different eco-geographical regions whereas as six in Table 1 were included in cluster II. The remaining six clusters *viz.*, III, IV, V, VI VII, VIII and IX had one genotype each.

The clustering pattern revealed that the genotypes originating from different geographical regions had been grouped in cluster I which indicated that there was no association between genetic diversity and geographical diversity. Similar results were reported by Anand and Chandra (1980), Yadav *et al.* (1988), Haile (1994) and Sankarapandian *et al.* (1996). The genotypes that originated in one region had been distributed into different clusters, indicating that genotypes with same geographic origin could have undergone change for different characters under selection. This could be due to genetic drift, selection pressure and environment, which creates greater diversity rather than genetic distance (Murthy and Arunachalam, 1966).

The intra- and inter-cluster distances among the genotypes studied was of varying magnitude (Table 2). Intra-cluster D^2 values were ranged from 0 to 21.623, cluster II has maximum intra-cluster distance (21.623) followed by cluster I (20.453) indicating that selection of parents for hybridization within the cluster is advisable. Low intra-cluster D^2 values were recorded for cluster III, IV, V, VI, VII, VIII and IX as they included only single genotype in each cluster. The maximum inter-cluster D^2 value (1656.24) was observed between cluster

Table 1. Distribution of 39 sunflower genotypes into different clusters along with their origin

Cluster number	Number of genotype	Genotype (accession number)	Origin
I	26	350, 38, 1227, 315, 342	USA
		1172, 1148, 1206, 1160	Turkey
		95	South Africa
		652	Russia
		16	Hungary
		146	Italy
		93, 2, 52, 183, 385, 216, 18, 174, 451, 390, 365, 150, 159	—
II	6	1156,1177	Turkey
		702, 1180, 666	USA
		61	Bulgaria
III	1	1144	Turkey
IV	1	30	—
V	1	780	Romania
VI	1	1164	Turkey
VII	1	433	Hungary
VIII	1	1217	Iran
IX	1	1220	Yugoslavia

Table 2. Intra- (diagonal) and inter-cluster average D^2 values of 39 genotypes of sunflower

Cluster	I	II	III	IV	V	VI	VII	VII	IX
I	418.32	957.59	597.65	649.74	1202.97	714.81	753.94	1344.33	1656.24
	(20.45)	(30.91)	(24.44)	(25.49)	(34.68)	(26.73)	(27.45)	(36.66)	(40.69)
II		467.77	1232.71	751.25	595.99	671.48	628.85	831.74	783.10
		(21.62)	(35.11)	(27.40)	(24.41)	(25.93)	(25.07)	(28.84)	(27.98)
III			0.00	769.89	1620.62	357.58	1063.21	1382.94	1524.66
				(28.74)	(40.25)	(18.91)	(32.60)	(37.18)	(39.04)
IV				0.00	873.79	909.08	471.32	667.49	1193.63
					(29.56)	(30.15)	(21.77)	(30.05)	(34.54)
V					0.00	1036.00	560.03	667.49	1402.27
						(32.18)	(23.66)	(25.83)	(37.44)
VI						0.00	852.99	839.26	752.40
							(29.20)	(28.97)	(27.43)
VII							0.00	944.76	934.76
								(30.73)	(30.57)
VIII								0.00	990.42
									(31.47)
IX									0.00

I and IX indicating wider genetic diversity between the genotypes in these groups. Since, these clusters have more inter-cluster distance among them, selection of parents from such clusters for hybridization programme would help to achieve novel hybrids. Inter-cluster distance is found to be minimum (357.58) between cluster III and VI indicating close relationship and similarly for most of the characters of the genotypes in these clusters, hence, selection of parents from these two clusters is to be avoided.

The cluster means for different characters under study revealed considerable genetic differences between the groups (Table 3). The cluster IX registered the highest mean value for days to flowering, days to maturity, plant height, number of leaves, leaf area index, total dry matter, and seed yield/plant. Whereas cluster VII recorded high mean values for total number of seeds/head, seed filling (%) and 100-seed weight. Cluster VI recorded high mean values for head diameter and harvest index and low mean value for oil content. Similarly, cluster V recorded high mean values for head diameter and oil content (%), total dry matter and seed yield/plant. Cluster VII recorded low mean values for leaf area index, seed filling (%) and harvest index. Cluster II had the low mean values for days to flowering and days to maturity. Similarly, the genotypes of cluster IV had the lowest number of seeds/head.

The characters contributing maximum to the D^2 values are to be given greater emphasis for deciding

Table 3. Cluster means for 14 characters in sunflower genotypes

Character / Cluster Number	Days to Floweing	Days to maturity	Plant height (cm)	No. of leaves	Stem diameter (cm)	Head diameter (cm)	Leaf area index	Total number of seeds/ plant	Seed filling (%)	100-seed weight	Oil content (%)	Total dry matter (g)	Harvest index (%)	Seed yield/ plant (g)
I	58.74	87.76	86.58	19.62	1.32	8.79	1.54	478.01	59.23	3.42	29.57	43.22	22.58	9.80
II	60.57	90.00	100.64	20.19	2.06	12.03	2.10	704.25	64.79	4.61	33.74	65.02	30.50	20.15
III	53.567	81.67	99.78	18.86	1.42	11.86	2.55	340.66	68.00	5.19	23.79	55.67	31.17	12.35
IV	63.67	94.67	94.38	19.53	1.69	11.44	1.54	397.40	67.93	5.31	37.56	62.88	23.06	14.52
V	58.33	85.33	103.13	22.27	2.24	15.06	1.23	670.66	56.35	5.80	42.45	59.67	31.52	17.72
VI	57.33	85.33	87.57	18.00	2.22	15.60	2.55	579.33	59.57	5.96	21.55	58.08	35.99	20.93
VII	62.00	90.00	105.29	20.93	1.40	10.07	0.90	508.33	53.57	5.03	33.76	77.97	16.35	12.80
VIII	55.67	85.67	109.50	20.20	1.97	13.66	1.16	750.00	69.00	7.69	31.67	48.13	35.44	17.02
IX	67.67	97.67	118.54	29.20	2.07	12.33	2.99	7.7.66	68.80	7.03	23.13	86.57	27.12	22.48

the clusters for the purpose of further selection and choice of parents for hybridization (Table 4). The highest contributor in this regard was oil content (24.27%), followed by total number of seeds/head (19.15%) and total dry matter (16.22%). Hence, oil content (%), total number of seeds/head and total dry matter were considered to be important traits contributing towards genetic divergence. The present study suggested that the future hybridization work in sunflower should involve the parents that displayed higher genetic divergence.

Table 4. Relative contribution of 14 characters to genetic diversity in sunflower

Character	Number of times ranked first	% contribution towards divergence
Days to flowering (No.)	75	9.15
Days to maturity (No.)	86	10.49
Plant height (cm)	0	0.00
Number of leaves	3	0.37
Stem diameter (cm)	0	0.00
Head diameter (cm)	0	0.00
Leaf area index	76	9.27
Total no. of seeds/head	157	19.15
Seed filling (%)	8	0.98
100-seed weight (g)	76	9.27
Oil content (%)	199	24.27
Total dry matter (g)	133	16.22
Harvest index (%)	4	0.49
Seed yield/plant	3	0.37

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Somaclonal Variation in Three Varieties of Scented Rice

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Suspended protoplast culture was made from callus culture of four scented rice varieties *viz.* Basmatibahar, Gourav, Kalimochi and Muskbudhi. A good yield of protoplast up to 0.6 x 10^6 and 4 x 10^6 protoplasts/ml were obtained from callus and cell suspension cultures respectively after 4 h of incubation. The protoplast cultured from Gourav exhibited best colony formation *i.e.* 16.2 from callus and 62.4 from cell suspension and 38.52% plant regeneration. The protoplasts derived from regenerated plants exhibited substantial magnitude of variability for five economic characters. Grain yield followed by grain number/plant and panicle number/plant showed significant variability.

Key Words: Callus/Cell Suspension Culture, Plant Regeneration, Protoplast Culture, Scented Rice

The scented rice has a premium value in international market for its aroma and slenderness. India is the second largest exporter of Basmati rice next to Thailand. It also shares a major part of total agricultural export in our country. The success of crop improvement programme largely depends upon the extent of exploitable variability in the germplasm of crop concerned. In the past, conventional breeding methods were followed in improvement of crop production. Conventional hybridization has its own limitations. Tissue and protoplast culture provides avenues to create a wide genetic variability in the improvement of export quality scented rice. The present experiment was undertaken to generate the variability in scented rice by protoplast isolation, culture and regeneration of plants from four scented rice varieties.

Materials and Methods

The protoplast isolation and culture were carried out in four scented rice varieties *viz.*, Basmatibahar, Gourav, Kalimochi and Muskbudhi. Mature seeds were used as explants for callus induction. MS medium (Murashige and Skoog, 1962) was supplemented with 2-4-D 2.0 mg/l and KIN 0.5 mg/l. The cell suspension was carried out to a 500 mg of actively growing callus into a 150 ml flask containing 30 ml of liquid R-2 (Ohira *et al.*, 1973) medium supplemented with 2-4-D 2.0 mg/l and KIN 0.5 mg/l. The protoplasts were isolated from the callus as well as from cell suspension cultures. Some 500 mg of cellulage (Onozuka R-10) was added with 50 mg pectolyase Y23 and 29 mg of EMS (buffer) in 50 ml of CPW 13 m salt solution at pH 5.5 at room temperature. The protoplasts were cultured at a density ranging from 5 x 10^5 protoplasts/ml to 2x 10^6 protoplasts/ml in Milipore filter membrane (0.2 µm) placed in feeder cells 8% PCV and are embeded in K.P.R. medium solidified with 0.8% agar. The callus were incubated at 25° ± 2 in dark till the formation of colonies. After 3-4 weeks of culturing the individual colonies were transferred to regeneration medium (MS + NAA 0.2 mg/l) to obtain regenerated plants. The plants were transferred to field, raised and grown to maturity. Variation for yields and its component characters were recorded from the individual plants. The observations from the 10 parent plants and also from all the regenerated plants were recorded. The range, mean, CV were calculated as per standard procedures.

Results and Discussion

Protoplast Isolation

The callus were incubated at 25°C and were shaken with a speed of 100 RPM. After 4 h of shaking, the protoplasts were isolated. Good protoplasts were

Table 1. Number of colonies obtained from the callus and cell suspension derived protoplast of four scented rice

Variety	I	II	III	IV	V	Mean ± SE
Callus derived-protoplast						
Basmatibahar	12	10	4	7	12	9.0 ± 1.55
Gourav	15	12	18	14	22	16.2 ± 1.74
Kalimochi	8	7	5	6	11	7.4 ± 1.03
Muskbudhi	0	5	3	2	2	2.4 ± 0.81
Cell suspension derived-protoplast						
Basmatibahar	65	53	40	32	28	43.6 ± 6.85
Gourav	82	70	43	65	52	62.4 ± 6.83
Kalimochi	45	35	30	21	25	31.2 ± 4.18
Muskbudhi	15	21	10	18	16	16.0 ± 1.82

Table 2. Shoot regeneration from protoplast derived colonies from four scented rice

Variety	Number of calli cultured	Number of calli showed shoot regeneration	Shoot regeneration (%)
Basmatibahar	102	32	31.37
Gourav	135	52	38.25
Kalimochi	65	16	24.62
Muskbudhi	28	4	14.29

collected from four scented rice varieties. Gourav gave the highest protoplast yield 0.6 x 10^6 followed by Basmatibahar 0.5 x 10^6, Kalimochi 0.4 x 10^6 and the Muskbudhi lowest 0.3 x 10^5 protoplast/ml. Similar type of work were done by Ghose and Zapata (1993) and Kaur *et al.* (1999). The protoplast yield was affected by sub-culturing of suspension cultures because at this stage the cell suspension cultures exhibited exponential growth.

Protoplast Culture

The isolated protoplasts were cultured at a density of 5 x 10^5 to 2 x 10^6 protoplasts/ml when placed under milipore filter paper. The cultured protoplasts were examined at different periodic interval during incubation period. The cell wall formation and cell divisions occurred 2 and 5 days after incubation, respectively. The colonies appeared 4 weeks after incubation. The protoplast with plating efficiency were compared with callus-derived protoplast. From callus-derived protoplasts, best colony formation was observed for Gourav (16.2) followed by Basmati bahar (9.0), Kalimochi (7.4) and lowest for Muskbudhi (2.4). In cell suspension protoplast, colony formation was maximum in Gourav (62.4) followed by Basmatibahar (43.6), Kalimochi (3.12) and minimum in Muskbuhi (16.0) (Table 1).

Plant Regeneration from the Protoplast-derived Calli

After 5 weeks, the protoplast derived calli were transferred to regeneration medium (MS + 0.5 mg/l NAA + 2 mg/l KIN) and were incubated under high light intensity 5000 lux with 16 h light and 8 h dark. After 2 weeks of incubation, shoots and roots came out and after 5 weeks of incubation complete plants were obtained. The regenerated shoots were maximum in Gourav (38.25%) and the lowest in Muskbudhi (14.29%) (Table 2).

Table 3. Variability in regenerated plants in four scented rice

Variety	Parents			Regenerated Plants		
	Range	Mean	CV	Range	Mean	CV
Days to 50% flowering						
Basmatibahar	83-92	88.0	3.71	75-95	86.5	7.16
Gourav	93-100	95.5	2.85	85-106	95.0	6.25
Kalimochi	96-105	102.0	3.55	84.108	98.13	6.16
Muskbudhi	79-96	83.0	3.06	78-92	86.25	7.23
Plant height (cm)						
Basmatibahar	98-115	110.0	5.72	94-129	109.0	8.70
Gourav	85-102	95.3	6.32	82-108	93.88	10.07
Kalimochi	118-132	125.0	3.71	110-135	122.81	6.09
Muskbudhi	75-87	81.1	6.51	78-95	87.25	8.25
Panicle number/plant						
Basmatibahar	5-9	7.33	18.32	4-15	9.45	37.51
Gourav	6-10	7.70	18.41	4-12	9.31	23.10
Kalimochi	5-9	6.70	21.17	4-12	8.0	31.75
Muskbudhi	4-7	5.00	21.08	6-8	6.75	14.18
No. of grains/panicle						
Basmatibahar	80-116	101.2	12.07	75-140	111.63	17.56
Gourav	60-92	78.0	14.72	75-120	99.69	14.66
Kalimochi	50-85	67.7	17.71	45-115	84.13	21.23
Muskbudhi	45-65	55.3	12.11	55-70	62.5	10.33
1000-grain weight (g)						
Basmatibahar	11.95-15.00	13.48	7.84	12.25-19.65	15.18	14.59
Gourav	18.75-22.50	20.93	6.71	18.65-24.35	21.31	8.34
Kalimochi	15.75-18.65	17.27	5.94	14.50-20.00	17.73	10.23
Muskbudhi	17.80-21.15	19.23	6.18	18.50-22.10	20.53	7.65
Grain yield/plant (g)						
Basmatibahar	6.45-8.15	7.15	8.16	6.00-9.80	7.93	14.85
Gourav	7.65-9.15	8.32	7.22	8.35-12.15	10.11	11.77
Kalimochi	6.55-9.00	7.66	12.36	6.30-10.60	8.34	15.72
Muskbudhi	7.55-10.95	9.15	12.92	6.50-9.15	8.35	14.90

The protoplast-derived plants were transferred to soil for normal growth till maturity. Normal package and practices were followed. The magnitude for genetic variability for all the economic characters were studied. There was no consistency in economic characters between normal parents and with the regenerated plants obtained from protoplast culture. The range mean and CV fluctuates on both the side of the parents for all the characters studied (Table 3).

The regenerated population except in Muskbudhi indicated their earliness for days to 50% flowering. Early flowering provides scope for early maturity in regenerated plants. The mean plant height in regenerated plants varied in all the four scented rice. Significant higher population mean were noticed in all the four scented varieties as compared to the parents. Number of grains/panicle and 1000-grain weight in regenerated plants were higher in comparison to that of the parents. There was change in shape (long slender) than the parents in Basmatibahar and Gourav, which is a desired character in scented rice.

The mean and CV for grain yield/plant was higher in Basmatibahar, Gourav and Kalimochi. This variation provides a scope for grain yield in above three varieties.

From comparison of normal parents with that of the regenerated plants (somaclonal variants) the later showed a wide range of variability for different economic characters. There was no consistency in behaviour and mean of different characters of parents with that in the regenerated plants of all the scented rice. The yield is as such a complex character which depends upon several combining factors in physiological process of scented rice. So the protoplast-derived plants contributed better physiological efficiency for grain/plant. The seeds obtained from the protoplast-derived plants need to be grown further to test the stability in somaclonal variation induced through protoplast culture.

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Metroglyph Analysis in Pear Germplasm

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Metroglyph and index score analysis was carried out for different characters like trunk girth, yield, tree height, spread, fruit weight, length, breadth, TSS, acidity, sugar, time of flowering, time of maturity, sugar acid ratio and taste in pear germplasm. A total of 29 pear accessions were used and in scatter diagram 4 groups were formed. Lowest score was recorded against *Pyrus ussuriensis*. There was great deal of variability among groups, as well as within the groups, index score value varied between 1-12 and 2-8.

Key Words: Index Score, Metroglyph, *Pyrus*, Tree and Fruit Characters, Variability

Pear (*Pyrus* spp.) is a delectable fruit, next only to apple in importance. The genus *Pyrus* belongs to family Rosaceae and probably originated in the mountainous regions of western China from where it moved both in east and west directions. Later, evolution took place in different regions under isolation, ecological tolerance, introgression and interspecific hybridization (Bell and Hough, 1986; Layne and Quamme, 1975). The pear available in market belongs either to *Pyrus communis* or *Pyrus pyrifolia* or to the hybrid group of the two species. The importance of pear lies in good amount of carbohydrates, protein, organic acid, vitamins, minerals, pectic substances, aroma constituents, tannin and enzymes. The world production of pear is 13069 thousand MT while India contributes only 130 thousand MT (FAO, 1997). Because of its tolerance to a wide range of soil and climatic conditions, it is grown both in temperate and subtropical conditions. The genus *Pyrus* has many species which are important for improvement of different traits.

Materials and Methods

The present investigations were carried out at pear germplasm collection block of Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan which is situated at an altitude of 1275 m above mean sea level, latitude 30°50N and longitude 77°8 E. The material was introduced from different parts of the world, grown here and evaluated for different traits. The data was collected in 1998 for trunk girth, yield, tree height, fruit weight, fruit length, fruit breadth, TSS, acidity, sugar, time of flowering, time of maturity and for taste. The metroglyph and index score analysis was carried out according to the method suggested by Anderson (1957). The germplasm which was evaluated is given as below:

1. Autumn of Yokolove, 2. Babugosha, 3. Bartlett, 4. Buttira Giffor, 5. Beloved of Michurin, 6. Beurre Hardy, 7. Beurre Bose, 8. Beurre Diel, 9. Beurre-de-Amanlis, 10. China pear, 11. Chojuro, 12. Conference, 13. Durandeau, 14. Godara sand pear, 15. Jargonelle, 16. Kashmiri, 17. Kieffer, 18. Laxton's Superb, 19. Le Conte, 20. Monarch, 21. Napolean, 22. Noveau Pointeau, 23. *Pyrus ussuriensis*, 24. Sentya Brpskaya, 25. Shinsui, 26. Smajkanska pozdniaza, 27. Starking Delicious, 28. W.B. Chorte and 29. Winter Nellis.

The class intervals and index score values for different traits is given in Table 1 and 2. The metroglyph analysis for different traits was carried out in two steps by taking 10 characters in one and rest in the other. The trunk girth and yield were taken common in both the analyses.

Results and Discussion

The results of metroglyph analysis are presented in Fig. 1 and Fig. 2. Each germplasm is represented by a semi-circle, the X coordinates of each circle being trunk girth and Y coordinates the yield. The other characters have been represented by rays at different positions on the glyph. Both the scattered diagrams show four complexes.

Complex I

This complex consists of medium trunk girth and high yield (Fig. 1). It contains three germplasm (16, 18, 24). The main characteristics of the complex were medium tree height, tree spread, fruit weight, fruit length, fruit breadth, TSS and high acidity and sugar (Fig. 1). While Fig. 2 indicates medium tree spread (NS), mid to late flowering, mid to early maturity, low to high sugar acid ratio and sub-acidic to sweet in taste.

Complex II

Complex II contains 6 germplasm (2, 9, 19, 20, 21, 29). In this group tree height (medium), E.W. (East-West) tree spread (medium) fruit weight medium, fruit length

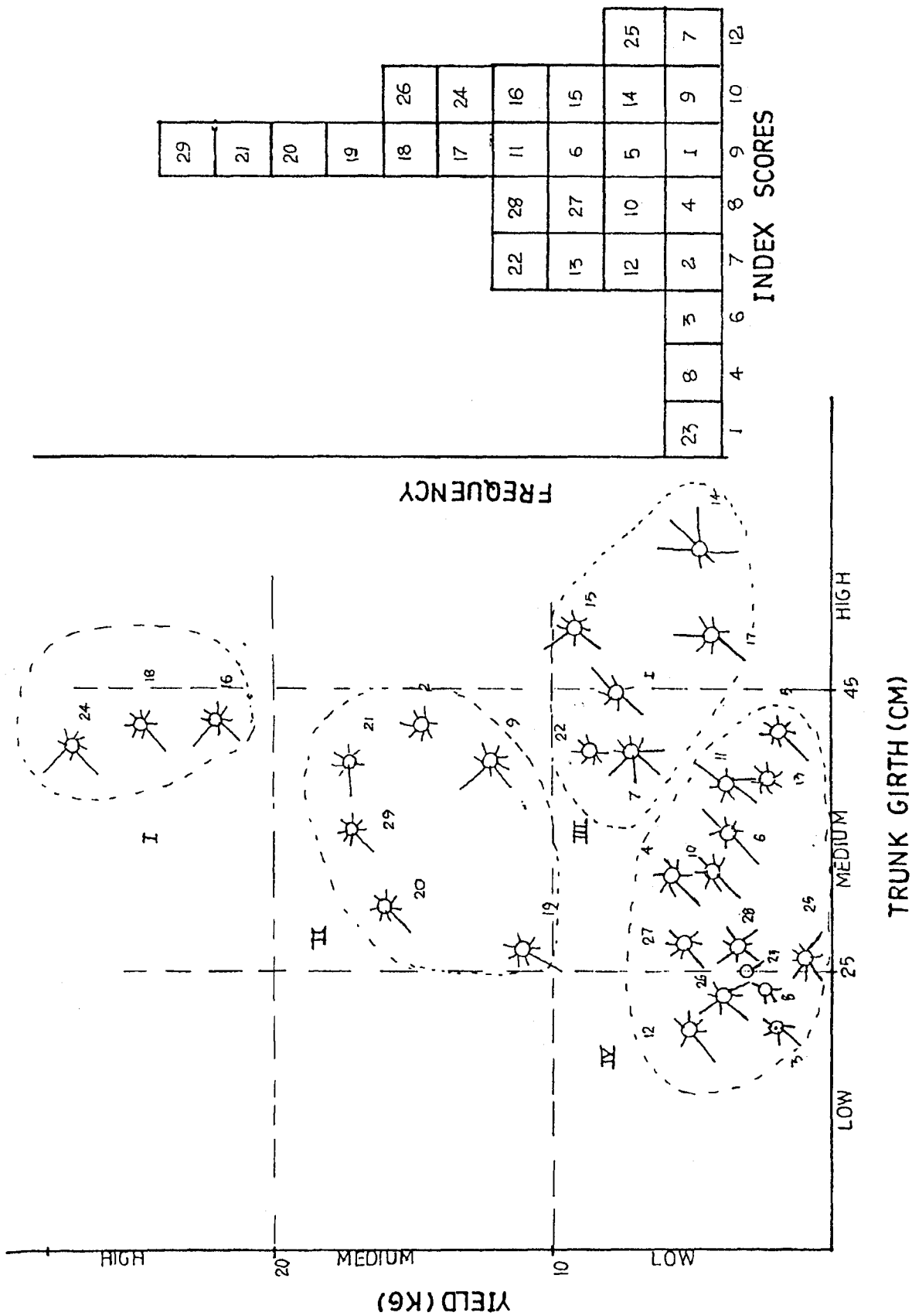

Fig. 1. Scatter diagram of metroglyph for tree and fruit characters

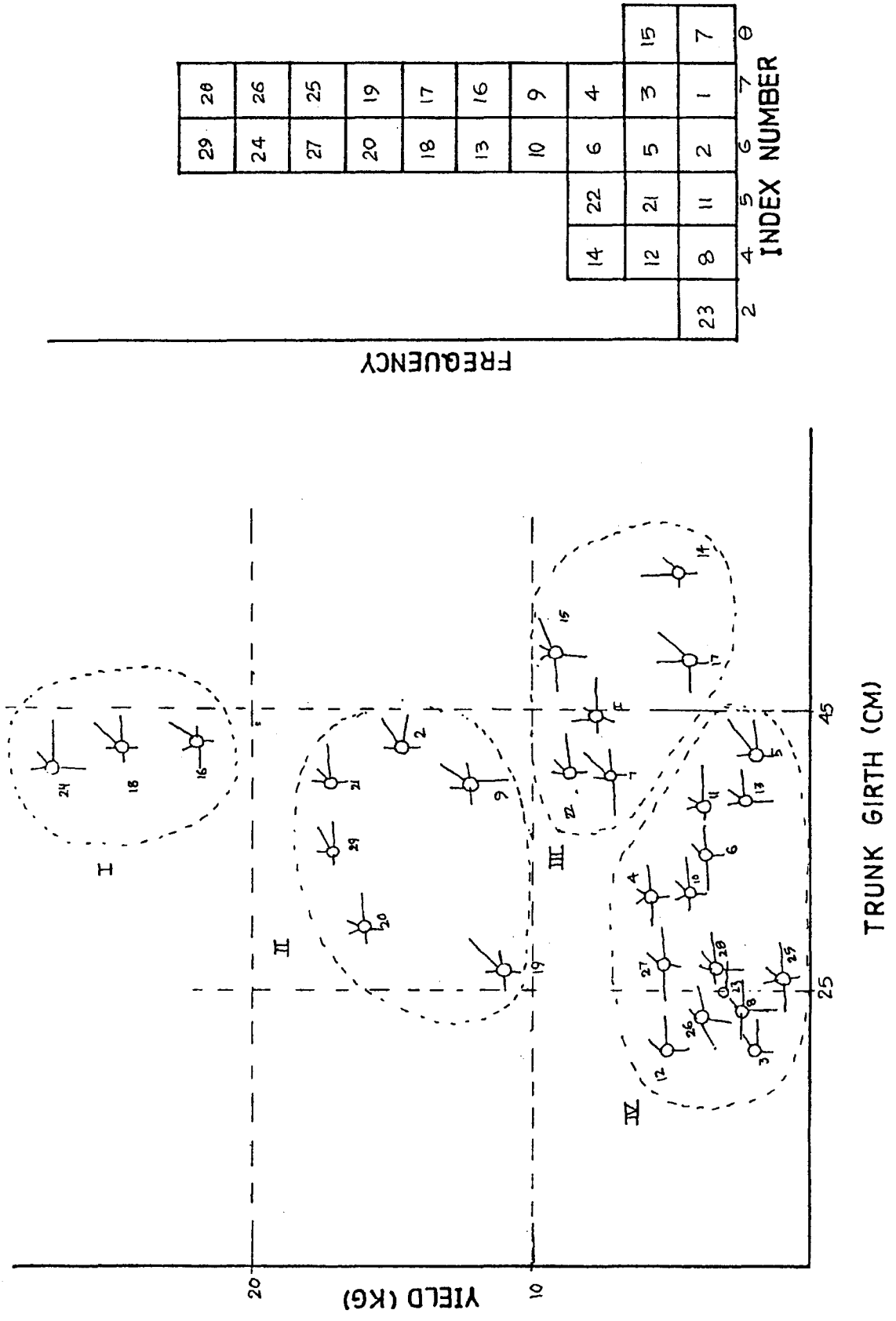

Fig. 2. Scatter diagram of metroglyph for tree, floral and fruit characters

(medium to high) fruit breadth medium, TSS (low to medium), acidity (low to high) and sugar, medium to high (Fig. 1). Fig. 2 of the complex 2 indicates that this group has minimum of 5 rays and maximum of 7 rays for the traits like tree spread NS, time of flowering, time of maturity, sugar acid ratio and taste.

index score value in both the figures. This is due to the fact that it is a separate species having most of the traits of inferior quality. But it is an important source of improvement as far as germplasm point of view is concerned. The great deal of variability in the germplasm indicates better chances for future improvement. It

Table 1. Class intervals and index values for different characters in pear germplasm

Characters	Index value 0	Symbol	Index value 1	Symbol	Index value 2	Symbol
Trunk girth (cm)	Low (<25)	-	Medium (25-45)	-	High (>45)	-
Yield (kg)	Low (<10)	-	Medium (10-20)	-	High (>20)	-
Tree height (m)	Low (<3)	Ó	Medium (3-6)	Ó	High (>6)	Ó
Tree spread EW (m)	Low (<2)	O-	Medium (2-5)	O-	High (>5)	O—
Fruit weight (g)	Low (<75)	Ọ	Medium (75-150)	Ọ	High (> 150)	Ọ
Fruit length (cm)	Low (<5)	-O	Medium (5-8)	-O	High (>8)	—O
Fruit breadth (cm)	Low (<5)	Ơ	Medium (5-7)	Ơ	High (>7)	Ơ
TSS (°Brix)	Low (<12)	Ọ	Medium (12-13)	Ọ	High (<13)	Ọ
Acidity (%)	High (>80)	Ọ	Medium (60-80)	Ọ	Low (<60)	Ọ
Sugars (%)	Low (<8)	Ọ	Medium (8-9)	Ọ	High (>9)	Ọ

Table 2. Class intervals and index values for different characters in pear germplasm

Characters	Index value 0	Symbol	Index value 1	Symbol	Index value 2	Symbol
Trunk girth (cm)	Low (<25)	-	Medium (25-45)	-	High (>45)	-
Yield (kg)	Low (<10)	-	Medium (10-20)	-	High (>20)	-
Tree spread NS (m)	Low (<2)	O	Medium (2-4)	Ó	High (>4)	Ó
Time of flowering	Early (before 10th March)	O	Medium (10th to 20th March)	O-	Late (after 20th March)	O—
Time of maturity	Late (after 31st July)	O	Medium (25th to 31st July)	Ọ	Early (before 25th July)	Ọ
Sugar-acid ratio	Low (<15)	O	Medium (15-20)	-O	High (>20)	—O
Taste	Acidic	O	Sub-acidic	Ơ	Sweet	Ơ

Complex III

This complex contains 6 germplasms (1, 7, 14, 15, 17, 22) having low yield and medium to high trunk girth. Most of the characters in these complexes are of high value. Their index score values lie between 7 to 12 and 4-8 (Fig. 1 and 2).

Complex IV

This complex consists of maximum number of germplasm as high as 14 (3, 4, 5, 6, 8, 10, 11, 12, 13, 23, 25, 26, 27, 28). This group has low yield and low to medium trunk girth. There is a lot of variability in this complex. Its index score value varied between 1 to 12 (Fig. 1) while in another scatter diagram it ranged between 2 to 7 (Fig. 2). The minimum score in both the figures is recorded against the germplasm No. 23 (*Pyrus ussuriensis*).

There were both similarities and dissimilarities among the complexes. *Pyrus ussuriensis* had clear cut distinction from all other germplasms as it has lowest

appears from these studies that metroglyph and index score analysis of 29 pear accessions can be divided into different complexes on account of trunk girth and yield. Similar studies have also been carried out in almond (Sharma *et al.*, 1989) and in seedling walnut (Sharma and Sharma, 1997).

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Genetic Variability, Character Association and Path Analysis of Yield and its Component Characters in Six-rowed Barley

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Genetic variability, character association and path analysis between yield and its component traits were carried out in 55 genotypes of six-rowed barley (*Hordeum vulgare* L.). Highly significant differences between genotypes were recorded for all the characters studied. High phenotypic and genotypic coefficient of variation coupled with high heritability and high genetic advance in grain yield/plant and moderate for grains/spike, spikelets/spike, tillers/plant, flag leaf area and plant height. Correlation and path coefficient analysis revealed that harvest index, tillers/plant, grains/spike and 1000-grain weight, were the most important characters for realizing improvement in grain yield in six-rowed barley.

Key Words: Barley, GCV, Genetic Variability, PCV, Path Analysis

Development of high yielding cultivars requires knowledge of the existing genetic variation and also the extent of association among yield contributing characters. The observed variability is a combined estimate of genetic and environmental causes of which only the former one is heritable. However, the estimate of heritability alone does not provide an idea of the expected gain in the next generation but it has to be considered in conjunction with genetic advance. Correlation and path analysis will establish the extent of association between yield and its component and also bring out the relative importance of their direct and indirect effects and, thus, give a clear understanding of their association with yield. The present study deals with the above genetic constant and character association in 55 genotypes of six-rowed barley.

Materials and Methods

Fifty five genotypes including 10 parents and 45 F_1s of six-rowed barley were grown in a randomized block design with three replications in three environments (date of sowing) at the Research Farm Asalpur, SKN College of Agriculture, Jobner, Jaipur, during *rabi* 2000-01. Observations were recorded on 10 random plants/genotype in each replication and environment separately for 10 quantitative characters, namely, days to heading, plant height (cm), tillers/plant, flag leaf area, spike length, spikelets/spike, grainyield/plant (g). The data were pooled and standard statistical procedures followed for estimating genetic components, phenotypic and genotypic coefficient of variation (Burton, 1952), heritability (Hanson *et al.*, 1956) and genetic advance (Johnson *et al.*, 1955). Genotypic and phenotypic correlation coefficients were calculated following Searle (1961) and path analysis following the method of Dewey and Lu (1955).

Results and Discussion

A wide range of phenotypic variability was observed for all the characters studied. The analysis of variance recorded highly significant differences between genotypes for all the characters studied. This suggested that there is considerable amount of inter-varietal variability in six-rowed barley.

The data on yield and its contributing traits, genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability (h^2_{bs}) and genetic advance (GA) are presented in Table 1. The variability estimates, in general, revealed that the phenotypic variation (PCV) was higher than the corresponding genotypic variance (GCV) for different characters though the extent of difference between the two was relatively low. The estimates of PCV and GCV indicated the existence of fairly high degree of variability for grain yield/plant. Moderate variability was observed for tillers/plant, plant height, grains/spike, spikelets/spike and flag leaf area. Relatively low PCV and GCV were recorded for spike length, 1000-grain weight, days to heading and harvest index. The genotypic coefficient of variation ranged from a minimum of 3.44% for harvest index to a maximum 21.44% for grain yield/plant. The grain yield/plant showed the highest PCV value of 21.74 in comparison to GCV of 21.44

Table 1. Data on mean, range and genetic parameter in 55 genotypes of six-rowed barley

Characters	Mean	Range	GCV (%)	PCV (%)	GA	h^2 (bs) (%)
Days to heading	82.03	70.33 - 92.33	4.38	5.15	6.24	72.20
Plant height (cm)	74.25	61.31 - 99.32	10.47	12.00	13.94	76.00
Tillers/plant	7.14	5.40 - 8.87	10.62	11.48	1.41	85.50
Flag leaf area	6.70	5.63 - 8.25	7.39	8.54	0.92	74.90
Spike length	7.87	6.31 - 8.96	6.48	8.11	0.83	63.80
Spikekets/spike	51.07	42.31 - 60.60	7.79	8.45	7.49	85.00
Grains/spike	48.39	39.38 - 57.63	8.24	8.82	7.61	87.30
1000-grain weight	48.58	41.71 - 55.43	5.13	5.36	4.91	91.80
Harvest index	40.07	36.29 - 43.48	3.44	3.81	2.54	81.50
Grain yield	15.64	9.87 - 24.78	21.44	21.74	6.70	97.20

suggesting less environmental influence on this character, which was confirmed by its high heritability. The difference between PCV and GCV was minimum for 1000-grain weight, grain yield/plant, harvest index, grains/spike and spikelets/spike suggesting that these traits were least affected by environment. This observation draws support from the very high value of heritability (>81.50) recorded for these traits (Table 1). The observations are in agreement with the findings of Arbi *et al.* (1992).

Grain yield of a crop is the result of interaction of a number of inter-related characters. Therefore, selection should be based on these component characters after assessing their correlation with grain yield. Character associations revealed the mutual relationship between two characters, and it is an important parameter for taking a decision regarding the nature of selection to be followed for improvement in the crop under study. In the present investigation, grain yield/plant was found to be significantly and positively correlated with harvest index, tillers/plant, spikelets/spike, grains/spike, spike length, 1000-grain weight and flag leaf area (Table 2). Therefore, these characters should be considered while making selection for yield improvement in barley. Harvest index showed positive and highly significant correlations with tillers/plant, spike length, spikelets/spike, grains/spike, flag leaf area and 1000-grain weight at both

Table 2. Phenotypic (P) and genotypic (G) correlation coefficient among 10 characters in six-rowed barley

Characters		Plant Height	Tillers/ plant	Flag leaf area	Spike length	Spikelets/ spike	Grains/ spike	1000-grain weight	Harvest index	Grain yield/ plant
Days to	P	0.220	0.102	-0.085	-0.048	0.032	0.022	-0.074	0.077	0.062
Heading	G	0.301*	0.132	-0.090	-0.011	0.031	0.009	-0.098	0.133	0.081
Plant height	P		0.271*	0.027	0.160	0.118	0.129	-0.176	0.151	0.161
	G		0.361**	0.073	0.237	0.154	0.157	-0.202	0.170	0.180
Tillers/	P			0.675**	0.565**	0.616**	0.613**	0.329*	0.807**	0.844**
Plant	G			0.777**	0.775**	0.701**	0.696**	0.363*	0.945**	0.927**
Flag leaf area	P				0.465**	0.491**	0.491**	0.216	0.631**	0.617**
	G				0.637**	0.582**	0.582**	0.267	0.767**	0.724**
Spike length	P					0.695**	0.682**	0.345**	0.642**	0.676**
	G					0.866**	0.855**	0.457**	0.807**	0.842**
Spikelets/	P						0.981**	0.339*	0.718**	0.822**
spike	G						0.999**	0.398**	0.769**	0.868**
Grains/	P							0.347*	0.704**	0.819**
Spike	G							0.405**	0.760**	0.860**
1000-grain	P								0.514**	0.574**
weight	G								0.599**	0.607**
Harvest Index	P									0.905**
	G									0.965**

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

(genotypic and phenotypic) level. On the other hand, 1000-grain weight showed positive and significant correlations with spike length, grains/spike, spikelets/spike and tillers/plant at both levels. Grains/spike showed positive and significant correlations with spikelets/spike, spike length, tillers/plant and flag leaf area, whereas spikelets/spike was positive and significantly correlated with spike length, tillers/plant and flag leaf area. Significant positive correlation of spike length with tillers/plant and flag leaf area; flag leaf area with tillers/plant, tillers/plant with plant height at both levels, whereas plant height with days to heading at genotypes level only (Table 2). Vazquez and Sanchez (1987) also reported similar findings.

Yield is the sum total of the several component characters which directly or indirectly contributed to it. The information derived from the correlation studies indicated only mutual association among the characters. Whereas, path coefficient analysis helps in understanding the magnitude of direct and indirect contribution of each character on the dependent character like grain yield. Partitioning of correlation coefficient into direct and indirect effects provides the information about the nature and magnitude of effects of other characters on grain yield. The results of the present investigation on path coefficient analysis (Table 3) revealed the characters like grains/spike, tillers/plant, 1000-grain weight and days to heading had maximum positive direct effect on grain yield at both the level, while the harvest index, spikelets/spike, plant height and flag leaf area have positive direct effect at phenotypic level whereas spike length has positive direct effect on genotypic level. Spikelets/spike, harvest index, plant height and flag leaf area at genotypic level whereas spike length at phenotypic level had direct but negative effect on grain yield. On the other hand, positive indirect effects on grain yield were realized from characters including grains/spike, 1000-grains weight, harvest index and tillers/plant. The residual effect at genotypic (-0.00002) and phenotypic (0.0591) levels were a very low magnitude, which indicates that variables included in this study were significant.

Table 3. Path coefficient analysis of phenotypic (P) and genotypic (G) correlation coefficient to determine the direct (in bold face) and indirect effects of different traits on grain yield in barley

Characters		Days to heading	Plant height	Tillers/ plant	Flag leaf area	Spike length	Spikelets/ spike	Grains/ spike	1000-grain weight	Harvest index	Correlation with grain yield/plant
Days to heading	P	**0.008**	0.005	0.033	0.000	0.000	0.005	0.004	-0.015	0.022	0.062
	G	**0.127**	-0.050	0.140	0.003	0.000	-0.067	0.022	-0.031	-0.063	0.081
Plant height	P	0.002	**0.023**	0.088	0.000	-0.002	0.020	0.024	-0.036	0.044	0.161
	G	0.038	**-0.166**	0.383	-0.003	0.003	-0.339	0.407	-0.063	-0.081	0.181
Tillers plant	P	0.001	0.006	**0.324**	0.003	-0.006	0.103	0.113	0.068	0.233	0.844**
	G	0.017	-0.060	**1.062**	-0.029	0.009	-1.539	1.802	0.114	-0.449	0.927**
Flag leaf area	P	-0.001	0.001	0.219	**0.004**	-0.005	0.082	0.090	0.045	0.182	0.617**
	G	-0.011	-0.012	0.825	**-0.037**	0.008	-1.276	1.507	0.087	-0.365	0.724**
Spike length	P	0.000	0.004	0.183	0.002	**-0.010**	0.116	0.125	0.071	0.185	0.676**
	G	-0.001	-0.039	0.823	-0.023	**0.012**	-1.901	2.212	0.143	-0.384	0.842**
Spikelets/ spike	P	0.000	0.003	0.200	0.002	-0.007	**0.167**	0.180	0.070	0.207	0.822**
	G	0.004	-0.026	0.744	-0.021	0.010	**-2.195**	2.592	0.125	-0.366	0.868**
Grains/ spike	P	0.000	0.003	0.199	0.002	-0.007	0.164	**0.184**	0.072	0.203	0.819**
	G	0.001	-0.026	0.739	-0.021	0.010	-2.198	**2.589**	0.127	-0.361	0.860**
1000-grain weight	P	-0.001	-0.004	0.107	0.001	-0.003	0.056	0.064	**0.206**	0.148	0.574**
	G	-0.012	0.003	0.386	-0.010	0.005	-0.873	1.049	**0.314**	-0.285	0.607**
Harvest index	P	0.001	0.003	0.262	0.003	-0.006	0.120	0.129	0.106	**0.288**	0.905**
	G	0.017	-0.028	1.004	-0.028	0.010	-1.688	1.968	0.188	**-0.475**	0.965**

Residual, Genotypic = -0.0002, Phenotypic = + 0.0591

** Significant at 1%.

In the light of above findings it may be concluded that improvement in characters like tillers/plant, grains/spike, 1000-grain weight and harvest index will help in improving the grain yield in six-rowed barley both directly and indirectly. Therefore, these characters should be considered for yield improvement in barley breeding programme.

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Geographical Distribution of Indian Mulberry Species

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Extensive explorations were undertaken in different regions of India. A total of 367 mulberry germplasm were collected through 38 explorations covering 5 zones, 21 states and 58 districts. The wild collections of *Morus serrata* was confined to North-western Himalaya. *M. laevigata* in natural forms are available in North-eastern, North-western and South India including Andaman and Nicobar Islands. Introduced genepool of mulberry were collected from Madhya Pradesh, Chhattisgarh, Tamil nadu, Kerala, Karnataka, Maharashtra and other parts of India which are maintained as avenue trees, shade trees, social forestry and fruit trees mainly in coffee and tea estates. *M. alba* and *M. indica* are mostly found in cultivated forms throughout India. Considerable diversity was observed in *Morus* germplasm collected through explorations. The variability in the Indian collections of *Morus* germplasm and the scope of utilization are discussed.

Key Words: Geographical Distribution, Mulberry Species, Utilization, Variation

In India, the genus *Morus* is represented by four species *viz., M. indica, M. alba, M. serrata* and *M. laevigata* (Hooker, 1885; Brandis, 1906). The natural distribution of the genus has considerably changed because of its extensive cultivation for silkworm rearing. Vavilov (1926) while reviewing the centres of origin of crop plants placed the genus *Morus* in "China-Japan" region which includes East China, Korea and Japan. There are about 68 species recognized in the genus of which 24 species are represented in China, 19 in Japan, 6 in Korea, 4 each in Taiwan and India, 3 each in Myanmar and Indonesia, 2 each in Thailand, Vietnam and Afghanistan and 1 each in Arabia, Oman and Muscat. Further, 14 species are found in North America and 7 in Central and South America (Sanjappa, 1989). Parkinson (1923) reported the availability of *M. leavigata* in Andaman and Nicobar Islands. The occurrence of mulberry is reported in different regions of India (Kanjilal *et al.,* 1940; Gamble and Fischer, 1957; Nair, 1977).

Explorations for mulberry genetic resources were undertaken in Central Himalayas (Balakrishna and Ramesh, 1989), North-eastern India (Jain and Kumar, 1989; Ravindran *et al.,* 1997), North-western Himalayas (Dhar and Ahsan, 1989); reported the distribution of *M. indica, M. serrata* and *M. laevigata* in forest flora of Kumaon region and North-eastern India, respectively, (Sreekumar *et al.,* 1995) have extensively explored Kerala for mulberry resources and collected from farm backyard/cultivated gardens, tea and coffee estates. Widespread urbanization, agricultural uses and denudation of forest areas threatens the natural habitats of mulberry particularly the primitive and obsolete varieties available in different parts of the country. Explorations are essential to identify the locations of mulberry resources available in natural and cultivated habitats and to document the diversity of mulberry for further utilization in mulberry crop improvement programme.

Materials and Methods

Regular surveys and explorations were conducted in various geographical regions of the country in two different seasons (February-April and September-November) every year during 1993-2000. The exploration sites are indicated in Fig. 1. Before conducting the survey, the published literature and herbarium records of Botanical Survey of India at Shillong, Dehradun, Port Blair, Pune, Coimbatore, Forest Research Institute, Dehradun, Institute of Forest Genetics and Tree Breeding, Coimbatore, State Forest Research Institute, Itanagar and North-eastern Hill University, Shillong were consulted. The genus *Morus* is distributed naturally in the Sub-Himalayan regions up to an altitude of 2200 m extending between Indus and Brahmaputra rivers with varying climate from temperate to tropical. To expedite the process of exploration in different areas, the geographical regions of the country were grouped into 5 zones, *viz.,* North-east, North-west, Central and South India. Accordingly, the zones were covered to identify the natural, cultivated, primitive landraces and obsolete varieties of mulberry germplasm. In addition, passport data, ethnobotanical notes on special uses with sericultural utilization were recorded in standard collection format. The same collection format was used by each team member. The plants were sampled based on distinct morphological, reproductive and other features. Random sampling in case of wild forms and biased sampling procedure were used when the population was more in number *i.e.,* at least 10% of

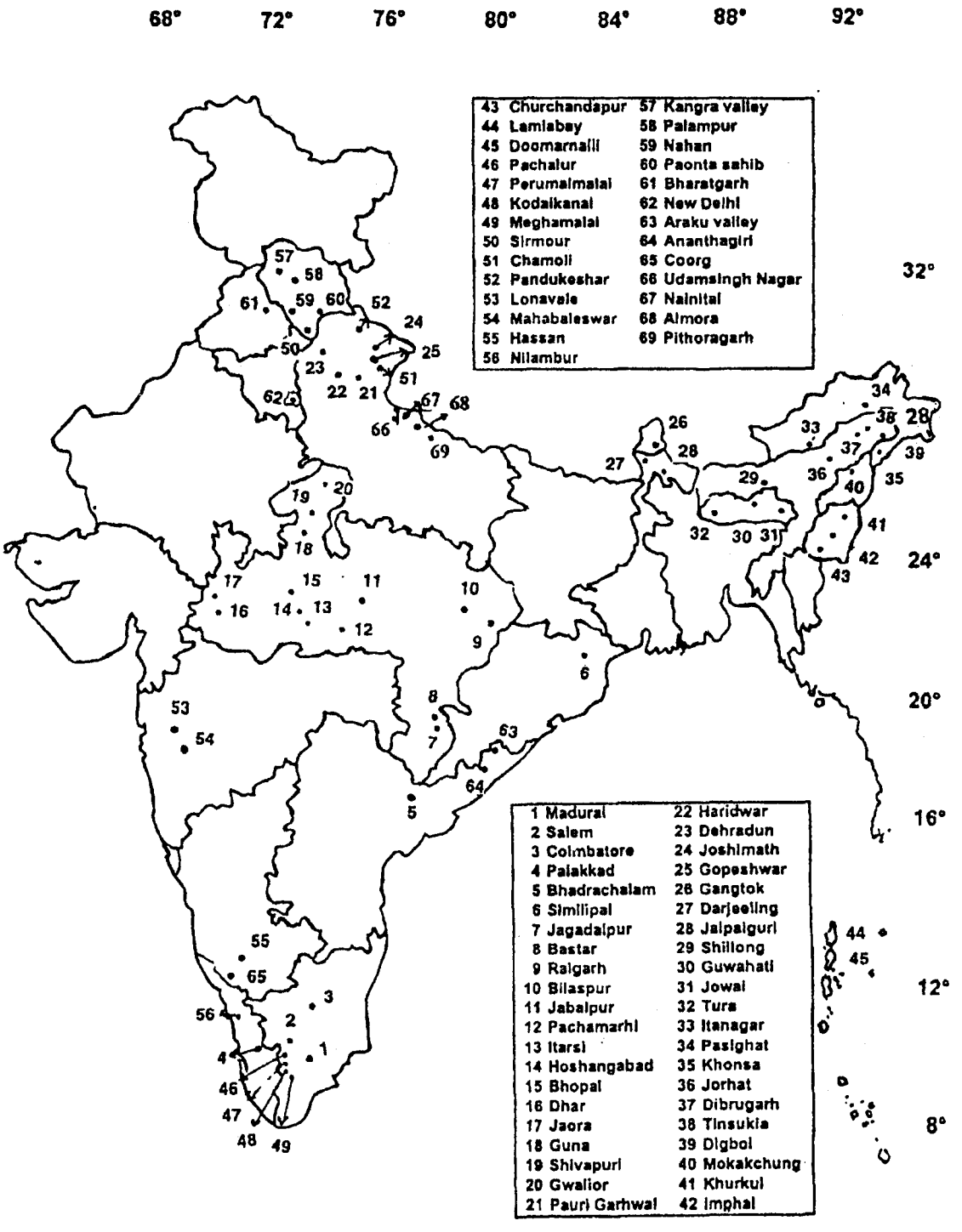

Fig. 1. Exploration sites of Morus spp. in India

the population was sampled. Herbarium specimens were made from the collected samples. Healthy, mature, disease-free shoots with dormant buds were collected for further multiplication in nursery and subsequent establishment from nursery to field genebank for *ex situ* conservation and utilization.

Results and Discussion

A total of 367 mulberry germplasm were collected from different zones and states which are presented in Table 1. The distribution of *Morus* species is indicated in Fig. 2. The distribution pattern revealed that in India the two species *M. laevigata* and *M. serrata* are available

Table 1. Mulberry collections in different states of India (1993-2000)

North-east India	West Bengal	11
	Sikkim	06
	Assam	08
	Manipur	07
	Meghalaya	30
	Nagaland	01
	Arunachal Pradesh	06
North-west India	Uttaranchal	105
	Uttar Pradesh	01
	Himachal Pradesh	12
	Punjab	01
	New Delhi	03
	Haryana	02
Central India	Madhya Pradesh	14
	Orissa	01
	Maharastra	03
South India	Tamil Nadu	63
	Karnataka	14
	Kerala	30
	Andhra Pradesh	03
	Andaman and Nicobar Islands	46
Total		367

as wild trees. *M. serrata* is available in North-western India at a higher altitude (Dandin *et al.*, 1993; Tikader *et al.*, 1999, 2000). *M. laevigata* is available throughout the country both in natural and as developed genopool. In Andaman and Nicobar Islands, wild trees of *M. laevigata* are abundantly available which differs in characteristics from main land forms (Ravindran *et al.*, 1997). Wild form of *M. laevigata* was recorded earlier in Andaman and Nicobar islands and reported by Parkinson (1923). The distribution of mulberry species is presented in Table 2. It is observed that *M. alba, M. Indica* and *M. laevigata* represent North-east, North-west, Central and South India except Andaman and Nicobar Islands. In Andaman and Nicobar Islands, only natural resource of *M. laevigata* is available. *M.serrata* is the only representative of North- west India and confined to higher altitude in Sub-Himalayan belt (800-2200 m).

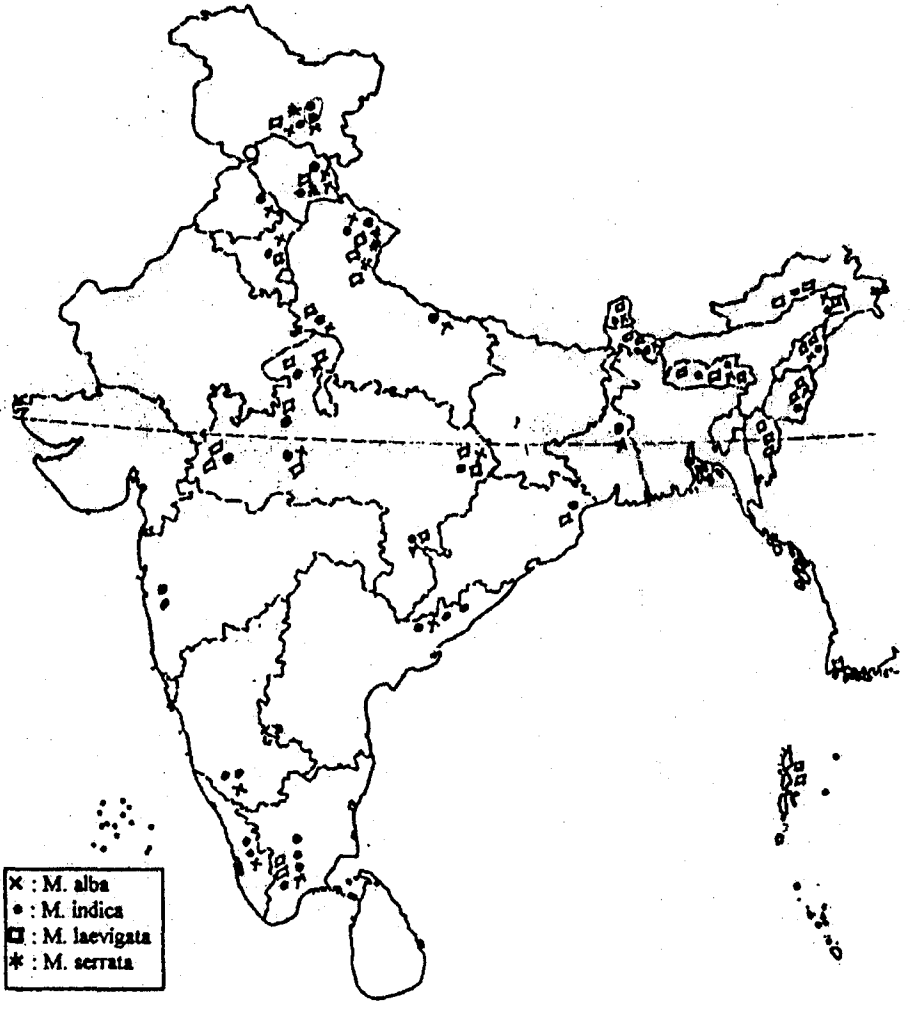

Fig. 2. Distribution of Morus species in India

Table 2. Species-wise distribution in mulberry collection (1993-2000)

Zone	Species					
	M. alba	*M. indica*	*M. laevigata*	*M. serrata*	Unidentified	Total
North-east India	—	32	33	—	04	69
North-west India	16	60	14	34	—	124
Central India	02	08	08	—	—	18
South India (A & N Islands)	02	49	57	—	46	110
Total	20	151	112	34	50	367

The natural distribution of *M. laevigata* was observed in Eastern Himalaya wet temperate forests in Rhenok, Tarpin (East Sikkim), Mamring, Turung, Sipsu (South Sikkim), Jume and Chakung (West Sikkim). *M. laevigata* trees were observed in West Bengal in Kalimpong sub-division (Lava and Algara), Jalpaiguri district (Murthy and Imdong forest). It was also observed in Pengaree, Dibrunadhi near Digboi in Assam, Umpling and Nongpoh in Meghalaya, Sung Valley, Mynso, Jowai, Khurkhul and Churchandapur are the places from where *M. laevigata* was collected in Manipur State (Ravindran *et al.*, 1990).

In central India developed genepool of *M. laevigata* is observed in Jaora, Shivpuri, Gwalior, Panchmari, Jabalpur and Raigarh districts of Chhattisgarh and Madhya Pradesh States. It is utilized for fruit purposes. In South India, *M. laevigata* is mainly grown as shade tree in tea and coffee estates of Tamil Nadu and Kerala (Yadav and Pavan Kumar, 1996). It is also grown as fruit tree.

M. serrata also called Himalayan mulberry is confined to Uttaranchal, Himachal Pradesh and Jammu and Kashmir in natural habitats. The sacred mulberry tree at Joshimath is the oldest and about 1200 years old (Rau, 1967; Tikadar *et al.*, 1999). *M. serrata* is naturally distributed at Salna, Urgam Valley, Chakrata, Pandukeshar, Almora, Pithoragarh, Nainital at higher altitude. This species is grown in association with oak, pines and conifers. Watt (1891) reported the species at higher altitudes in North-western Himalayas. The distribution of *M. serrata* was also reported in Rajouri, Sunderbani, Poonch, Batote in Jammu and Kashmir, Kangra, Chamba, Nahan and Kullu of Himachal Pradesh and Garhwal and Kumaon Himalayas of Uttaranchal (Balakrishna and Ramesh, 1989; Dandin *et al.*, 1993).

M. indica, is the most domesticated species and commonly cultivated for sericultural purposes from Kashmir to Sikkim. Most of the cultivated forms are distributed in the states of West Bengal, Assam, Meghalaya, Manipur, Arunachal Pradesh, Maharashtra, Karnataka, Tamil Nadu, Kerala, Andhra Pradesh, Uttar Pradesh, Uttaranchal, Delhi and Punjab. The survey and exploration revealed that the distribution of natural resources of *M. indica* have reduced due to introduction of improved varieties.

Morus alba is indigenous of China (Watt, 1891; Parker, 1956) and extensively cultivated throughout the plains of India and the hilly areas of Himalayas. It is not exactly known how the variety was introduced in India. *M. alba* is widely cultivated for sericulture and fruit purposes besides avenue, fodder and other uses. The different mulberry species collected during the explorations are maintained in field genebank for further studies and utilization in mulberry crop improvement programme.

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Evaluation of Important Mango Cultivars of Diverse Origin for their Fruit Set Behaviour under Lucknow Conditions

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Twenty-six commercially important cultivars of mango were evaluated for fruit set in Lucknow conditions for 2 years. A wide range of variability was observed for fruit set behaviour. The cultivars like Amrapali, Chausa, Dashehri, Fazri, Banglora, Kishanbhog, Neelam exhibited satisfactory performance.

Key Words: Barren Panicles, Fruit Set, Mango Cultivars

Fruit set is one of the important factors affecting final yield of mango (Thimmappaiah and Suman, 1987). It is influenced by several factors like cultivars, pollination and weather conditions. Apart from these, mango cultivars exhibit eco-geographical dependence for growth, flowering and fruiting (Singh and Singh, 1988; Yadav and Rajan, 1993 and Singh *et al.*, 1994) and some of these may be erratic in fruiting under specific geographical locality and *vice versa.* Since, in India, more than a thousand cultivars are in existence and about 30 of these are grown on commercial scale, there is a scope for introducing suitable cultivars in a region, Therefore, before selecting suitable commercial cultivars for large-scale plantation or using them in breeding programme, study of their fruit set behaviour under the conditions where they are to be grown is of immense importance. The purpose of this study was to evaluate cultivars for their fruit set potential under Lucknow conditions.

Materials and Methods

The experiment was conducted during 1994 and 1995 at the Central Institute for Subtropical Horticulture, Rehmankhera, Lucknow, on full-grown trees of 26 important commercial mango cultivars (Table 1), representing various parts of the country. Hundred panicles of each cultivar were tagged before opening of the flowers. Observations on fruit set were recorded at 40 days after the mustard stage of the fruit. Data was recorded on percentage of barren panicles, fruit bearing panicles and number of normal fruits per panicles.

Results and Discussion

A wide range of variability was observed for fruit set behaviour in mango cultivars under Lucknow conditions. The analysis of variance recorded highly significant difference between cultivars for percentage of barren panicles, normal fruits/panicle and fruit set (%)

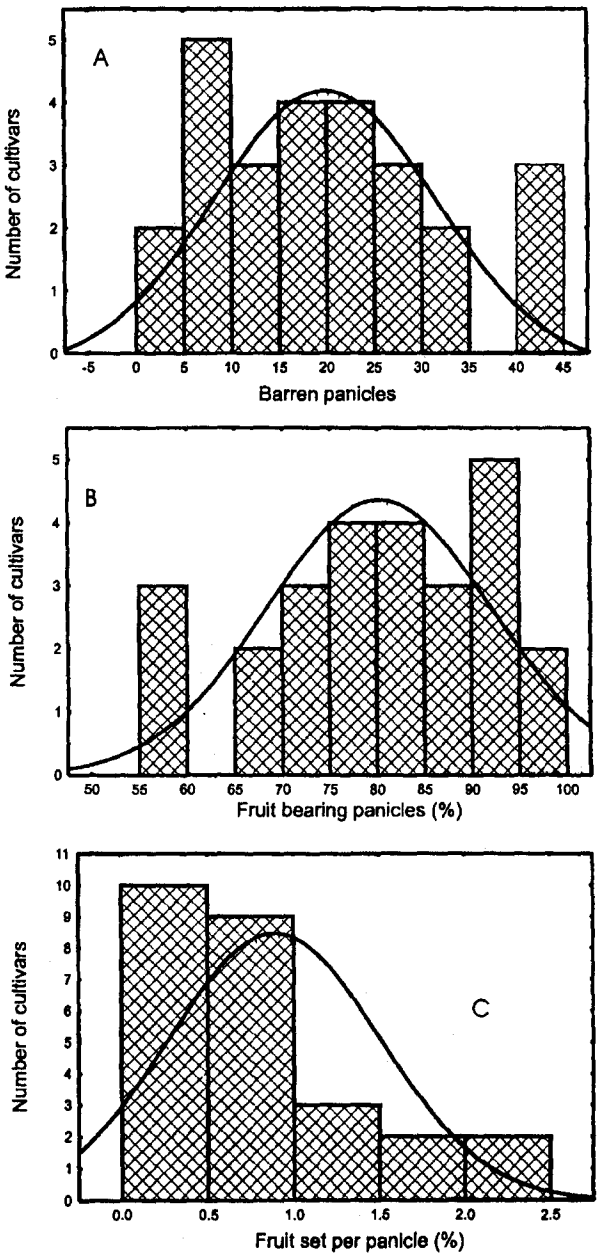

Fig. 1. Frequency distribution of A: barren panicles (%), B: fruit bearing panicle (%) and C: fruit set/panicle (%)

Table 1. Fruit set behaviour of some important Indian mango cultivars

Cultivar	Barren panicles (%)			Fruit bearing panicles (%)			Normal fruit set/panicle		
	1994	1995	Mean	1994	1995	Mean	1994	1995	Mean
Alphonso	72.75	8.00	40.38	27.35	92.00	59.63	0.20	0.35	0.28
Amrapali	11.00	12.75	11.88	89.75	87.00	88.38	2.03	2.08	2.05
Bangnapalli	65.50	19.50	42.50	34.50	80.00	57.25	0.20	0.75	0.48
Bangalora	32.00	0.00	16.00	68.00	99.75	83.88	0.70	1.23	0.96
Bombay	11.25	12.75	12.00	87.25	98.00	88.13	0.90	0.98	0.94
Bombay Green	19.50	0.00	9.75	80.75	100.00	90.38	0.40	1.38	0.89
Chausa	6.25	0.00	3.13	94.00	100.00	97.00	0.70	1.88	1.29
Dashehari	20.00	12.00	16.00	80.00	88.00	84.00	1.10	1.30	1.20
Fazri	11.50	8.00	9.75	88.50	92.00	90.25	1.23	2.70	1.96
Fernandin	65.25	20.00	42.63	34.50	80.00	57.25	0.30	0.68	0.49
Gulab Khas	22.75	16.00	19.38	77.25	84.00	80.63	090	1.05	0.98
Himsagar	14.00	0.00	7.00	86.00	100.00	93.00	0.70	1.25	0.98
Kesar	59.25	8.25	33.75	40.75	92.00	66.38	0.30	0.40	0.35
Khas Ul Khas	10.00	12.00	11.00	90.00	88.00	89.00	0.85	0.75	0.80
Kishan Bhog	6.00	0.00	3.00	92.00	100.00	96.00	2.10	2.85	2.48
Langra	25.00	24.00	24.50	75.25	786.00	75.63	0.50	0.13	0.30
Lucknow Safeda	0.00	12.00	6.00	100.00	88.00	94.00	0.60	0.53	0.56
Mallika	33.50	12.00	22.75	66.75	88.00	77.38	0.25	0.43	0.34
Mankurad	30.00	21.00	25.50	70.00	80.00	75.00	0.50	0.43	0.46
Mulgoa	7.00	7.50	7.25	93.00	92.50	92.75	0.50	1.48	0.99
Neelum 2	42.75	0.00	21.38	56.00	100.00	78.00	0.40	3.33	1.86
Nisar Pasand	47.00	4.25	25.63	53.00	96.00	74.50	0.40	0.14	0.27
Rataul	0.00	41.00	20.50	100.00	59.00	79.50	0.50	0.65	0.58
Suvernrekha	40.50	19.75	30.13	59.25	72.00	65.63	0.30	0.45	0.38
Vanraj	47.75	8.00	27.88	52.25	92.00	72.13	0.38	0.12	0.25
Zardalu	34.00	4.00	19.00	66.00	96.00	81.00	1.00	1.03	1.01
Mean	28.02	11.15	19.59	71.84	88.61	80.23	0.68	1.09	0.88
CD (5%)	3.98	2.81	2.46	4.55	4.40	3.23	0.25	0.19	0.15
Minimum	0.00	0.00	3.00	27.25	59.00	57.25	0.20	0.12	0.25
Maximum	72.75	41.00	42.63	100.00	100.00	97.00	2.10	3.33	2.48
SD	21.43	9.59	11.71	21.40	10.00	11.87	0.49	0.86	0.61
SE	4.20	1.88	2.30	4.20	1.96	2.33	0.10	0.17	0.12
Skewness	0.61	1.20	0.53	-0.61	-1.17	-0.54	1.75	1.20	1.17
Kurtosis	-0.66	2.44	-0.51	-0.66	1.80	-0.60	3.10	0.88	0.73

(Table 1). It is clear from Fig. 1A that 3 cultivars have 40-45% barren panicles whereas 5 cultivars have 5-10% barren panicles. This shows the suitability of these cultivars under the evaluation conditions. Fig. 1B exhibited that there are good number of cultivars with high percentage of fruit bearing panicles. Fruit set/ panicle was more than 1% in 7 cultivars whereas 9 cultivars had 0.5-1% fruit set. Ten cultivars exhibited poor fruit set (>0.5%).

During the investigations on 26 important mango cultivars, it was observed that the percentage of barren and fruit bearing panicles varied year to year. This may be due to erratic weather conditions in some of the years at the time of flowering. In 1994, the highest percentage (72.75%) of barren panicles was recorded in Alphonso followed by Bangnapalli (65.50%) and Fernandin (65.25%) whereas during 1995 it was more in Ratoul (41.00%). Mean value of both the years indicated that the Fernandin (42.63%), Bangnapalli (42.50%) and Alphonso (40.4%) produced the highest percentage of barren panicles. Maximum number of fruit bearing panicles (100.00%) was recorded in Lucknow Safeda and Ratoul during 1994 but in 1995 it was 100.00% in Bombay Green, Chausa, Himsagar, Kishanbhog, Neelam and Bangalora. Mean value showed that the cultivar Chausa produced the maximum percentage (97.00%) of fruit bearing panicles followed by Kishanbhog (96.00%) and Lucknow Safeda (94.00%) and was less in Bangnapalli (57.25%) and Fernandin (57.25%). The highest percentage of normal fruit set/panicle was observed in Kishanbhog (2.48%) followed by Amrapali (2.05%), Fazri (1.96%) and Neelum (1.86%) and it was least in Vanraj (0.25%. These results are in support with the findings of Singh *et al.* (1994) and Yadav and Rajan (1993). The study showed that, in general, varieties from western India like Alphonso and Vanraj exhibited poor fruit set under Lucknow conditions. The variation in fruit set and yield due to change locality was also reported by Macioas Gonzalez and Hernandez (1986), Thimmappaiah and Suman (1987) and Singh and Singh (1988).

The study indicated that profuse flowering is not the only pre-requisite factor for high yield but the extent of fruit set is also important. Thus, the trees bearing large number of panicles may not set satisfactory number of fruits under some of the geographical area due to poor adaption. The cultivars like Amrapali, Chausa, Dashehari, Fazri, Bangalora, Kishanbhog, Neelam exhibited satisfactory fruit set as well as less number of barren panciles under Lucknow conditions. Out of these cultivars, Kishanbhog, Bangalora and Neelum are not commonly grown under Lucknow conditions but exhibited their potential for fruit set and they can yield a good crop.

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Comparative Evaluation of Different Sorghum (*Sorghum bicolor* L. Moench) Cultivars on the Basis of Chemical Tests

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Twelve varieties of sorghum (*Sorghum bicolor*) were studied by chemical tests *viz.* phenol and modified phenol test, $FeSO_4$ test, KOH-bleach test, and response of GA_3 and 2, 4-D. The varieties included were HC-136, HC-171, HC-260, HC-308, PC-1, PC-6, PC-9, PC-23, PC-121, SSG59-3, CSV-15 and MP-Chari. Based on phenol test sorghum varieties can be grouped into four categories *viz,* light brown (PC-6, PC-9), brown and black (SSG 59-8). In the case of modified phenol test, two groups were identified *i.e.* group A and group B, group A is characterized into dull grey, light grey, dark grey and brown colour and group B included light buff colour, yellow colour light brown, brown and brownish red. Seven varieties showed light grey colours, one variety (PC-6) showed yellow colour, two grey and two black colour in response to ferrous sulphate test. KOH-bleach test broadly divided these varieties into two groups, off white colour (seven varieties) and red colour (five varieties). Response to GA_3 and 2,4-D in comparison to control helped to differentiate the varieties from each other on the basis of effect on germination (plumule and radicle length).

Key Words: Ferrous Sulphate, Forage Sorghum, Phenol, Potassium Hydroxide

The importance of cultivar identification was recognized in the late 19th century and early 20th century when new field crop varieties often lost their identity due to their admixture with other varieties or general types. Hence, there is a need to develop rapid and accurate laboratory techniques which can supplement the plant morphology. The various laboratory techniques which are employed range from simple method of examining seed and seedling morphology to the more advanced procedure of analyzing DNA polymorphism (Smith and Smith, 1992; Cooke, 1995). Seed morphology studied by visual examination and under magnification (by scanning electron microscopy SEM) can provide useful information for differentiating genotypes (Bahadur *et al.,* 1994). Examination of seedling morphology under controlled conditions of growth can be useful and cost-effective for describing and distinguishing cultivars (ISTA, 1992). Practically, a variety should be distinct, uniform and stable (DUS) with respect to the characteristics for use in varietal identification. Therefore, it is of paramount importance for those engaged in quality seed production and certification that they should be well acquainted with the diagnostic characteristics of different varieties.

An attempt has been made in this paper to identify the important sorghum (*Sorghum bicolor*) cultivars by subjecting them to different chemical tests and preparing schematic flow diagrams.

Materials and Methods

Phenol Test

Seeds were soaked in water for 16-24 h and 50 seeds of each genotype were placed in 15 cm Petri dish on two layers of filter paper soaked in 1% phenol solution. The Petri dishes were immediately covered. Seed colour was observed after 8 and 24 h. The procedure for modified phenol test is similar as above except the seeds were pre-soaked in 0.4% solution of $CuSO_4$ and 0.6% solution of Na_2CO_3 for addition of Na^+ ions instead of water.

Modified phenol test A = Pre-soaking in 0.4% $CuSO_4$.

Modified phenol test B = Pre-soaking in 0.6% Na_2CO_3.

Ferrous-sulphate ($FeSO_4$) Test

Fifty seeds were soaked in 1% $FeSO_4$ solution and kept in an incubator for four hours at 25°C. Varieties were categorized on the basis of change in the colour of the solution, namely, yellow, light grey, grey and black.

Potassium-hydroxide (KOH) Bleach Test

The presence or absence of a darkly pigmented testa or undercoat layer can be used to help in differentiating sorghum cultivars. The dark pigment in the testa has been identified as tannic acid. The test was conducted by preparing (1:5 w/v) solution of potassium hydroxide and fresh house hold bleach (5.25% NaOCl). Seeds were put into a glass container and were completely covered with KOH-bleach solution and kept at room temperature for the test. The seeds with brown seed coat soaked for 10 min and the seeds with the white seed coat for 5 min. in this solution and the mixture gently swirled periodically. Then the seeds were transferred to a sieve and rinsed with tap water. The seeds were placed on a paper towel and allowed to

air dry. The dry seeds were not patted to avoid removal of the pigment. After the seeds had dried results were recorded (number of dark seeds and number of light seeds).

Gibberelic Acid (GA_3) Test

Twenty five seeds were sown in Petri dishes lined by two layers of filter paper moistened with GA_3 (100 ppm). The Petri dishes were kept in a germinator at 25°C. The data was recorded at regular interval of 2 days up to 10 days for both plumule and radicle length.

2,4 Dichlorophenoxy Acid (2,4-D) Test

Solution of 2,4-D (1 ppm) was used in this method. The method was similar to that used for GA_3 test. The effect of 2,4-D on different cultivars was seen as the response of plumule and radicle emergence.

Results and Discussion

Advantage of phenol test is that it serves as an easy, quick and reliable test for the identification of different genotypes. The study of phenol test revealed that sorghum varieties could be grouped into four types: very light brown (2 varieties), light brown (4 varieties), brown (5 varieties) and black (1 variety) and in case of modified phenol test-A, four distinct categories *viz,* dull grey (2 varieties), light grey (4 varieties), dark grey (3 varieties), brown (3 varieties) and in the case of modified phenol test-B also four categories *viz,* light buff colour (3 varieties), yellow colour (2 varieties), light brown (3 varieties), brown (3 varieties) and brownish red (1 variety) could be recognized, as shown in flow chart 1 and Table 1. Our results suggest that the modified phenol tests are better for the categorization of different varieties into different colour groups more critically. Banerjee (1974) studied 61 wheat varieties and grouped them into black, brown, light brown and negative on the basis of phenol reaction. Miyagawa and Yasue (1980) grouped rice into Japanese, Chinese and Indian on the basis of phenol colour reaction. Twenty-nine varieties of paddy were divided into different groups on the basis of phenol colour reaction (Gupta and Agrawal, 1988). The other eighty-five varieties of paddy were also studied and grouped into different colour categories (Vanagamudi *et al.,* 1988). Similar work has been done on wheat (Singhal and Prakash, 1988), rice (Chauhan and Nanda, 1984) and pearlmillet (Rao *et al.,* 1989).

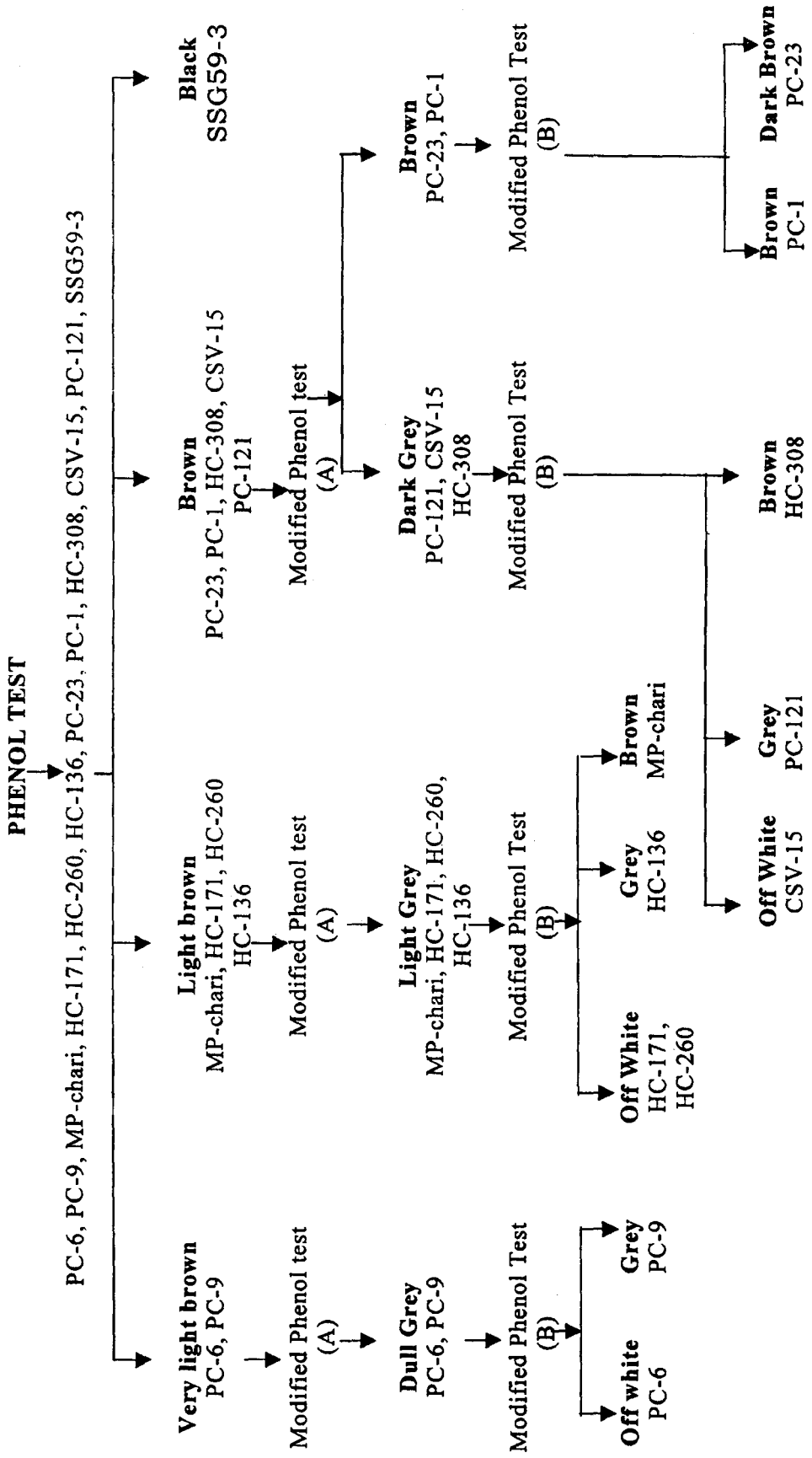
The use of ferrous sulphate colour reaction was also found to be a useful method in differentiating sorghum varieties (flow chart 2). Four different colour groups were made on the basis of $FeSO_4$ reaction. Seven varieties showed light grey colour, one variety (PC-6) showed yellow colour, two varieties showed grey and two varieties showed black colour (Table 1). Fe++ ions give different colour reactions with different genotypes in paddy husk. Saharan (1991) used the ferrous sulphate test in rice for varietal identification and reported 5 groups *viz.,* brown spots, brown streaks, grey, grey spot and grey streaks on kernels. Kumar (1992) applied $FeSO_4$ test in pearlmillet and grouped the hybrids into five colour groups.

On the basis of KOH test two major groups were identified. Seven varieties *i.e.,* HC-171, HC-171, HC-260, HC-308, PC-6, PC-9, CSV-15 and MP-Chari showed off white colour and five varieties *i.e.,* HC-136, PC-1, PC-23, PC-121 and SSG59-3 showed red colour reaction as shown in Table 1 and flow chart 1.

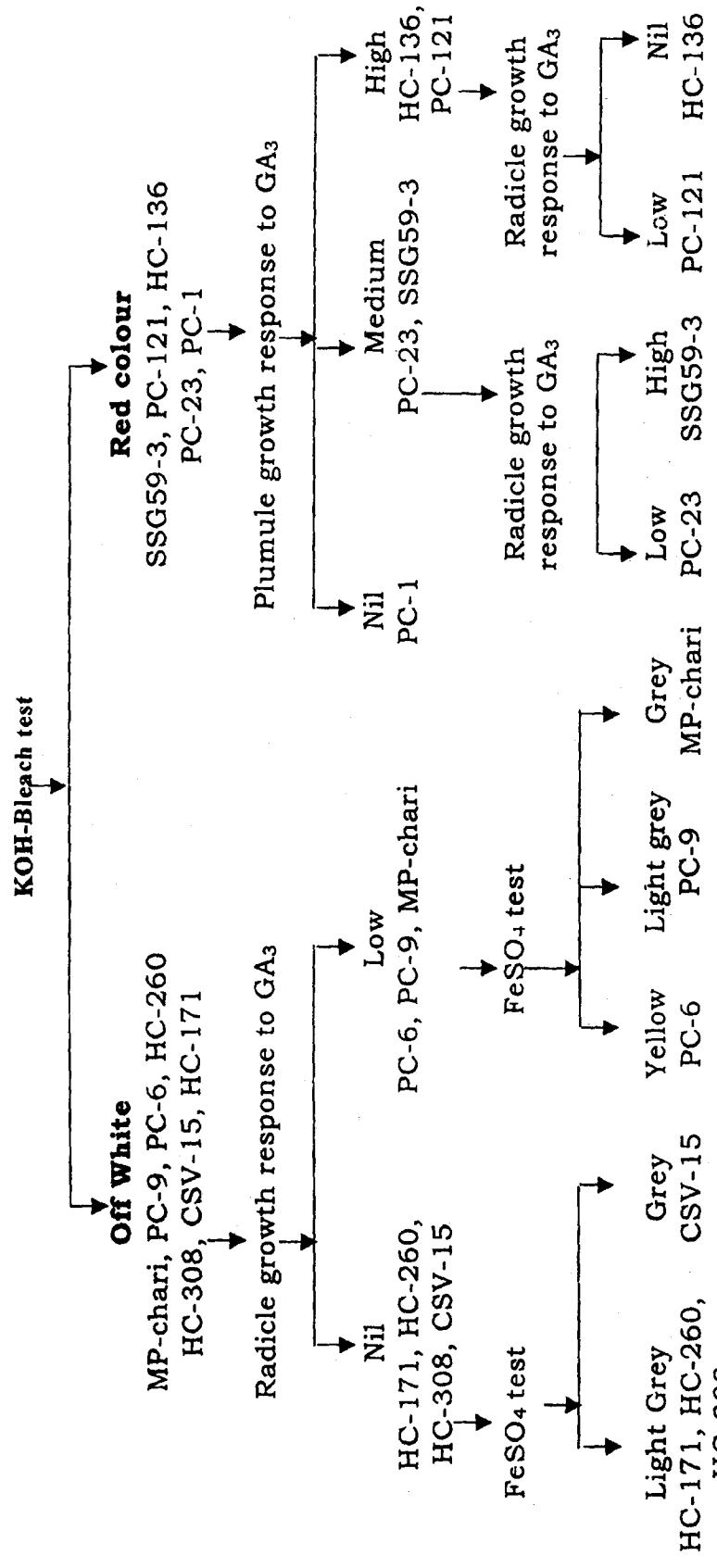
These varieties were classified into four groups on the basis of plumule and radicle growth response to GA_3 in comparison to control. The varieties were classified into four groups, as nil/no response (<10% increase over control), low (10-30% increase over control), medium (30-50% increase over control) and high (>50% increase over control) for both hypocotyl and radicle growth as

Table 1. Distinguishing sorghum varieties on the basis of chemical tests

Varieties	Phenol test	Modified Phenol test		Ferrous sulphate test	KOH-Bleach test
		(a)	(b)	$FeSO_4$	
HC-136	Light brown	Light grey	Brown	Light grey	Red
HC-171	Light brown	Light grey	Yellow	Light grey	Off white
HC-260	Light brown	Light grey	Light buff	Light grey	Off white
HC-308	Brown	Dark grey	Yellow	Light grey	Off white
PC-1	Brown	Brown	Brownish red	Light grey	Red
PC-6	V. Light brown	Dully grey	Light brown	Yellow	Off white
PC-9	V. Light brown	Dull grey	Light brown	Light grey	Off white
PC-23	Brown	Brown	Brown	Black	Red
PC-121	Brown	Dark grey	Brown	Light grey	Red
CSV-15	Brown	Dark grey	Light buff	Grey	Off white
SSG 59-0	Black	Brown	Light brown	Black	Red
MP-Chari	Light brown	Light grey	Light buff	Grey	Off white



Flow Chart 1. Varietal identification of sorghum on the basis of phenol and modified phenol test



Flow Chart 2. Varietal identification of sorghum on the basis of KOH-test $FeSO_4$-test, plumule and radicle growth response to GA_3

shown in Table 2 and flow chart 2. GA_3 is a growth regulator and stimulates the coleoptile growth whereas 2,4-D inhibits the root length. In case of 2,4-D test, all the varieties responded in the same manner *i.e.*, plumule were insensitive and root growth inhibited. Even in the presence of 2,4-D solution plumule were found to be least affected in comparison to radicle. But this test was found least effective in distinguishing 12 varieties from each other. Singh and Afria (1990) reported the GA_3 enhanced seedling growth, emergence and establishment in cotton; Agrawal and Pawar (1990) in soybean, Nagapadma *et al.* (1996) in maize, Walker *et al.* (1992) in sorghum, Shinde and Bhalerao (1990) in sorghum.

Based on these results it is concluded that the chemical tests such as phenol test, $FeSO_4$ test, KOH-bleach test, treatments with growth regulator were found to be useful in classifying the sorghum cultivars. The order of reliability to classify the above 12 sorghum varieties on the basis of chemical tests, KOH test showed marked differentiation followed by the phenol test, modified phenol test and growth response to GA_3. This information would be useful to the plant breeders, seed testing laboratories and seed certification agencies.

Table 2. Distinguishing sorghum varieties on the basis of seedling characters

Varieties	Control		Growth response to GA_3	
	Hypocotyl length	Radicle length	Plumule length	Radicle length
HC-136	Medium	Medium	High	Nil
HC-171	Short	Long	Low	Nil
HC-260	Short	Long	Medium	Nil
HC-308	Short	Long	High	Nil
PC-1	Short	Long	Nil	Nil
PC-6	Long	Medium	Medium	Low
PC-9	Short	Short	Low	Low
PC-23	Short	Short	Medium	Low
PC-121	Short	Long	High	Nil
CSV-15	Long	Long	Low	Nil
SSG59-3	Long	Short	Medium	High
MP-chari	Long	Short	Low	Low

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Genetic Variability Studies in Banana-1. Mysore Subgroup (AAB)

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Eleven accessions Mysore subgroup (AAB) of *Musa*, representing variability of different banana growing regions of the country were used in the present study, conducted at the National Research Centre on Banana (NRCB), Trichy, Tamil Nadu. This study revealed highly significant differences for most of the characters studied. Moderate GCV values were obtained for bunch weight, no. of leaves at harvest, total no. of fingers, no. of hands and no. of leaves at shooting. The characters bunch weight, breadth of leaf, no. of leaves at shooting, no. of leaves at harvest, no. of hands and total no. of fingers, showed high to moderate heritability and moderate GA. Among these traits, bunch weight should be emphasized during selection owing to its high genotypic coefficient of variability (GCV) values, heritability and genetic advance (GA).

Key words : Genomic Group, Germplasm, Heritability, *Musa*, Selection, Variability

Banana is the premier fruit crop in the country with the highest production of 13.2 million tonnes across the globe. Though the Indian sub-continent harbours more than 100 varieties, Mysore subgroup (AAB) dominates the banana industry with 18.42% area and a production of 16.19% only next to the Cavendish subgroup (AAA). Unlike the Cavendish cultivars, this bispecific subgroup has a wider adaptability and is grown up to an altitude of 1800 m above msl without any significant yield reduction.

Accordingly, great variation has been observed with respect to a number of characters attributing towards the yield. Apart from this, this subgroup exhibits high female fertility in terms of seed yield and a prolonged female phase unlike in other subgroups *i.e.* after completion of the female phase bearing fruits, there is a barren male phase. At the end of the male phase, a female phase bearing fruits reappears just above the male bud. These traits make Mysore subgroup, a potential parent in banana breeding programmes. So the present study was undertaken to collect all the variability present in Mysore subgroup across the country and to study their genetic variability by determining Phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV), heritability (h^2) in broad sense and genetic advance (GA) in order to select suitable genotypes for utilization in *Musa* improvement programme.

Material and Methods

Eleven accessions of Mysore subgroup were collected from the secondary centres located in Karnataka, Kerala, Tamil Nadu, Andhra Pradesh, Bihar, Assam and Maharashtra. They were evaluated in Randomized Complete Block Design with a spacing of 2m x 2m and with four replications at NRCB farm, Trichy, situated at an altitude of 90 m above msl. A recommended dose of fertilizers of 250:50:300 of NPK was given and crop was raised under wetland system of cultivation. Observations were recorded on eleven quantitative traits.

Height and pseudostem girth of the plant were recorded at harvest, length and breadth were recorded for the fully opened third leaf. Phyllochron is a major parameter in broad leaved plants like banana directly contributing towards yield, so the number of photosynthetically active leaves was recorded at shooting and at harvesting stages to estimate the no. of leaves spent towards bunch maturation. Number of days taken from planting to bunch maturation was recorded as crop duration.

Bunches were harvested at 80% maturity when fruit skin turned pale green, bloom disappeared and stigmatic remnants dropped off from the fruit tip. The parameters like weight of the bunch, number of hands per bunch, number of fingers per hand and total number of fingers per bunch were recorded. Analysis of variance was carried out following the standard procedures. The PCV and GCV coefficients of variability were computed by the method suggested by Burton (1952), heritability (broad sense) and genetic advance were worked out as per the procedure adopted by Johnson *et al.*, (1955).

Results and Discussion

Range, mean and standard error for all the characters studied are presented in Table 1. Analysis of variance

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and comparison of F-ratio revealed that highly significant differences were noticed for breadth of leaf, no. of leaves at shooting, number of leaves at harvest, crop duration, bunch weight, number of hands and total number of fingers (Table 2). This indicated the presence of high genetic variability among the accessions. Non-significant difference was noticed for the trait, plant height. Differences were significant for the remaining three characters *viz.*, pseudostem girth, length of leaf and number of fingers/hand. Bunch weight ranged from 4.88 kg to 16.62 kg with a mean of 9.93 kg. The range of variation for number of hands was from 6.25 to 12.5 with a mean of 9.86. The average total number of fingers was 142.34 with a range of 102 to 179.75.

Table 1. Range, mean and standard error values of Mysore subgroup of genus *Musa*

Characters	Range	Mean	S.Em
Plant height (cm)	240.50-274.0	261.86	15.35
Girth (cm)	51.0-61.50	57.68	2.43
Leaf length (cm)	146.5-202.75	185.81	19.46
Leaf breadth (cm)	58.75-80.75	66.52	4.35
No. of leaves at shooting	8.25-13.0	11.77	1.10
No. of leaves at harvesting	3.75-8.25	6.25	1.04
Duration (days)	374.5-480.25	436.86	11.28
Bunch weight (kg)	4.88-16.62	9.93	1.38
No. of hands	6.25-12.50	9.86	1.24
No.of fingers/hand	13.0-18.25	15.72	1.37
Total no. of fingers	102-179.75	142.34	17.8

Phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV), heritability (h^2) in broad sense and genetic advance (GA) as per cent over mean for various characters were studied (Table 3). In general, PCV values were relatively higher than GCV values indicating influence of environment on the expression of the character. The GCV helps in the measurement of the range of genetic diversity in a character and provide a means to compare the genetic variability in quantitative characters. Maximum GCV was observed for bunch weight (32.33) whereas least was for plant height (1.77) followed by pseudostem girth (4.2). Studies of Rajeevan and Geetha (1982) has also supported this view, emphasizing the importance of bunch weight. Moderate values of GCV were observed for leaves at harvest, number of hands and total number of fingers/bunch.

Table 3. Genetic parameters (PCV, GCV, h^2 and GA) of Mysore subgroup of *Musa*

Plant height	Phenotypic co-efficient of variability	Genotypic co-efficient of variability	Heritability (h^2)	Genetic advance (% over mean)
Plant height (cm)	8.48	1.77	4.4	0.76
Girth (cm)	7.30	4.20	33.1	4.97
Leaf length (cm)	17.73	9.73	30.1	11.0
Leaf breadth (cm)	12.79	8.82	47.5	12.52
No. of leaves at shooting	16.70	10.18	37.2	12.83
No. of leaves at harvesting	31.74	21.29	45.0	29.44
Duration (days)	9.48	8.75	85.2	16.62
Bunch weight (kg)	37.83	32.33	73.0	56.89
No. of hands	23.39	15.09	41.6	20.08
Fingers/hand	14.95	8.36	31.3	9.67
Total no. of fingers	23.36	15.15	42.1	20.25

But heritability estimates in broad sense are not the true indicators of genetic potentiality of an accession. Still their scope is restricted as they are prone to changes with the change in environment. Hence, if heritability values are considered in conjunction with predicted genetic gain, the reliability of the parameter as a tool in selection programme will increase.

Values of genetic advance (% over mean) ranged from 0.76 (plant height) to 56.89 (bunch weight). Higher value was obtained for bunch weight followed by no. of leaves at harvest, total number of fingers and number of hands. Bunch weight with high values of GCV, heritability coupled with high genetic advance indicated that it is predominantly controlled by additive gene action, meaning simple selection can be effective in improving this character. This is supported by hypothesis proposed by Panse (1957) who suggested that characters showing high heritability and GA are governed by additive gene effects. Additive effect of bunch weight in banana was also observed by Rosamma (1982).

Table 2. Analysis of variance for different characters of *Musa* subgroup (Mysore)

Source	Degrees of freedom	Plant height	Girth	Length	Breadth	No. of Lvs. at shooting	No. of Lvs. at harvest.	Dura-tion	Bunch weight	No. of hands	Fingers/ hand	Total no. of fingers
Replication	3	604.2	122.2	1232.1	71.9	1.06	2.26	65.0	9.52	2.75	3.82	1007.50
Treatment	10	557.8^{NS}	353.07*	2065.1*	175.6**	8.17**	9.25**	6095.0**	45.04**	11.97**	1.07*	2501.2**
Error	30	471.4	11.86	758.0	37.9	2.42	2.16	254.5	3.81	3.10	3.80	639.90
S.Em.		15.35	2.43	19.46	4.35	1.10	1.04	11.28	1.38	1.24	1.37	17.80
CD at 5%		31.35	4.96	39.75	8.88	2.24	2.12	23.03	2.81	2.53	2.79	36.34
CD at 1%		42.21	6.68	109.30	11.96	3.02	2.86	31.02	3.79	3.41	3.76	48.95

Though the crop duration has shown a high heritability estimate of 85.2%, moderately low estimates of GCV and GA infer that this character is governed by non-additive gene action or the presence of high genotype-environment interaction and simple selection will not be effective for improvement of this character. Moderate estimates of GCV, heritability and GA were observed for leaves at harvest, number of hands, total no. of fingers, leaf breadth and leaves at shooting. This suggests that these characters are influenced by environmental factors to certain extent. But still the improvement in these parameters could be brought about by rigid selection in the collection. Parameters like plant height with lowest values of GCV, heritability and GA is highly influenced by the environment and should not be considered for selection.

Acknowledgements

The authors acknowledge the facilities provided by the Director, NRCB for conduct of this research.

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Designing of Exotic Germplasm Database Using Client/Server Technology

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An efficient management of large volume of data related to Plant Genetic Resources (PGR) has become very essential for researchers, agricultural scientists and policy makers for research and reference purposes. An attempt is made to address the problem of managing data related to germplasm material imported by National Bureau of Plant Genetic Resources. A relational information system is designed and developed based on client-server approach. The detailed study also includes the taxonomic details and the addresses of national and international institutes. Some issues and steps related to the database designing of information management in the area of import of exotic material have been discussed. The detailed Entity-Relationship (ER) diagram and Data-Flow Diagrams (DFD) are also included which can help in the detailed designing of the database.

Key Words: Data Flow Diagram (DFD), Database Management System, Diagram, Entity Relationship (ER), Germplasm Exchange, Plant Genetic Resources

National Bureau of Plant Genetic Resources (NBPGR, hereafter referred to as Bureau) is the only nodal agency for import/export of germplasm material for agricultural research in India. It maintains a large number of crop species which include the "local" species (that grow naturally and collected from within the country) called "*Indigenous Collections*" (IC) and the "foreign" species (species that have been brought in/imported from various parts of the world) called "*Exotic Collections*" (EC). A wide variety of crop species have been imported and distributed by the Bureau for research purposes against requests by researchers and scientists in the area of agricultural sciences. The Bureau has been engaged in this activity since 1946 and nearly 0.5 million of samples have been received and distributed under import.

Any scientist, researcher or organization requiring to import some material has to make a formal request to the Exchange Division of the Bureau which in turn after scrutiny, issues an Import Permit (IP) and forwards the same to the source institute/country with a copy for information to the indentor. Imported exotic material may be received first-hand only at the Bureau where it undergoes for quarantine procedures to screen for interceptions of any pathogen. Any infected material is either cleaned or immediately destroyed. Only clean(ed) samples are returned to the Exchange Division where this material is accessioned before being distributed to the indentor. Accessioning is a process of giving a unique sample number called "EC number" to each and every sample to be used for any future reference. Each recipient including the original indentor needs to provide a feedback on the utility of material received by them.

Till date, information about all the exotic collections were maintained manually, the volume of which has reached around 200 registers. One of the major hurdles faced by the scientists and research management people is the management of this large amount of EC data. The EC data includes a variety of information such as the crop and species name, crop variety, type of material (such as seed, fruit, stem, root, culture etc.), alternate identity, other characteristics (such as plant quarantine, grow conditions etc.) and place of collections for material imported from various countries. The EC data may, therefore, be classified into six inter-related groups, namely, the *taxonomy* data (which includes details of all the crop species, their classifications and characteristics etc.), the *germplasm material* data (which includes the taxonomic details, quantity and other characteristics of the material imported from abroad), the *indentor* data (which includes details of the scientist, researcher or organization placing a request for import, namely, national addresses) the *source* data (which includes details of the source institute, organization from where the material is to be imported, namely, international addresses), the *import* data (which includes information about the material actually received and quarantined) and the *feedback* data (which includes information about feedback on material received and utilized by the indentor).

Maintaining and accessing above information in record books poses several data problems. Hence, what is required is a system to manage the voluminous exotic data in an efficient way and to provide quick retrieval, is an imperative. Apart from the need to aid the Bureau in proper and efficient management, maintenance of

information such as whether a species is a local or foreign species, it has become essential for documentation of such information in view of the recent global developments such as *General Agreement on Trade and Tariffs (GATT).*

In this paper we attempted to explain some issues and steps related to the database designing of information management regarding import of exotic material. Keeping in view the above mentioned facts, the following objectives were defined.

(i) ***Primary objectives:*** (a) to study and analyze the current manual system (requirement analysis), (b) to design and normalize various data tables to a reasonable degree, (c) to create and maintain a database of plant genetic material imported by the NBPGR and (d) to develop and implement a multi-user, user-friendly web enabled information management system.

(ii) ***Other objectives:*** (a) to facilitate the Bureau in bringing it at par with documentation capacities of other international organizations of repute engaged in similar research activities, (b) to assist NBPGR in maintaining a strong documentation base to tackle problems related to IPR (Intellectual Property Rights), Patents etc in the changing global scenario, and (c) to assist researchers, agricultural scientists and policy makers to access online the information about germplasm for research and reference purposes.

The detailed Entity-Relationship (ER) diagram and Data-Flow Diagrams (DFD) are also included which can help in the detailed designing of the database.

Problem Statement and Requirement Analysis

Any indentor, who wants to import some germplasm, has to make a formal request to the Bureau which after scrutiny issues an Import Permit for the purpose. The steps currently being followed manually and problems anticipated by the client in the process were identified and are listed below:

(1) Indentor places a request by filling a pre-printed form available at Germplasm Exchange (GEX) Division of the Bureau for import, giving the details of material required. The indentors request for material may be very vague or specific e.g. some samples of tropical fruits or say 5-6 samples of Tomato (*Lycopersicon esculentum* L.) exhibiting resistance to a particular disease. However, at a time same indentor may request for importing multiple materials from a single source. The client wishes to see the probable source(s) of requested material, which in the current manual system is difficult. Each request is registered and a Diary No. is assigned to the indentor for any further reference.

(2) GEX Division scrutinizes the request. Here, the client wishes to verify a history of material(s) imported by same indentor in recent past (up to 5 years) which in the current manual system is difficult.

(3) For valid requests, an Import Permit is generated and issued by the Bureau. An acknowledgement along with the Import Permit *number* (for reference) and a copy to this effect is sent to the indentor for his/her information. Separate permit is issued against each request for import from one country.

(4) The Import Permit is forwarded to the source country/ institute for sending the material. The supplier institute may send the requested material along with necessary documentation. The client needs to issue acknowledgement to the indentors and reminders to non-responding source(s) and keep a track of pending requests. The imported material can be received first-hand only by the Bureau and not directly by the indentor. The client requires crop-wise, country-wise and year-wise reports of imported material.

(5) Material (Consignment) received from abroad is given a *PQ number* and forwarded by GEX Division to the Plant Quarantine (PQ) Division to screen for any possible infection (due to virus, bacteria, disease etc.). Only clean(ed) samples out of the consignment are returned by the PQ Division to GEX Division. Here the Bureau needs to maintain a record of material sent to and cleared by PQ Division concerning quarantine. Status of cases pending with PQ Division is also needed. Thus the correspondence between PQ and GEX is mainly on the basis of PQ number.

(6) Each sample received by GEX Division after quarantine is accessioned *i.e.*, given a unique identification number called Exotic Collection (EC) number. From here onwards this *EC number* is the reference for all future operations of these samples.

(7) After accessioning, the material is passed on to the original indentor. **Multiple material distributions** are to be handled. Here, the client also needs to maintain a record of material distributed crop-wise, country-wise, and year-wise and category-wise which in the current manual system is a very cumbersome process.

(8) Each recipient of the material is expected to provide a feedback on the material utilized by him/her. The client needs to send reminders to non-responding parties in the matter. All feedback responses are to be compiled and made available for reference by other researchers. This is expected to be an EC number or crop name-based activity.

(9) Periodic reports and a versatile query system are also imperative needs of the client.

Advantages of the Information System over the Manual System

There are many drawbacks in the existing system. The present system was completely manual and all the records were kept in paper files that stand at a risk of getting damaged through gradual deterioration. The system, like other manual systems has some limitations, which can be enumerated as follows:

(i) Since the volume of data is very large, it is very difficult and inefficient to maintain them, (ii) The process of generating report is very time consuming, (iii) Retrieving information is time consuming, (iv) Time to time updating of records is very difficult, (v) Involvement of lots of manual works, (vi) Manipulation and repudiation possible and (vii) Lack of structured storage of data and efficient summarization.

The proposed system shall overcome the drawbacks of the existing system (manual system) in the following ways:

(i) Increase efficiency and reliability by suitable electronic medium for data storage, (ii) Increased information security by using suitable security model for information storage and processing, (iii) Increased effectiveness by providing efficient and convenient information retrieval methods and by providing value added information output, (iv) Increased efficiency and convenience by computerizing processing, (v) Backup can be done easily, (vi) Updating of records is an easy task, (vii) Generating of Reports is quite simple, (viii) Recovery of data can be done after any system crash, (ix) Information can be available online, (x) Administration of database can be done online and (xi) Increased productivity expectancy with the changed work environment.

The Platform/tools Required

The system was developed with following hardware and software tools:

(a) Hardware

One of the available P-IV (@1.5 GHz, 256MB RAM, 40GB HDD) desktop machines was used as Server.

Server : Intel Pentium III or above, Min. 256 MB RAM and 40GB HDD

Client : PII or above desktop with minimum 32 MB RAM

(b) Software

Following is a reference list of software used to develop and implement the software:

Operating System : Linux 7.3 (Server)

Client-Side Interface : Browser (I.E., Netscape etc.)

Database Server *(Back-end)* : ORACLE 9i for Linux

Web Server : ORACLE HTTP Server (Middle Tier)

System Architecture

It is based on a 3-tier Client Server model (Fig. 1).

(a) Database Server

At the lowest layer PGR-IMS employs the Database Server. The Server receives requests from clients for various operations. The server is responsible for concurrency control, recovery, transaction and storage management. The Database Server is responsible for query processing and all the operations on PGR-IMS database. After initialization, the database server waits for a query from its client. The results of the query

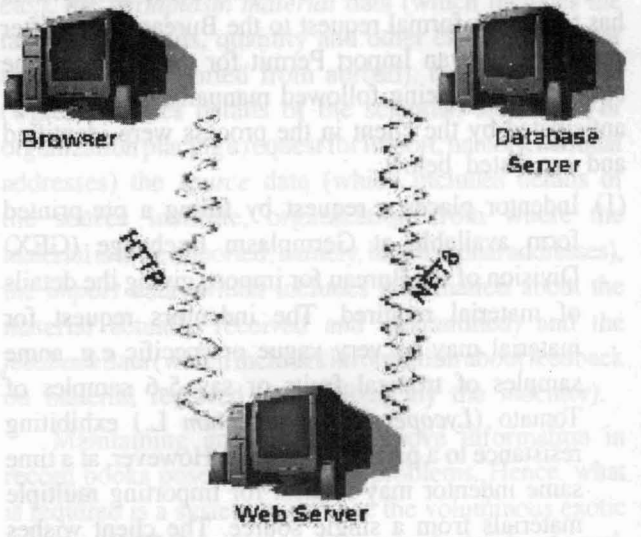

Fig. 1. Architectural design

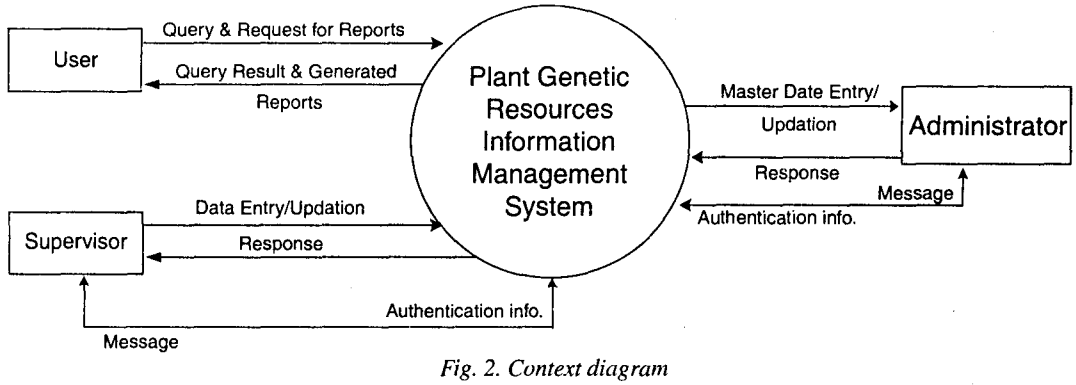

Fig. 2. Context diagram

that are obtained by processing it are sent back to the client.

(b) The Web Server

This is the middle tier between the browser and the Database Server. The user interacts with the Form based GUI through browser and the request that is sent to the Database Server is served by the Web Server. The Web Server waits for the result of the request from the Database Server and sends it back to the browser in suitable form when it is received.

(c) Browser

The browser is the client side interface for interacting with the database server.

Conclusions

The aim of this paper is to design and develop a Management Information System for National Bureau of Plant Genetic Resources to reduce the paper record filing works and for providing the safety for valuable data. The system is able to achieve quick and efficient processing of data, provision for multi-user data update/ entry, generation of quick and well-formatted reports, proper storage of data etc. Thus it enhances the performance in comparision to the existing system. A context diagram (Fig. 2) was drawn to show the process node (process 0) that generalizes the function of the entire system in relationship to external entities. Initially the existing system was thoroughly studied and observations recorded for use in the proposed system. Tools like DFD (Fig. 3) and ER diagram (Fig. 4) were use for requirement analysis. Following that was the design phase in which we designed the database schema for system.

The system is developed using Oracle 9i as RDBMS. The system should be developed in such a way that it becomes user friendly. If desired more enhancements can be made in the system in future to make it more fanciful, convenient and secure. An internet based SQLPLUS named *miSQL*PLUS* has been developed for Bureau which helps the administrators for maintain it online.

Apart from the above insights, we feel that there are other insights that could be gained from this project in the field of software application development. The importance of proper system design and the power of adhering to the correct software engineering development procedures have been made prominent in our mind.

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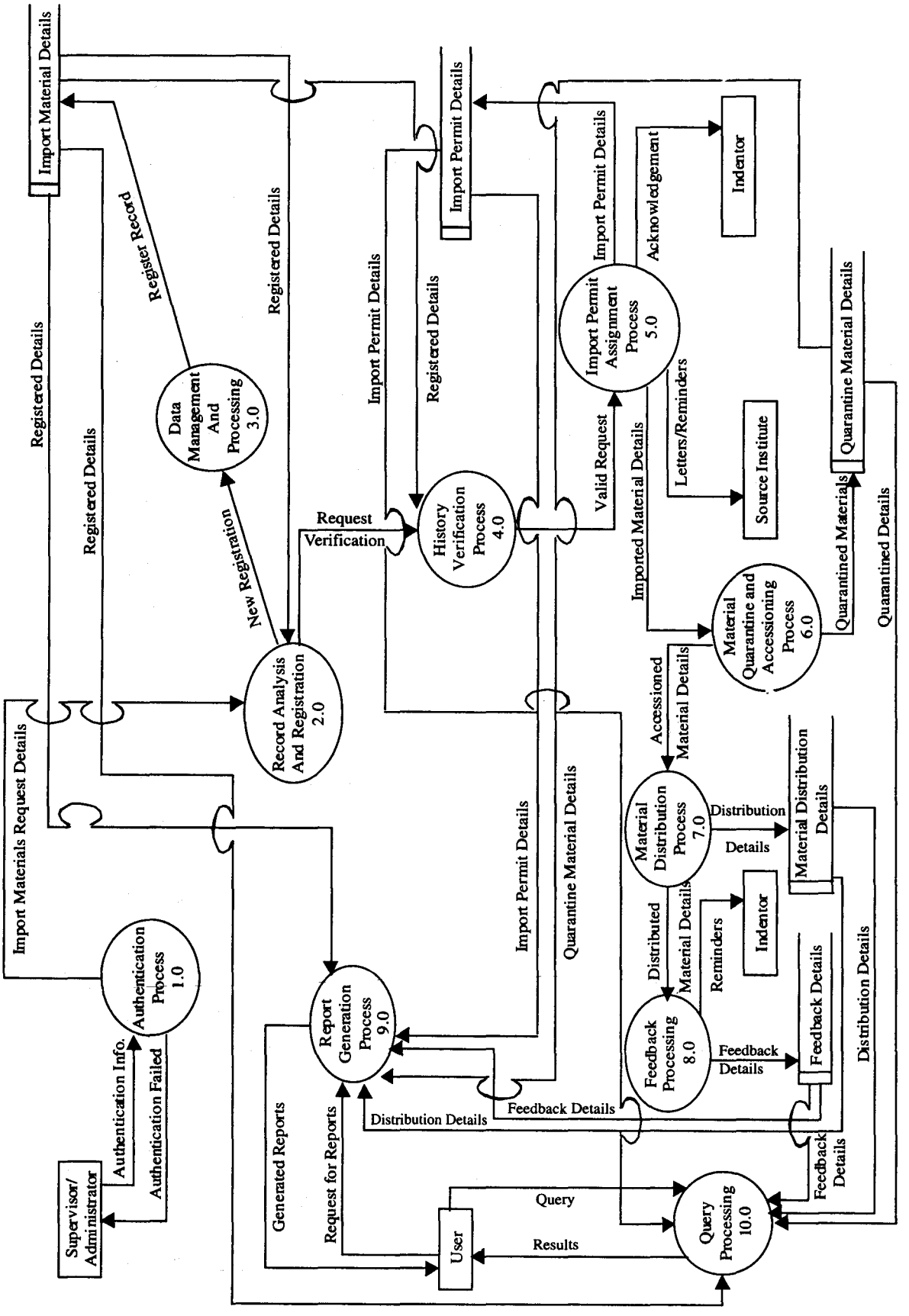

Fig. 3. Data flow diagram (Ist level)

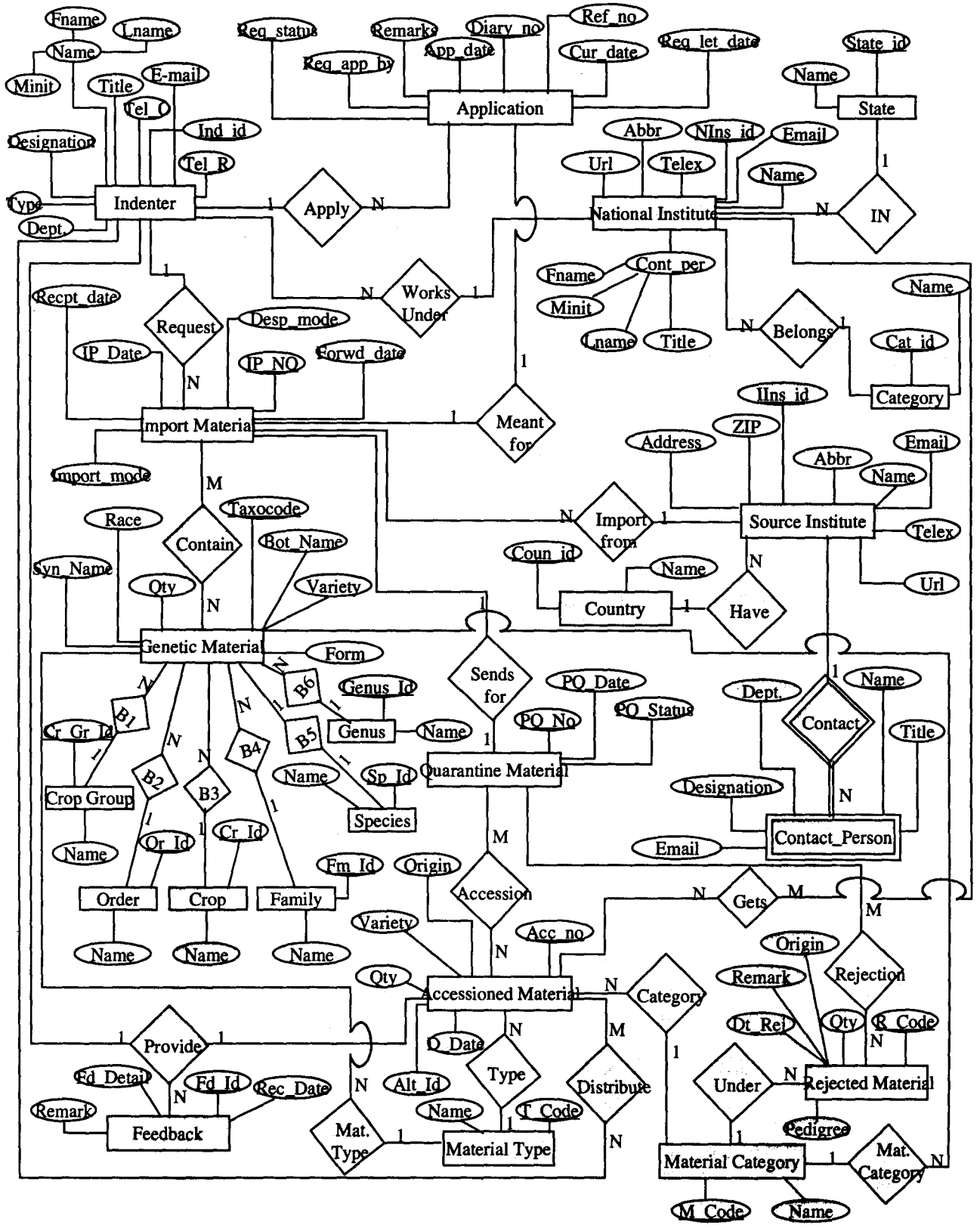

Fig. 4. Entity relationship model

SHORT COMMUNICATION

Glutamate Dehydrogenase Isozyme Pattern As a Unique Marker for Identifying Cold-Tolerant Wheat Genotypes

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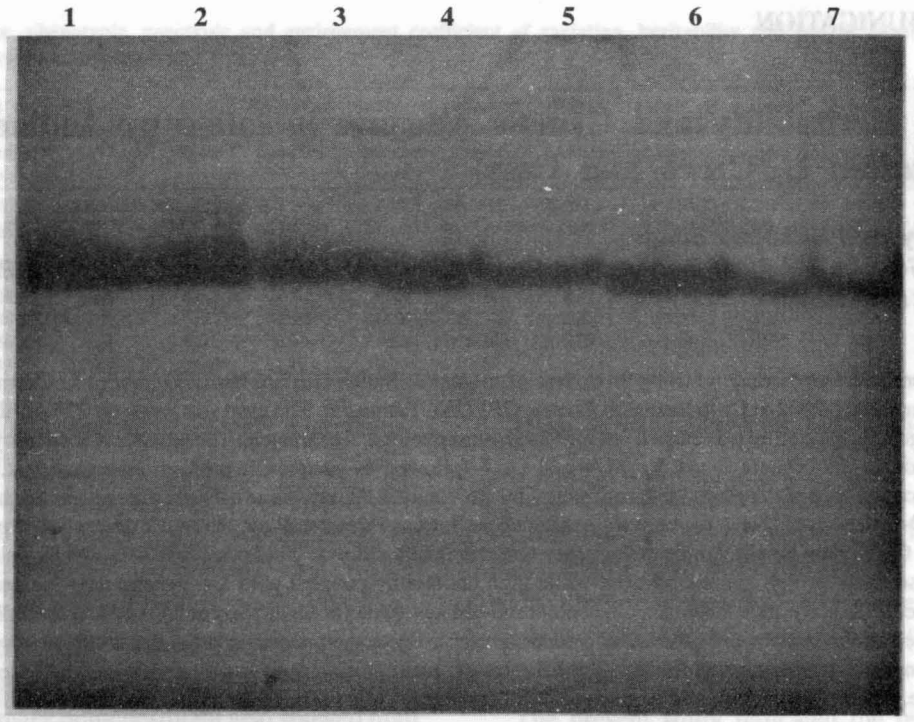
Identification of wheat genotypes that are tolerant to cold by using glutamate dehydrogenase isozyme pattern has been investigated. Glutamate dehydrogenase isozyme analysis of cold-tolerant wheat genotypes (VWFW1350 and HS240) and cold-sensitive wheat genotypes (VL404 and HD 1949) under cold-acclimated and non-acclimated conditions have shown that one unique glutamate dehydrogenase isozyme form was expressed in the cold tolerant genotypes under cold acclimated condition. This particular isozymic form has the potential to serve as a biochemical marker for selecting cold tolerant genotypes.

Key Words: Cold Tolerance, Glutamate Dehydrogenase, Isozyme, Marker, Wheat

The term isozyme refers to the multiple molecular forms of an enzyme which catalyze the same biochemical reaction (Scandalios, 1974). These multiple forms may occur in a single organism or in different members of the same species (Harris and Hopkinson, 1976). Isozymes can vary in size, structure, isoelectric point, amino acid composition, temperature and pH optima (Thorp and Duke, 1992). Isozymes serve as unique biochemical markers in a wide range of plant species. Biochemical markers in the form of isozymes have been correlated with stress adaptation and stress tolerance in different plant systems from time to time (Gangopadhyay and Basu, 2000). However, the study of isozyme patterns in identification of cold tolerance and cold-induced changes in isozyme profile are relatively few. We have established a way of identifying cold-tolerant wheat genotypes using the glutamate dehydrogenase isozyme pattern.

Wheat (*Triticum aestivum* L.) seedlings of four different genotypes that differ in cold tolerance were used as experimental material. Of the four genotypes, two genotypes (VWFW 1350, HS 240) were cold-tolerant and two other genotypes (VL 404, HD 1949) were cold-sensitive. All the four genotypes were obtained from Vivekananda Parvatiya Krishi Anushandhan Shala, Almora, India. The seedlings were grown in growth chamber with 22°C/18°C day/night temperature and with 12h photoperiod. Seven-day-old seedlings were cold acclimated for a period of 15 days with 4°C/2°C day/night temperature while another set of seedlings were grown at normal temperature. Cold-acclimated and non-acclimated seedlings were used for glutamate dehydrogenase (GDH) isozyme profiling. For glutamate dehydrogenase isozyme analysis the enzyme was extracted with 25 mM Tris buffer (pH 7.5), having 2.5 mM cysteine hydrochloride, 4.0 mM $MgSO_4$. $7H_2O$ and 0.25 mM EDTA in ice cold environment, and the enzyme extract was taken for acrylamide gel electrophoresis (PAGE) electrophoresis under non-denaturing condition. After electrophoresis, the gels were incubated in mixture containing 20 mg $NADP^+$, 30 mg nitroblue tetrazolium, 2 mg phenazine methosulfate, 25 ml of 0.5 M phosphate buffer (pH 8.0), 5 ml of 1 M sodium glutamate (pH 7.0) and 70 ml of water for 2h, and the bands were visualized.

Comparing the GDH isozyme bands of all the genotypes under both cold-acclimated and non-acclimated conditions reveal the presence of clear and distinct pattern associated with cold-acclimated tolerant genotypes. The tolerant genotypes VWFW-1350 and HS-240 under cold-acclimated conditions (Fig. 1 lane no. 1 and 2) produce a distinct GDH isozyme band which is not present in the cold-acclimated sensitive genotypes, and all non-acclimated genotypes. The density of the bottom most bands also differed between cold-tolerant and cold-sensitive genotypes and also between non-acclimated and cold-acclimated conditions. Among the cold-acclimated genotypes, the tolerant types had thicker GDH isozyme band than the sensitive genotypes. All the cold-acclimated genotypes had thicker band when compared to their non-acclimated condition. Among the non-acclimated genotypes, the



Lane No.1 Cold-acclimated tolerant genotype (VWFW1350)
Lane No.2 Cold-acclimated tolerant genotype (HS240)
Lane No.3 Cold-acclimated sensitive genotype (VL404)
Lane No.4 Cold-acclimated tolerant genotype (HD1949)

Lane No.5 Non-acclimated tolerant genotype (VWFW1350)
Lane No.6 Non-acclimated tolerant genotype (HS240)
Lane No.7 Non-acclimated sensitive genotype (VL404)
Lane No.8 Non-acclimated sensitive genotype (HD1949)

Fig. 1. Glutamate dehydrogenase isozyme pattern of cold tolerant and sensitive wheat genotypes under cold-acclimated and non-acclimated conditions.

tolerant genotypes had thicker GDH isozyme band when compared to the sensitive genotypes.

GDH isozyme analysis for cold-acclimated and non-acclimated tolerant and sensitive genotypes have shown the presence of a distinct GDH isozyme form in the cold-acclimated tolerant wheat genotypes. This unique isozyme band was not present in the non-acclimated tolerant genotypes and also in acclimated and non-acclimated sensitive genotypes. Also, the intensity of GDH bands that are common to cold-tolerant and sensitive genotypes was higher in the cold-acclimated genotypes. This increase correlated well with that of the GDH activity. The presence of unique isozyme band only in the cold-acclimated tolerant genotypes has the potential of using GDH isozyme pattern for the identification of cold-tolerant genotypes.

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SHORT COMMUNICATION

Variability, Heritability and Genetic Advance in late-sown Indian Mustard (*Brassica juncea* L. Czern and Coss)

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The experiment was carried out using 98 diverse genotypes of Indian mustard (*Brassica juncea* L. Czern and Coss) during *Rabi* 2001-2002 at Crop Research Centre, GBPUAT, Pantnagar. The crop was sown on 27th April 2001. The study of genetic variability was carried out for 13 agro-morphological characters. The number of secondary branches/plant recorded the highest values for PCV and GCV followed by number of primary branches/plant, siliqua on main shoot and seed yield/plant. Moderate values for PCV and GCV were shown by plant height, main shoot length, and 1000-seed weight. Days to maturity exhibited the lowest value for PCV while oil content showed the least value for GCV. Plant height, number of primary branches/plant and seed yield/plant revealed high heritability. Plant height also showed high genetic advance while high heritability coupled with low genetic advance was recorded for number of primary branches/plant. Oil content showed low values of heritability and genetic advance. The present study revealed the presence of substantial amount of variability in the material and the important yield components were number of primary and secondary branches/plant, plant height, main shoot length and 1000-seed weight. Therefore, greater emphasis should be given on these characters while selecting for higher yield and related characters.

Key Words: Genetic Advance, Heritability, Indian Mustard, Variability

The *Brassica* group of oilseed crops, commonly known as rapeseed-mustard are the second largest oilseed crop next to groundnut in terms of area and production in India. Indian mustard is the predominant crop among the *Brassica* oilseeds occupying nearly 90% of the total area among these crops. The low productivity can be substantially increased by the use of high yielding varieties/hybrids which in turn serve as potential donors for various qualitative and quantitative traits. In view of the above evaluation of variability present in the germplasm and its exploitation is a pre-requisite. Similarly, heritability of complex traits such as yield and its component characters is also useful in determining the selection criteria for improving the genotypes. Considering the above facts, the present study was conducted to assess the variability in Indian mustard germplasm under late sown conditions and have an idea of the heritability and genetic advance of yield and its component traits.

The experimental material consisting of 98 diverse genotypes of Indian mustard (*Brassica juncea* L. Czern and Coss), were grown during *rabi* 2001-2002 at Crop Research Centre, GBPUAT, Pantnagar. These genotypes, along with two checks Kranti and Varuna were sown in 10 x 10 simple lattice design with two replications under late-sown conditions (27th November, 2001). Each plot consisted of a single row of 3 m length with row to row distance of 30 cm and plant to plant distance of 10 to 15 cm was maintained by thinning. The crop was grown at a fertility level of 80:40:40 NPK/ha, respectively. Observations were recorded on five randomly selected plants from each plot for 13 quantitative characters *viz.* days to flower initiation, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches/plant, length of main shoot, siliqua length, siliqua on main shoot, seeds/siliqua, 1000-seed weight, oil content and seed yield/plant. The estimates of phenotypic coefficient of variations (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance were computed using standard statistical procedures.

The analysis of variance under late sown conditions exhibited highly significant differences among genotypes for all the characters studied. The range, mean and standard error of mean, genotypic and phenotypic coefficient of variability, heritability and genetic advance are presented in Table 1. The range of variability indicated the existence of variability for all the characters.

Secondary branches ranged from 3.2 to 18.9 with a mean value of 7.98 $\pm$ 1.58 and exhibited the maximum

Table 1. Range, mean, phenotypic, genotypic and environment coefficient of variation, heritability and genetic advance as per cent of mean of various characters

	Days to Flower Initiation (no.)	Days to 50% flowering (no.)	Days to maturity (no.)	Plant height (cm)	Number of primary branches	Number of secondary branches (cm)	Length of main shoot	Siliqua length (cm)	Siliqua on main shoot (cm)	Seeds/ siliqua (no.) (g)	1000-seed weight	Oil content (%) (g)	Seed yield/ plant
Range	47.3-71.3	52.5-83.5	117.8-133.9	101.8-176.8	3.2-11.4	3.2-18.9	20.6-53.1	2.7-5.5	15.7-36.7	6.8-16.1	2.1-4.9	35.7-42.8	1.5-6.9
Mean± SEM	55.82±2.48	61.97±2.34	128.61±2.74	132.7±7.80	4.82±0.66	7.98±1.58	40.73±5.05	4.33±0.42	23.99±2.63	12.16±1.10	3.63±0.27	37.87±1.31	3.75±0.32
PCV	9.65	6.70	3.56	13.65	31.22	41.52	18.53	16.37	23.92	15.44	15.33	4.79	21.38
GCV	7.32	4.04	1.89	10.83	24.44	30.64	5.94	8.77	18.24	8.65	11.21	1.39	17.67
ECV	6.28	5.35	3.01	8.30	18.43	28.01	17.55	13.82	15.47	12.80	10.46	4.99	12.03
h^2	0.58	0.36	0.28	0.63	0.61	0.54	0.70	0.29	0.58	0.31	0.53	0.08	0.68
GA	6.38	3.11	2.68	23.49	1.89	3.71	1.59	0.42	6.87	1.21	0.61	0.31	1.13

values for PCV (41.52) and GCV (13.64). Oil content and days to maturity showed the lowest values for PCV (4.79 and 3.56, respectively) and GCV (1.39 and 1.89, respectively). Similar results have been reported by Chauhan *et al.*, (1999).

Plant height varied from 101.8 cm to 176.8 cm with a mean value of 132.7 ± 7.80 cm. The corresponding PCV and GCV values were 13.65 and 10.83, respectively. The number of primary branches/plant also showed high PCV (31.22) and GCV (24.44) values, the range being 3.2 to 11.4 with a mean value of 4.82 ± 0.66.

Main shoot length varied from 20.6cm to 53.1cm with a mean value of 40.73 ± 5.05. The PCV and GCV values were 18.53 and 5.94, respectively. The siliqua length showed moderate values for PCV (16.37) and GCV (8.77) and ranged from 2.7 cm to 5.5 cm with a mean value of 4.33 ± 0.42.

The 1000-seed weight varied from 2.07 g to 4.87 g with a mean value of 3.63 ± 0.27. The character recorded moderate values for PCV (15.33) and GCV (11.21).

Seed yield/plant showed moderately high values for PCV (21.38) and GCV (17.67) and ranged from 1.47 g to 6.91 g with a mean value of 3.75 ± 0.32.

Plant height (0.63), number of primary branches/ plant (0.61) and seed yield/plant (0.68) showed high estimates of heritability. This indicated that these characters are less influenced by environment. Similar results have been reported by Bagrecha *et al.*, (1972), Ghosh and Gulati (2001). Moderate heritability (0.40 to 0.60) was recorded for number of secondary branches/plant (0.54), siliqua on main shoot (0.58) and 1000-seed weight (0.53). Oil content (0.08) showed the least heritability. This is supported by the findings of Sharma (1987).

High heritability coupled with high genetic advance (23.49) was recorded for plant height. Number of primary branches/plant (1.89) and seed yield/plant (1.13) showed low genetic advance but high heritability. Similar results have been reported by Bagrecha *et al.* (1972), Das *et al.*, (1998). Oil content showed low heritability with low genetic advance (0.31) supported by the findings of Sharma (1987).

The present study indicated the presence of wide range of variability for number of secondary branches/ plant, number of primary branches/plant, plant height, main shoot length, siliqua on main shoot, 1000-seed weight and seed yield/plant. Therefore, selection should be based on these characters in order to achieve greater productivity in this crop.

Acknowledgement

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SHORT COMMUNICATION

Addition to the Germplasm of *Allium roylei* Stearn

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The present communication adds to the existing germplasm of *Allium roylei* Stearn, a known source of genes for providing resistance to the common onion *A. cepa* against some pathogens. Problems encountered in its identification and some differences from the earlier collections have been recorded.

Key Words: *Allium roylei*, Collections, Germplasm

At the International symposium on *Allium* held at Gatersleben, Germany in 1991 *Allium roylei* was one of the most keenly debated species (de Vries, 1992) for reasons of its potential as the source of genes for resistance against downy mildew and leaf blight for incorporation into *A. cepa*. Its importance notwithstanding the taxonomic identity of the species is in jeopardy and the available germplasm limited (de Vries, 1992; de Vries *et al.*, 1992). The urgency to widen the germplasm of the species and establish its identity is so great that the group working on this plant had brought potted specimens of the species to elicit information, from the delegates attending the symposium. These plants have their origin in Mussoorie, India. One of us (RNG) had the opportunity to see the plant at Gatersleben. On his return to India he explored Mussoorie and other places in the Shivaliks for the species.

It was not possible to collect the material from Mussoorie partly because the actual location from where it has been collected is not known and also on account of urbanization and habitat destruction. However, some accessions of *Allium* collected from Bani and Mendhar areas of the Jammu and Kashmir Himalayas appear to resemble *Allium roylei*. In addition, an accession procured from the National Bureau of Plant Genetic Resources Regional Station, Bhowali (Uttaranchal) also matches the description of *A. roylei*. All the three accessions, which could not be studied in detail in their native habitats were transplanted to the University Botanical Garden, Jammu. After documenting their morphological characters, attempts were made to confirm their identity with the help of local flora and other literature available on the Indian Alliums (Hooker, 1892; Stearn, 1947; Nasir, 1975). This exercise confirmed the earlier views of de Vries (1992), and we also realized that on the basis of available data, it is not easy to assign relevant name to even the accessions collected by us. Despite that, based on most of the morphological features these plants could be identified only as *Allium roylei* Stearn. Morphological details of the plants collected by us are as follows:

Bulbs ovoid, 4-7 cm long and 1.2-2.5 cm broad, with a narrow but distinct rhizome, inner coats scaly, outer coats leathery and brown coloured. Scape hollow, covered with leaf bases, 45-52 cm long. Leaves 3-5, terete, 17-36 cm long and 2-3 mm broad. Inflorescence hemispherical, 4.5-5 cm across. Flowers pinkish and companulate, 5-6 mm long. Pedicels 12-17 mm long. Tepals oval. Filaments exerted, inner two toothed at the base, anthers large, stigma much above the flower and ovary trilocular with two ovules in each locule. Spathe persistent and acuminate. Flowering period July to August. Location slopes around village Dholka in Bani block (18 Km from Bani towards Bhaderwah between 1300–1400m), Mendhar and Bhowali. The reddish coloured flowers changed to pinkish white when cultured and maintained in Jammu for about one year.

The above details have been compared with those given for *Allium roylei* by Stearn (1947) and Nasir (1975).

Although, as is clear from the Table 1, there are differences in some quantitative characters, the plants collected and described by us fit the description of *A. roylei* Stearn. The Botanical Survey of India, Dehradun, have confirmed this identification.

The present collection add to the available germplasm of this important species. There is, however, a limitation for the utility of these accessions because unlike the Mussoorie accession, they are sterile on account of complex translocation heterozygosity. The purpose of this communication is to prompt botanists for exploring Western Himalayas for *A. roylei* and invite them to

share any information with the authors of this communication.

The authors are thankful to National Bureau of Plant Genetic Resources, Bhowali, for providing one accession of this species, Botanical Survey of India for confirming the identification and Department of Science and Technology, Government of India, for financing the project. We are also grateful to Professor AK Koul for critically going through this manuscript and giving useful suggestions.

Table 1. Morphological characterization of new collection of *A. roylei*

Character	New collection	Stearn (1947)	Nasir (1975)
Bulb length (cm)	4-7	Not mentioned	Not mentioned
Bulb breadth (cm)	1.2-2.5	Not mentioned	Not mentioned
Leaf	Fistular	Terete	Linear, grooved
Leaf length (cm)	17-36	Not mentioned	Not mentioned
Leaf breadth (cm)	2-3	Not mentioned	1 to 2
Scape length (cm)	42-52	20-26	20-40
Inflorescence diameter (cm)	4.5-5	2.5-2.8	2-3
Flower length (mm)	5 to 6	Not mentioned	Not mentioned
Pedicel length (mm)	12-17	6-8	Not mentioned
Tepal length (mm)	5-6	6	6-8
Location	Western Himalayas	Western Himalayas	Western Himalayas

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SHORT COMMUNICATION

Estimates of Variability Parameters in Strawberry (*Fragaria ananassa* Duch)

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Thirteen genotypes selected for variability parameters showed significant differences and a broad range of variation for all the traits studied. High heritability coupled with high genetic gains as observed for fruit weight/plant, number of fruits/plant, number of flowers/plant, number of marketable fruits/plant, pedicel length, fruit size, berry weight, plant genetic effects in the control of these traits. Contrary to it, soluble contents, titratable acidity showed comparatively low values of genotypic, phenotypic coefficients of variation and expected genetic gains, suggesting that phenotypic selection for these traits might not be rewarding.

Key Words: *Fragaria ananassa*, **Heritability, Strawberry,Variability**

The success of any crop improvement programme is directly dependent on the amount of genetic variability present in a crop. The coefficient of variability measures the extent of variation present among the genotypes within a particular trait, whereas the role of heritability coupled with genetic gains is very prominent in predicting the breeding value of an individual as well as predicting the genetic improvement expected in next generation as a result of the adoption of a particular scheme of selection. Galleta and Mass (1990) also emphasized the partitioning of a character into their components before selection. This study estimated the coefficient of variation, heritability and genetic gains in 13 genotypes of strawberry for prediction of selecting components of improvement for the next generation.

The experimental material comprised 13 genotypes (cultivars/hybrid/open-pollinated seedling selections) was grown on raised beds in a randomized block design with three replications during planting season, 1999. The experimental site was located at 1200 m above mean sea level and situated at 31°N latitude and 77°E longitude. The plot size was 2 x 1.6 m with spacing 50 x 40 cm between row to row and plant to plant, respectively. Observations were recorded on five randomly selected plants in each replication for growth and yield characters as per the standard procedure.

The analysis of variance was performed as per the method suggested by Panse and Sukhatme (1961). The variability parameters were determined as per the methodology suggested by Burton and de Vane (1953) and Johnson *et al.* (1955).

Results have been presented in Table 1. Analysis of variance showed significant mean sum of squares for all the traits, suggesting the presence of diversity among the genotypes assessed. The estimated of GCV were slightly lower in magnitude than the magnitude of phenotypic coefficient of variability (PCV) due to partial interaction of the genotypes with the environment or other environmental factors influencing the expression of these characters. As all the traits showed a narrow difference between GCV and PCV, phenotypic selection could be made effectively. Highest GCV and PCV for traits like fruit weight/plant, number of fruits/plant and number of flower/plant indicated the presence of diversity and offer good scope of enhancing productivity by selecting individuals for these traits.

However, estimate of heritability coupled with genetic gains would be useful for selection (Johnson *et al.*, 1955). The traits *viz.*, fruit weight/plant, number of fruits/plant, number of flowers/plant, number of marketable fruits/plant, pedicel length, fruit size, berry weight, plant height and leaf area studied in the present investigation showed high heritability (>90%) alongwith high expected genetic gains. The occurrence of such might be due to the presence of additive gene action (Panse, 1957). The above results are in agreement with the findings of Lal and Seth (1979). Spangelo *et al.* (1971) also reported high heritability estimates for average berry weight, number of berries/flower stem and yield/flower stem.

Contrary to it, total soluble contents, titratable acidity, pedicel thickness and leaf area showed comparatively low values of GCV, PCV and expected

Table 1. General mean, range and variability parameters for fruit yield and other traits in strawberry

Trait	Range	Mean	Mean sum of squares (12 d.f.)	GCV (%)	PCV (%)	Heritability (broad sense) (%)	Genetic advance	Genetic gain (%)
No. of flowers/plant	5.68-19.80	9.90	63.00*	45.95	47.01	95.6	9.16	92.8
Plant height (cm)	14.37-27.93	17.05	38.08*	20.58	21.52	91.4	6.91	40.5
Plant spread (cm)	25.33-47.57	29.65	97.78*	18.71	20.30	85.0	10.54	35.5
Leaf area (cm^2)	45.53-78.13	65.53	342.70*	16.68	17.10	95.1	21.29	33.5
No. of fruits/plant	4.0-15.47	7.05	37.17*	49.46	50.84	94.6	6.99	99.2
No. of marketable fruits/plant	2.53-8.13	4.25	6.22*	33.49	34.61	93.6	2.84	66.8
Fruit size (cm)	4.40-9.07	6.90	5.98*	20.32	20.78	95.7	2.83	41.0
Pedicel length (cm)	2.67-6.67	5.01	4.56*	24.22	25.40	90.9	2.38	47.5
Pedicel thickness (cm)	0.91-1.35	1.15	0.06*	12.18	14.25	73.0	0.25	21.7
Berry weight (g)	4.23-8.77	6.38	4.59*	19.20	19.75	94.5	2.45	38.4
Fruit weight/plant (g)	12.17-90.67	36.01	1621.40*	64.39	64.89	98.5	47.40	131.6
Total soluble solids (°Brix)	6.43-8.67	7.75	1.19*	7.83	8.67	81.6	1.13	14.6
Titratable acidity (%)	0.80-1.14	0.95	0.40*	11.34	13.25	73.2	0.19	20.0

genetic gains in the presence of high estimates of heritability (73-81.6%) giving an indication of non-additive gene action, suggesting that the phenotypic selection for these traits might not be rewarding.

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SHORT COMMUNICATION

Natural Aging Effect on Seed Germinabilty of Clusterbean Cultivars

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Seeds of eight varieties of clusterbean or guar (*Cyamopsis tetragonoloba* L. Taub.) stored for 7, 19 and 31 months, respectively, under ambient storage conditions were assessed for their germinability under field conditions. Almost complete loss of viability was observed in the seeds, which were stored for 31 months or three crop seasons. The best germination was recorded in the seeds that were stored for 7 months or one crop season. Differential response to germinability was observed in different varieties of guar. For achieving optimum germination and better crop stand, only one season old (about 7-8 months) seeds should be utilized for sowing in the fields.

Key Words: Clusterbean, Natural Aging, Seed Germination

The maintenance of viability of the seed embryo of any plant species is important for two main reasons *i.e.* for the utilization of carry-over quality seed for sowing in the next season and for long-term conservation of genetic resources owing to limitations in growing whole germplasm every year. Deterioration in the condition of the seeds prevents them from normal germination and vigorous growth due to certain physiological and biological changes occurring in the seeds during storage. But no published work is available on the effect of natural aging or variable storage period on seed germinability in guar. Hence, to assess the effect of natural aging and response of different cultivars on germinability, an experiment was conducted in field on eight genotypes of guar seeds stored for three consecutive seasons.

One (7 months), two (19 months) and three (31 months) seasons old seeds of eight diverse genotypes of guar were taken for this study. After threshing, the seeds were sun-dried and stored in cloth bags under ambient conditions in the field laboratory. The age of seed lots harvested in 1996, 1995 and 1994 were 7 months, 19 months, and 31 months, respectively. One hundred seeds of each genotype of three ages were sown in the dryland area of Forage Section, Department of Plant Breeding, CCS Haryana replications. The row to row and plant to plant spacings were 45 and 10 cm, respectively. Germination counts were made after 25 days of sowing.

The data for germination counts were transformed into square-root (X+1) values for statistical analysis.

The results of germination of eight genotypes of guar stored for 3 different durations are presented in Table 1. Data revealed that per cent mean germination was very low in 31-month-old seeds, which ranged from 0.00 to 14.33. Genotypes FS 277,

Table 1. Effect of natural aging and cultivars on seed germinability in guar*

Genotypes	7 months or one-season-old	19 month or two-season-old	31 months or three-season-old	Average
FS 277	8.50 (71.33)	1.00 (0.00)	1.00 (0.00)	3.50 (23.78)
CP 42	8,12 (65.00)	1.00 (0.00)	1.00 (0.00)	3.37 (21.67)
RGC 936	8.89 (78.00)	7.80 (60.00)	1.00 (0.00)	5.90 (46.00)
Naveen	8.72 (75.00)	1.00 (0.00)	1.00 (0.00)	3.57 (25.00)
HG 258	9.09 (81.67)	1.00 (0.00)	1.00 (0.00)	3.70 (27.22)
HGS 329	9.57 (90.67)	8.94 (79.00)	1.00 (0.00)	6.50 (56.56)
HG 365	8.20 (66.33)	1.00 (0.00)	1.00 (0.00)	3.40 (22.11)
HFG 156	9.22 (84.00)	8.92 (68.67)	3.91 (14.33)	7.35 (55.67)

SE (M) ±	Variety	: 0.08	CD at 5%	Variety	: 0.16
	Aging	: 0.05		Aging	: 0.10
	Variety x Aging	: 0.13		Variety x Aging	: 0.27

* Figures not in parentheses are square root (X + 1) (transformed values)
Figures in parentheses are actual germination per cent values (Untransformed values)

CP 42, RGC 936, Naveen, HC 258, HGS 329 and HC 365 did not germinate at all, whereas only one genotype HFG 156 gave 14.33% germination. In 19-month-old seeds, germination percentage varied from 0.00 to 79.00. Genotypes FS277, CP 42, Naveen, HG 258 and HG 365 did not germinate at all. The average germination percentage of all the eight genotypes of 19-month-old seeds was 25.96. In 7-months-old seeds, the germination (%) in the field ranged from 65.00 to 90.07 with an overall average of 76.50%.

From the above findings, it is clear that guar seeds appeared to be very fast deteriorating in their germinability with increase in the storage period. Therefore, for achieving optimum seed germination, one season old (7-8 months old) seeds should preferably be utilized for sowing in the field. However, there is a need for further research to find out the optimum storage conditions under which guar seeds could be stored for a longer period.

Acknowledgement

The supply of seed material by Dr Jaivir Singh, is thankfully acknowledged.

PLANT GERMPLASM REGISTRATION NOTICE

Rice Germplasm from Andamans

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Black Burma Rice (INGR No. 01019, IC 296798)

Black Burma rice, *Oryza sativa* is a very tall (174.4 cm), traditional, indica cultivar grown in middle and south Andamans. It has been identified to be tolerant to aluminium toxicity and moderately tolerant to salinity. The cultivar flowers after 150 days and matures within 190 days. Each plant possesses lesser tillers (6.8) with an average of 5 panicles indicating moderate tillering capacity. The flag leaf area is 38.25 cm^2. Panicles are small (25.9 cm) with low spikelet sterility (25.35%). Average grain yield is 2.1 tons/ha. The grain length is around 9.7 mm, while the width is 3.85 mm with a length/width ratio of 2.52. The dehusked rice is creamy white in colour with a length/width ratio of 2.2. The grains possess opaque endosperm. On cooking the grain showed 6.67% elongation, and 2.22 times volume expansion. Alkali digestion value was found to be high with low amylose content and low gelatinisation temperature. Gel consistency value was scored as 3 with very soft texture on a scale of 0-9.

The genotype is found to be tolerant to sheath blight (caused by *Rhizoctonia solani*), bacterial leaf spots (caused by *Cercospora oryzae*), sheath rot (caused by *Xanthomonas campestris* pv. *oryzae*), and neck and leaf blight (caused by *Pyricularia oryzae*), and tolerant to leaf folder (*Cnaphalocrocis medinalis*), gundhi bug (*Leptocorisa oratoria*), while moderately tolerant to stem borer (*Scirphophaga incertulas* Walker) under field conditions.

It has violet coloured ligules with pink margin. It is specially suited for preparation of breakfast items. In Andamans it is used for *lasa* preparation (a local food item). It can be a source for improving nutritional quality, and tolerance to excess salt and aluminium toxicities.

Nona Rice (INGR No. 01020, IC 296799)

Nona is a traditional dwarf (66 cm) variety of rice, *Oryza sativa* grown in north, middle and south Andamans. It belongs to indica group. In was identified to be moderately tolerant to salinity and iron toxicities. The cultigen's flowers after 80 days and matures within 110 days. Each plant possesses moderate number of tillers (8) with an average number of 7 panicles indicating abundance of productive tillers. Panicles are small (20.0 cm) with test weight of 36.0 g. The average yield of the Nona rice is 1.5 tons/ha. The grains are bold with light brownish coloured husk. The endosperm of the grain was opaque with chalkiness at the centre. The grain elongates up to 33.4% and expands 1.87 times on cooking. The alkali digestion and gelatinisation temperature values were found to be intermediate with soft gel consistency.

The cultigen is moderately tolerant to bacterial leaf blight (*Xanthomonas campestris* pv. *oryzae*), bacterial leaf spot (*Cercospora oryzae*), *Helminthosporium* leaf spot and blast (*Pyricularia oryzae*), and tolerant to stem borer caused by *Scirphophaga incertulas* Walker.

Basmati Quality Cytoplasmic Male Sterile Rice

FU Zaman, AK Singh, A Hariprasad, MJ Abraham, Anju Mehendru, F Mohammad, RA Singh, Jagbir Singh, G Ravindran, AK Mittal, A Haque, Mahadev Mahto, R Paramsivam
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PUSA 4A (INGR No. 01021, IC 296800)

PUSA 4A is a basmati type cytoplasmic male sterile line of paddy, *Oryza sativa* derived from IR 58025A/IET 10649 through back crossing and selection. The plant height is 95 cm with purple base. The grains possess ideal basmati characteristics and pollen grains are completely sterile. It is a semi-dwarf, high tillering type with dark green leaves and purple stigma with better exsertion. Number of spikelets are 175 per panicle. Days to 50 per cent flowering is between 95 to 100 and to maturity 135.

Plant Germplasm Registration Notice*

The IX meeting of the Germplasm Registration Committee of Indian Council of Agriculture Research was held on 22nd May 2002. The Committee considered 108 proposals and approved the registration of following 24 germplasm lines/genetic stocks.

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[2]*Rice Research Station, CCS Agricultural University, Hisar-125 004 (Haryana)*

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[4]*National Research Centre for Plant Biotechnology, Indian Agricultural Research Institute, New Delhi-110 012*

Registration of Paddy Germplasm, Pusa 1121 (INGR No. 02001; IC 296890)

Linear kernel elongation during cooking with minimum lateral swelling is one of the most desirable characters of rice varieties. By selective inter-mating of two kernel elongating advance breeding sister lines (Pusa 614-1- 2 and Pusa 614-2-4-3) of Pusa Basmati 1, followed by pedigree selection, a new breeding line, Pusa 1121-92-8-1-3-3 of paddy (*Oryza sativa*) has been developed at the Division of Genetics, Indian Agricultural Research Institute, New Delhi. The average milled rice kernel length of Basmati 370, Taraori Basmati, and Pusa Basmati 1 is 6.89, 7.15 and 7.30 mm, with elongation ratios of 1.94, 1.90, and 2.02, respectively.

Pusa 1121 has profuse tillering habit and dark green narrow leaves like Pusa Basmati 1. It has slow leaf senescence with leaves remaining green even after maturity. It has straight flag leaf and panicle remain below the leaf level. All plant parts are free from pigmentation. Grains have tip awning. Information on some of the main morpho-agronomic characteristics as compared to other varieties is presented in Table 1.

Pusa 1121 has field tolerance to major rice diseases. Milled rice is highly aromatic, with an alkali spreading score of 7. Unlike traditional Basmati varieties, Pusa 1121 requires less curing time and rice from fresh harvest, elongates well during cooking.

Table 1. Morpho-agronomic characteristics of Pusa 1121

Character	Pusa 1121	Basmati 370	Taraori Basmati	Pusa Basmati 1
Plant height (cm)	110-120	160-175	160-175	95-100
Total duration (days)	140-145	145-150	155-160	130-135
Average yield (t/ha)	4.0	3.0	2.5	5.5
1000-grain weight (g)	27.50	19.50	22.60	20.00

In contrast, Pusa 1121 has a milled rice kernel length of 8 mm and elongation ratio of 2.7 during cooking. Also, Pusa 1121 makes a better parental material for generating mapping populations to identify and locate genes for linear kernel elongation (Singh *et al.*, 2002).

Reference

Singh VP, AK Singh, SS Atwal, M Joseph and T Mohapatra (2002) Pusa 1121: a rice line with exceptionally high cooked kernel elongation and Basmati quality. *IRRN* **27**: 25-26.

* *Communicated by Dr AK Singh, Member Secretary, Plant Germplasm Registration Committee*

PLANT GERMPLASM REGISTRATION NOTICE

Rice Germplasm from Andamans

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Black Burma Rice (INGR No. 01019, IC 296798)

Black Burma rice, *Oryza sativa* is a very tall (174.4 cm), traditional, indica cultivar grown in middle and south Andamans. It has been identified to be tolerant to aluminium toxicity and moderately tolerant to salinity. The cultivar flowers after 150 days and matures within 190 days. Each plant possesses lesser tillers (6.8) with an average of 5 panicles indicating moderate tillering capacity. The flag leaf area is 38.25 cm^2. Panicles are small (25.9 cm) with low spikelet sterility (25.35%). Average grain yield is 2.1 tons/ha. The grain length is around 9.7 mm, while the width is 3.85 mm with a length/width ratio of 2.52. The dehusked rice is creamy white in colour with a length/width ratio of 2.2. The grains possess opaque endosperm. On cooking the grain showed 6.67% elongation, and 2.22 times volume expansion. Alkali digestion value was found to be high with low amylose content and low gelatinisation temperature. Gel consistency value was scored as 3 with very soft texture on a scale of 0-9.

The genotype is found to be tolerant to sheath blight (caused by *Rhizoctonia solani*), bacterial leaf spots (caused by *Cercospora oryzae*), sheath rot (caused by *Xanthomonas campestris* pv. *oryzae*), and neck and leaf blight (caused by *Pyricularia oryzae*), and tolerant to leaf folder (*Cnaphalocrocis medinalis*), gundhi bug (*Leptocorisa oratoria*), while moderately tolerant to stem borer (*Scirphophaga incertulas* Walker) under field conditions.

It has violet coloured ligules with pink margin. It is specially suited for preparation of breakfast items. In Andamans it is used for *lasa* preparation (a local food item). It can be a source for improving nutritional quality, and tolerance to excess salt and aluminium toxicities.

Nona Rice (INGR No. 01020, IC 296799)

Nona is a traditional dwarf (66 cm) variety of rice, *Oryza sativa* grown in north, middle and south Andamans. It belongs to indica group. In was identified to be moderately tolerant to salinity and iron toxicities. The cultigen's flowers after 80 days and matures within 110 days. Each plant possesses moderate number of tillers (8) with an average number of 7 panicles indicating abundance of productive tillers. Panicles are small (20.0 cm) with test weight of 36.0 g. The average yield of the Nona rice is 1.5 tons/ha. The grains are bold with light brownish coloured husk. The endosperm of the grain was opaque with chalkiness at the centre. The grain elongates up to 33.4% and expands 1.87 times on cooking. The alkali digestion and gelatinisation temperature values were found to be intermediate with soft gel consistency.

The cultigen is moderately tolerant to bacterial leaf blight (*Xanthomonas campestris* pv. *oryzae*), bacterial leaf spot (*Cercospora oryzae*), *Helminthosporium* leaf spot and blast (*Pyricularia oryzae*), and tolerant to stem borer caused by *Scirphophaga incertulas* Walker.

Basmati Quality Cytoplasmic Male Sterile Rice

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PUSA 4A (INGR No. 01021, IC 296800)

PUSA 4A is a basmati type cytoplasmic male sterile line of paddy, *Oryza sativa* derived from IR 58025A/IET 10649 through back crossing and selection. The plant height is 95 cm with purple base. The grains possess ideal basmati characteristics and pollen grains are completely sterile. It is a semi-dwarf, high tillering type with dark green leaves and purple stigma with better exsertion. Number of spikelets are 175 per panicle. Days to 50 per cent flowering is between 95 to 100 and to maturity 135.

Registration of Chakuwa Paddy Germplasm

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The Chakuwa rice (*Oryza sativa*) germplasm collected from various parts of Assam are characterized by semi-glutinous endosperm. They can be used in preparation of instant rice.

Boga Chakuwa (INGR No. 02014; IC 342353)

Boga Chakuwa, a traditional landrace from Assam has high 1000-grain weight with long bold grains with an alkali spreading value of 6.0 and 16.74% of amylose. It was collected from Sibsagar district of Assam. The plant is tall with a height of 137 cm; average tillers/plant are eight and panicles/square meter are 167. It flowers in 120 days with intermediate panicle types, which are well exerted without awning; apiculus colour is purple with 1000-grain weight of 40 g. Kernel colour is white with a length of 6.8, width 3.1 mm and L/B ratio of 2.2. Hulling recovery is 68 and the milling recovery is 60.

Boka Chakuwa – 1 (INGR No. 02015; IC 342354)

Boka Chakuwa possesses red kernel and very low amylose content of 4.69% and alkali spreading value of 6.0. Geographically, it is distributed in Golaghat district. It is a tall type with plant height of 147 cm, an average of seven tillers/plant and 160 panicles/sq. m. It flowers within 120 days with intermediate panicles that are well-exerted and awnless. The apiculus colour is black. The kernel length is 5.56 mm with a width of 2.52 mm and L/B ratio of 2.21. Hulling recovery is 69%, milling recovery 65%, while the head rice recovery is 60%.

Saru Chakuwa (INGR No. 02016; IC 342359)

It is one of the landrace which has long bold grain with low to intermediate alkali spreading value of 3.5 and high amylose content (22.89%). It is a tall type with a plant height of 158 cm and on an average six tillers/plant and 165 panicles/sq. m. It flowers in 120 days with well-exerted intermediate panicles without an awn. The apiculus is purple in colour. The kernels are white with a length of 6.28 mm, width of 2.28 mm, L/B ratio of 2.76 and 1000-grain weight of 16 g. The hulling recovery is 66%, milling recovery 62% and head rice recovery 59%.

Kalamadani Chakuwa (INGR No. 02017; IC 342361)

It is the only long cylinder grain type among Chakuwa rice germplasm with an alkali spreading value of 7.0 and medium amylose content of 14.26%. It is a tall type with a plant height of 157 cm and an average of seven tillers/plant and 170 panicles/sq. m. It flowers in 120 days with well-exerted intermediate panicles without an awn. The apiculus is brown in colour. The kernels are white with a length of 7.44 mm, width of 2.08 mm, L/B ratio of 3.58 and 1000-grain weight of 20 g. The hulling recovery is 65%, milling recovery 60% and head rice recovery 55%.

Misimi Chakuwa (INGR No. 02018; IC 342367)

Misimi Chakuwa has red kernels with very low amylose content of 4.36% and an alkali spreading value of 7.0. It is cultivated in Sibsagar district of Assam. It is a tall type with a plant height of 159 cm and an average of eight tillers/plant and 190 panicles/sq. m. It flowers in 120 days with well-exerted intermediate panicles without an awn. The apiculus is black in colour. The kernels are black with a length of 5.66 mm, width of 2.72 mm, L/B ratio of 2.08 and 1000-grain weight of 28 g. The hulling recovery is 70%, milling recovery 65 per cent and head rice recovery 62%.

Nepali Chakuwa (INGR No. 02019; IC 342368)

Nepali Chakuwa is a traditional landrace grown in Assam. It has a high 1000-grain weight of 40 g with alkali spreading value of 7.0 and 13.75% of amylose content. However, the grains are short and bold. Nepali Chakuwa was collected from Golaghat district of Assam. It is a tall type with plant height of 160 cm. On an average, it has six tillers/plant and produces 175 panicles/sq. m. The panicle is of intermediate height, well-exerted without awns. Apiculus is straw coloured. The kernel length is 7.10 mm and the width 2.78 mm. with a L/B ratio of 2.56. The kernels are white in colour. Hulling recovery is 67%, milling recovery 63% and the head rice recovery is 59%.

Thermo-Sensitive Genic Male Sterile Rice

JP Singh, SC Mani, MP Pandey, Harpal Singh, Surendra Singh, Li Rongbai
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Two-line hybrid breeding system, utilizing thermo-sensitive genic male sterility (TGMS) is simpler and highly efficient for hybrid seed production and obtaining heterotic combinations than three-line hybrid breeding in rice, *Oryza sativa*. TGMS line should combine important features of low critical temperature for fertility transformation and high critical temperature for sterility induction. To achieve this the G B Pant University of Agriculture and Technology, Pantnagar developed two TGMS lines viz., UPRI 95-140 TGMS and UPRI 95-167 TGMS.

UPRI 95-140 TGMS (INGR No. 01022, IC 296801)

UPRI 95-140 TGMS is a spontaneous thermo-sensitive genic male sterile line identified from UPRI 95-140. It was a single plant selection. The plants are semi-dwarf (72 cm), early maturing (107 days from seed to seed) with purple base and narrow erect flag leaves. The plants are vigorous and have high tillering capacity. The panicles are fully exserted and awnless. The grains are long and slender. UPRI 95-140 TGMS expresses thermo-sensitive reaction with male fertility. The average thermo-sensitive temperature for complete sterility is 27.1^0C in dry season (DS) to 28.7^0C wet season (WS) and 21.8^0C in DS to 26.2^0C in WS under northwestern Indian conditions. Optimum spikelet fertility is more than 40% and the period of complete male sterility is 104 days (May-Sept). These features are desirable for two-line hybrid rice breeding programme.

UPRI 95-167 TGMS (INGR No. 01023, IC 296802)

UPRI 95-167 TGMS has been developed from *in vitro* non-pollinated F_1 ovary culture of the cross between UPRI 95-140 TGMS and UPRI 95-117. The plant type is semi-dwarf (73 cm), early maturing type (107 days from seed to seed) with good panicle and stigma exsertion and long slender grains. It transforms from complete sterility to fertility between an average temperature of 24.2 and 28.7^0C respectively during late wet season, while transformation of fertility to complete sterility occurs at mean minimum or average temperatures of 18.2^0C and 26.5^0C respectively during dry season. UPRI 95-167 TGMS has stable and long male sterility stage between May 1 to September 5, suitable for hybrid development in early wet season and partial line multiplication during dry season and late wet season. It is an ideal TGMS line of commercial potential for two lines hybrid development.

Moth Bean Germplasm

D Kumar
Central Arid Zone Research Institute (CAZRI), Jodhpur-342 003 (Rajasthan)

CZM-32 (INGR No. 01024, IC 296803)

CZM-32 is a mutant of moth bean *Vigna aconitifolia* (Jacq.) Marechal variety Jadia, developed by treating seeds with 30 kR Co^{60} gamma ray. The mutant was isolated in M_3 generation during 1992 at CAZRI, Jodhpur. The mutant exhibited higher drought tolerance potential in terms of maintaining high y plant (-1.50) than RMO-40 and Maru Moth-1 (-1.35 and 1.30 y plant, respectively) at 9th day of water stress (Garg *et al.*, 2001). CZM-32 has erect and upright growth behaviour, early partitioning (28-30 days) and maturity (58-60 days). It has higher productivity per day (10.3 g day^{-1}) than the parental line (4.5 g day^{-1}). In All India Co-ordinated trials during *Kharif* seasons of 1995 and 1996, it yielded 450 kg ha^{-1} retaining green foliage till maturity, making it, suitable both for grain and fodder. Due to early maturity it can escape yellow mosaic virus.

Two-year evaluation of 3 moth bean genotypes, including CZM-32, Maru Moth-1 and RMO-40 under rainfed conditions at CAZRI confirmed higher grain and fodder yield (Anonymous, 1997). This was attributed to better utilization of available soil moisture and nutrient, leading to higher photosynthetic efficiency and better leaf metabolism. Also, the mutant requires lesser macro-

Registration of a New Wheat Plant Type, DL 1266-5 (INGR No. 02002; IC 296889)

SS Singh, DN Sharma, Nanak Chand and JB Sharma
Division of Genetics, Indian Agricultural Research Institute, New Delhi-110 012

The genotype DL 1266-5 of wheat (*Triticum aestivum*) represents a new plant type of wheat for increased yield potential. The new plant architecture has been designed through hybridization of released wheat variety Vaishali with local wheat, Sirsa Farm Wheat (SFW) which has characteristic features *viz.*, very few tillers with long and lax spike and spikelet number ranging between 23 to 26 with shrivelled grains. This local germplasm is also susceptible to major wheat diseases.

The new plant type DL-1266-5 possesses dark green broad leaves, thick stem, no unproductive tillers, higher biomass, bold and very long ear heads, high 1000-grain weight, high grain number/ear and genes (*Lr 24/Sr 24*) conferring resistance to leaf and stem rust. It possesses on an average 100 grains/ear with an ear weight of 5.56 g, while 1000-grains weight is 55 g. This indicates that the negative correlation between grain weight and grain number/ear has been broken with optimum tillering capacity. The genotype contains around 13% protein, which further suggests the breakdown of negative correlation between higher grain weight and protein percentage.

Evaluation results indicate that physiological efficiency in terms of post anthesis source-sink relationship in this genotype has been achieved. DL 1266-5 is resistant to leaf and stem rusts, derived from *Agropyron elongatum* (*Lr 24/Sr 24*) of which *Lr 24* is highly effective in the Indian sub-continent.

Registration of Multiple Resistant Barley Germplasm

Dalvir Singh, VS Malik, Krishan Kumar and MS Beniwal
CCS Haryana Agricultural University, Hisar-125 004 (Haryana)

BH 462 (INGR No. 02023; IC 335830)

BH 462 is a six-rowed, multiple disease resistant line of spring barley (*Hordeum vulgare*). It was developed at the Chaudhary Charan Singh Haryana Agricultural University, Hisar, through single plant selection in Arizona 5908/ATHS//LIGNEE 640. BH 462 is a multiple resistant line with resistance to yellow rust (*Puccinia striiformis hordei*), brown rust (*Puccinia hordei*), black rust (*Puccinia graminis tritici*) and blights *i.e.* spot blotch (*Pyrenophora sativum*) and net blotch (*Pyrenophora teres*). Tests for resistance to these diseases were conducted in the National Barley Disease Screening Nursery (NBDSN)/ Elite Barley Disease Screening Nursery (EBDSN) under Barley Network Programme during 1998-99 and results are reported in Barley Network Progress Report 1998-99 and Annual Report 1999-2000 of the Directorate of Wheat Research, Karnal.

BH 462 has erect growth habit, medium plant height (90 cm), medium-sized light green leaves, long parallel lax spikes with rough awns, early maturity, light blue hulled oval grains and 1000-grain weight of 38 g.

BH 490 (INGR No. 02024; IC 335831)

BH 490, is another six-rowed, multiple disease resistant line of spring barley (*Hordeum vulgare*) developed at the Chaudhary Charan Singh Haryana Agricultural University, Hisar, through pedigree selection method from single cross BH 87/ Ratna. It has multiple resistance to all the three rusts of barley *i.e.* yellow (*Puccinia striiformis hordei*), brown (*Puccinia hordei*) and black (*Puccinia graminis tritici*). Testing for resistance to rusts was conducted in the National Barley Disease Screening Nursery (NBDSN)/Elite Barley Disease Screening Nursery (EBDSN) under the Barley Network Programme during 1998-99 and results are reported in Barley Network Progress Report 1998-99 and Annual Report 1999-2000 of the Directorate of Wheat Research, Karnal.

BH 490 has semi-erect growth habit, medium plant height (90 cm), narrow, light green leaves, long parallel spikes with smooth awns, medium maturity and yellow hulled elongated grains having 1000-grain weight of 45 g.

References

Anonymous (1999) Barley Network (Indian Council of Agricultural Research) Progress Report 1998-99, Directorate of Wheat Research, Karnal, pp 3, 11,14 &17.

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nutrients compared to spreading and late type checks (GMO-9102 and GMO-9103) and more or less the same or higher in comparison to erect but late type mutants in unfertilised rainfed arid lands (Table 1); depicting better nutritional partition towards sinks (Kumar, 1996). CZM-32, therefore, is a good example of fine source-sink relation in terms of nutritional partitioning and higher productivity.

Table 1. Nutrient requirement for one kg seed of moth bean (Kharif 1996 CAZRI, Jodhpur)

Group	Strains	N	P	K	Ca (mg g^{-1})	Mg	Cu	Fe	Mn (m g^{-1})	Zn
Spreading	GMO-9102	2.69	0.09	0.91	1.07	0.56	1.01	42.48	4.63	3.58
and late	GMO-9103	1.34	0.08	0.23	0.27	0.09	2.48	22.79	1.93	0.96
	Mean	**2.01**	**0.09**	**0.57**	**0.67**	**0.33**	**1.75**	**32.64**	**3.28**	**2.27**
Erect and	CZM-32 E	0.38	0.03	0.28	0.16	0.22	0.40	3.69	1.37	1.51
early	CZM-18 E	0.24	0.03	0.30	0.36	0.05	0.48	18.33	1.44	2.43
	Mean	**0.31**	**0.03**	**0.29**	**0.26**	**0.14**	**0.44**	**11.01**	**1.41**	**1.97**
Erect, late,	CZM-225	1.12	0.09	0.65	0.84	0.18	1.1	39.92	9.01	4.75
unbranched	CZM-170	0.86	0.02	0.62	0.53	0.14	1.4	3.86	2.64	2.82
	Mean	**0.99**	**0.06**	**0.64**	**0.69**	**0.16**	**1.3**	**21.89**	**5.83**	**3.79**

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Cytoplasmic Genic Male Sterile Line and their Restorers in Pigeonpea

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Cytoplasmic Genic Male Sterile Line of Pigeonpea, GT 290A (INGR No. 01025, IC-296804)

GT 290A is the second stable cytoplasmic genic male sterile line of pigeonpea, *Cajanus cajan* developed at S.K. Nagar. It has been developed from a cross between *C. scarabaeoides* x *C. cajan,* wherein F_2 was back-crossed with GT 100, followed by repeated back-crossing with GT 290 until BC_8 generation. The screening for restorer has resulted in identification of a restorer line designated as GT 290B.

Morphologically, it has determinate growth habit with plant height ranging from 115-130 cm. It matures between 140 to 150 days and produces pods in bunch with an average of 150-180 pods per plant. The pods are 4 to 5 cm long, green in colour with black strip, while the seeds are red. Average number of seeds per pod is 4, and 100 seed weight is 10 g.

Fertility Restorer, GTR-3 (INGR No. 01026, IC 296805) for GT 288A

GTR-3 is a fertility restorer line identified for a stable cytoplasmic genic male sterile line GT 288A. It is a selection from SKNP-9902 and can be used for developing commercial hybrids.

Morphologically, it has non-determinate growth habit with plant height ranging from 140-150 cm. It matures between 130 to 140 days and produces pods in scattered fashion with an average of 162-180 pods per plant. The pods are 5 to 6 cm long and green in colour, while the seeds are white in colour. Average number of seeds per pod is 4, and 100 seed weight is 10 g.

Fertility Restorer, GTR-4 (INGR No. 01027, IC 296806) for GT 288A

GTR-4 is a fertility restorer line of stable cytoplasmic genic male sterile line GT 288A. It is a selection from SKNP-9813.

Registration of a New Wheat Plant Type, DL 1266-5 (INGR No. 02002; IC 296889)

SS Singh, DN Sharma, Nanak Chand and JB Sharma
Division of Genetics, Indian Agricultural Research Institute, New Delhi-110 012

The genotype DL 1266-5 of wheat (*Triticum aestivum*) represents a new plant type of wheat for increased yield potential. The new plant architecture has been designed through hybridization of released wheat variety Vaishali with local wheat, Sirsa Farm Wheat (SFW) which has characteristic features *viz.*, very few tillers with long and lax spike and spikelet number ranging between 23 to 26 with shrivelled grains. This local germplasm is also susceptible to major wheat diseases.

The new plant type DL-1266-5 possesses dark green broad leaves, thick stem, no unproductive tillers, higher biomass, bold and very long ear heads, high 1000-grain weight, high grain number/ear and genes (*Lr 24/Sr 24*) conferring resistance to leaf and stem rust. It possesses on an average 100 grains/ear with an ear weight of 5.56 g, while 1000-grains weight is 55 g. This indicates that the negative correlation between grain weight and grain number/ear has been broken with optimum tillering capacity. The genotype contains around 13% protein, which further suggests the breakdown of negative correlation between higher grain weight and protein percentage.

Evaluation results indicate that physiological efficiency in terms of post anthesis source-sink relationship in this genotype has been achieved. DL 1266-5 is resistant to leaf and stem rusts, derived from *Agropyron elongatum* (*Lr 24/Sr 24*) of which *Lr 24* is highly effective in the Indian sub-continent.

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Dalvir Singh, VS Malik, Krishan Kumar and MS Beniwal
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BH 462 has erect growth habit, medium plant height (90 cm), medium-sized light green leaves, long parallel lax spikes with rough awns, early maturity, light blue hulled oval grains and 1000-grain weight of 38 g.

BH 490 (INGR No. 02024; IC 335831)

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BH 490 has semi-erect growth habit, medium plant height (90 cm), narrow, light green leaves, long parallel spikes with smooth awns, medium maturity and yellow hulled elongated grains having 1000-grain weight of 45 g.

References

Anonymous (1999) Barley Network (Indian Council of Agricultural Research) Progress Report 1998-99, Directorate of Wheat Research, Karnal, pp 3, 11,14 &17.

Anonymous (2000) Annual Report, Directorate of Wheat Research, (Indian Council of Agricultural Research) 1999-2000, Karnal, 74p.

Registration of Sorghum Germplasm (INGR No. 02022; EC No. 434430)

B Sarath Babu[1], HC Sharma[2], RDVJ Prasada Rao[1] and KS Varaprasad[1]

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The sorghum aphid, *Melanaphis sacchari* (Zehntner) is an important pest of sorghum (*Sorghum bicolor*) in several sorghum growing countries like Africa, America, Asia and Europe. Outbreaks of aphid populations are unpredictable and can result in 46 to 78% yield losses where insecticides are not used. The identification of resistant lines was undertaken at National Bureau of Plant Genetic Resources, Regional Station, Hyderabad and International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru. Nine accessions of sorghum germplasm imported for a different purpose from Indonesia, Thailand and China were sown in the post-entry quarantine isolation area. At maturity, three entries from Thailand *viz.*, EC 434430, EC 434431 and EC 434432 sown in the middle three blocks between the entries from Indonesia and China were found to be totally free from infestation by the yellow sugarcane aphid, *M. sacchari* and the sooty mould (*Capnodium* sp.). The honeydew secreted by aphids favours the development of sooty mould, which hinders photosynthesis by enveloping the green leaves leading to reduction in fodder quality and grain yield. The thick black sooty mould had completely covered the leaves of the other six entries from China (EC 434433, EC 434434 and EC 434435) and Indonesia (EC 434436, EC 434437 and EC 434438). The affected plants appeared to be burnt up in contrast to the unaffected plants from Thailand.

Aphid population on the susceptible entries covered the panicles and the tender shoots. While EC 434430, EC 434431 and EC 434432 were highly resistant to the yellow sugarcane aphid. The remaining six entries from China and Indonesia were susceptible or highly susceptible to aphid infestation ranging from 91.9 to 100%. Selections were made from the agronomically better performing entry EC 434430, multiplied for two seasons and the resistance was confirmed both under artificial and field conditions at two locations *viz.*, Patancheru in the Medak district and Rajendranagar in the Ranga Reddy district. The morpho-agronomic features of EC 434430 are listed in Table 1.

Table 1. Chief botanical and morpho-agronomical characters of sorghum germplasm

Character	Resistant entry EC 434430 (Registered)	Susceptible entry EC 434434
Early plant vigour	Good	Good
Total leaves	12	8.6
Leaf length (cm)	71.75	68.5
Leaf width (cm)	6.48	6.8
Leaf colour	Light green	Dark green
Leaf orientation	Drooping	Erect
Number of tillers	6.8	4.8
Earhead compactness	Loose	Compact
Earhead length (cm)	20.8	25.4
Earhead width (cm)	6.0	5.98
Earhead shape	Oblong	Oblong
Glume colour	Straw	Straw
Glume covering	Half grain covered	1/4th grain covered
Plant height (cm)	141.8	98.2
Grain colour	Chalky white	Brownish white
Grain shape	Spherical	Spherical
Grain length/height (mm)	4.5	4.6
Grain breadth/width (mm)	4.3	3.7
Grain thickness (mm)	2.97	2.5
100-seed weight (g)	3.64	3.13
Stay green	Senescence	Non-senescence
Presence of seed sub-coat	Absent	Absent
Biotic stress	Highly resistant to *Melanaphis sacchari*	Highly susceptible to *Melanaphis sacchari*

Distinct variability was observed in morpho-agronomic characters of resistant and susceptible genotypes. Tsumuki *et al.* (1995) reported that although leaf surface wax was similar among all varieties, the total sugar content and the free amino acid concentrations were slightly more in the aphid-resistant, than the susceptible types. Hagio (1992) classified six varieties as highly resistant and reported that resistance in the two varieties (PE 954 177 and Senkinshiro) may be conditioned by a dominant gene. Mote and Shahane (1994) reported that the varieties with greater height, greater distance between 2 leaves; smaller leaf angle and presence of waxy lamina were less susceptible to the aphid. EC 434430 matches with the traits attributed to the aphid resistant lines as described by Mote and Shahane (1994).

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Registration of Foxtail Millet Germplasm, GS 1953 (SIC 24) (INGR No. 02010; IC 296900)

A Seetharam, BTS Gowda, VR Shashidhar, BM Ramakrishna, M Krishnappa and KR Vasanth

All India Coordinated Small Millet Improvement Programme, University of Agricultural Science, GKVK, Bangalore- 560 065

The germplasm line, GS 1953 (SIC 24) of foxtail millet (*Setaria italica*) provides a new source of dwarfing gene. The dwarf differs from the normal tall types in having an altered constellation of characters. This unique germplasm was identified from the vast collection maintained at the National Active Germplasm Site for small millets in All India Coordinated Small Millet Improvement Programme, University of Agricultural Science, GKVK, Bangalore. It is a collection from Maharashtra.

One major recessive gene appears to be responsible for the dwarf growth habit (Dinesh Kumar *et al.*, 1992).

GS 1953 is stable over environments (Anon., 1989) and showed superiority for most of the agronomic attributes with performance comparable to any good tall variety. Its high yield and superior morphological frame makes it an ideal parent for hybridization with tall types for further genetic enhancement, particularly in breeding high yielding, non-lodging foxtail millets.

Table 1. Agronomic features of GS 1953 in comparison with standard tall checks

Genotypes	Plant height (cm)	Tillers/ plant	Leaves/ plant	Leaf area/m/ row (dm^2)	Dry matter m. row (kg)	Nodes on main tiller	Internodal length (cm)	Harvest index (%)	Grain yield (q/ha)
GS 1953	77.5	9	64	172.4	0.33	11	4.9	42	53.5
GPUS 9*	126.0	7	61	141.0	0.38	11	11.6	38	56.4
RS 118*	124.6	4	33	121.2	0.31	10	11.8	39	46.6

GS 1953 is significantly distinct in plant height, internode length and tillering potential. The reduced plant height was due to shorter internodal length, but not the number. Tillering potential was significantly higher resulting in more leaves and higher leaf area at anthesis besides enhanced harvest index compared to normal tall types (Table 1). The dwarf was insensitive to GA_3 application indicating that GA_3 synthesis was not impaired.

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nutrients compared to spreading and late type checks (GMO-9102 and GMO-9103) and more or less the same or higher in comparison to erect but late type mutants in unfertilised rainfed arid lands (Table 1); depicting better nutritional partition towards sinks (Kumar, 1996). CZM-32, therefore, is a good example of fine source-sink relation in terms of nutritional partitioning and higher productivity.

Table 1. Nutrient requirement for one kg seed of moth bean (Kharif 1996 CAZRI, Jodhpur)

Group	Strains	N	P	K	Ca (mg g^{-1})	Mg	Cu	Fe	Mn (m g^{-1})	Zn
Spreading	GMO-9102	2.69	0.09	0.91	1.07	0.56	1.01	42.48	4.63	3.58
and late	GMO-9103	1.34	0.08	0.23	0.27	0.09	2.48	22.79	1.93	0.96
	Mean	**2.01**	**0.09**	**0.57**	**0.67**	**0.33**	**1.75**	**32.64**	**3.28**	**2.27**
Erect and	CZM-32 E	0.38	0.03	0.28	0.16	0.22	0.40	3.69	1.37	1.51
early	CZM-18 E	0.24	0.03	0.30	0.36	0.05	0.48	18.33	1.44	2.43
	Mean	**0.31**	**0.03**	**0.29**	**0.26**	**0.14**	**0.44**	**11.01**	**1.41**	**1.97**
Erect, late,	CZM-225	1.12	0.09	0.65	0.84	0.18	1.1	39.92	9.01	4.75
unbranched	CZM-170	0.86	0.02	0.62	0.53	0.14	1.4	3.86	2.64	2.82
	Mean	**0.99**	**0.06**	**0.64**	**0.69**	**0.16**	**1.3**	**21.89**	**5.83**	**3.79**

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Cytoplasmic Genic Male Sterile Line and their Restorers in Pigeonpea

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Main Pulses Research Station, Gujarat Agricultural University, Sardar Krushinagar-385 506 (Gujarat)

Cytoplasmic Genic Male Sterile Line of Pigeonpea, GT 290A (INGR No. 01025, IC-296804)

GT 290A is the second stable cytoplasmic genic male sterile line of pigeonpea, *Cajanus cajan* developed at S.K. Nagar. It has been developed from a cross between *C. scarabaeoides* x *C. cajan,* wherein F_2 was back-crossed with GT 100, followed by repeated back-crossing with GT 290 until BC_8 generation. The screening for restorer has resulted in identification of a restorer line designated as GT 290B.

Morphologically, it has determinate growth habit with plant height ranging from 115-130 cm. It matures between 140 to 150 days and produces pods in bunch with an average of 150-180 pods per plant. The pods are 4 to 5 cm long, green in colour with black strip, while the seeds are red. Average number of seeds per pod is 4, and 100 seed weight is 10 g.

Fertility Restorer, GTR-3 (INGR No. 01026, IC 296805) for GT 288A

GTR-3 is a fertility restorer line identified for a stable cytoplasmic genic male sterile line GT 288A. It is a selection from SKNP-9902 and can be used for developing commercial hybrids.

Morphologically, it has non-determinate growth habit with plant height ranging from 140-150 cm. It matures between 130 to 140 days and produces pods in scattered fashion with an average of 162-180 pods per plant. The pods are 5 to 6 cm long and green in colour, while the seeds are white in colour. Average number of seeds per pod is 4, and 100 seed weight is 10 g.

Fertility Restorer, GTR-4 (INGR No. 01027, IC 296806) for GT 288A

GTR-4 is a fertility restorer line of stable cytoplasmic genic male sterile line GT 288A. It is a selection from SKNP-9813.

Morphologically, it has non-determinate growth habit with plant height ranging from 130-150 cm. It matures between 120 to 140 days and produces pods in scattered fashion with an average of 150-160 pods per plant. The pods are 6 to 7 cm long and green in colour, while the seeds are red in colour. Average number of seeds per pod is 5, and the 100 seed weight is 10.5 g.

Fertility Restorer, GTR-5 (INGR No. 01028, IC 296807) for GT 288A

GTR-5 is a fertility restorer line of stable cyptoplasmic genic male sterile line GT 288A. It has been developed from cross *C. scarabaeoides* x *C. cajan* followed by back-crossing of F_2 progenies with ICPL- 87119 until BC_6 generation.

Morphologically, it has non-determinate growth habit with plant height ranging from 140-150 cm. It matures between 160 to 180 days and produces pods in scattered fashion with an average of 170-180 pods per plant. The pods are 5 to 6 cm long and green in colour with black strips, while the seeds are red in colour. Average number of seeds per pod is 4, and 100 seed weight is 10 g.

Fertility Restorer, GTR-6 (INGR No. 01029, IC 296808) for GT 288A

GTR-6 is a fertility restorer line of stable cytoplasmic genic male sterile line GT 288A. It has been developed from cross *C. scarabaeoides* x *C. cajan* followed by back crossing of F_2 progenies with GT-100 and further back-crossing with GUT 88-9 until BC_8 generation.

Morphologically, it has non-determinate growth habit with plant height ranging from 170-180 cm. It matures between 150 to 160 days and produces pods in scattered fashion with an average of 180-200 pods per plant. The pods are 5 to 6 cm long and green in colour with dark strips, while the seeds are white in colour. Average number of seeds per pod is 4, and 100 seed weight is 8.5 g.

Fertility Restorer, GTR-2 (INGR No. 01030, IC 296809) for GT 288A

GTR-2 is a fertility restorer line of stable cytoplasmic genic male sterile line GT 288A. It has been developed from cross *C. scarabaeoides x C. cajan* followed by back crossing of F_2 progenies with QMS-2 until BC_8 generation.

Morphologically, it has non-determinate growth habit with plant height ranging from 125-140 cm. It matures between 160 to 180 days and produces pods in scattered fashion with an average of 170-180 pods per plant. The pods are 5 to 6 cm long and green in colour with black strips, while the seeds are brown in colour. Average number of seeds per pod is 4, and 100 seed weight is 9.5 g.

Foliar Disease Resistant Spanish Bunch, Derived from Interspecific Derivative of Groundnut

MVC Gowda, BN Motagi, GK Naidu, R Sheshagiri and SB Diddimani
Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwar (Karnataka)

GPBD 4 (INGR No. 01031, IC 296810)

GPBD 4 (D39d), (*Arachis hypogaea* L. Subsp. *hypogaea* var. *fastigiata*), is an improved Spanish bunch line resistant to late leaf spot [*Phaeoisariopsis personata* (Berk. & M. A. Curtis) Deighton] and rust (*Puccinia arachidis* Speg.). It was developed at the Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad. It scores 3.0 and 4.0 for rust and late leaf spot respectively on a 0-9 scale, compared to 8.0 and 9.0 for JL 24, a susceptible check at Dharwad. GPBD 4 is derived from a cross between KRG 1 (selection from cultivar Argentine), an early maturing, Spanish bunch and an interspecific derivative, CS16 (ICGV 86855) involving wild *Arachis* species, *A. cardenasii*, a virginia bunch foliar disease resistant interspecific derivative developed at International Crops Research Institute for Semi-Arid Tropics (ICRISAT). GPBD 4 was developed by pedigree selection method in F_2 generation.

GPBD 4 has erect growth habit and sequential branching with medium sized wide-elliptical dark green leaves (IBPGR and ICRISAT, 1992). On an average

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GPBD 4 has erect growth habit and sequential branching with medium sized wide-elliptical dark green leaves (IBPGR and ICRISAT, 1992). On an average

it has four primary and two secondary branches and matures between 100-110 days. It has medium sized pods (22.3 and 8.9 mm average pod length and width) with slight reticulation and beak, and moderate constriction. The majority of pods are two-seeded with few one-seeded with an average shelling out-turn of 76%. The seeds are tan in colour with 100 seed weight of 42 g. The seeds contain 48% oil with a 1.76 oleic/ linoleic acid ratio (Motagi et al. 2000c). In trials conducted at three locations in northern transitional tract of Karnataka during the 1998, 1999 and 2000, crop seasons, GPBD 4 out-yielded the national check variety JL 24 for pod (16.0%), kernel (18.0%), oil (18.75%) and fodder (19.2%) yield (Motagi et al. 2001 and 2000a).

Further, it was also found free from early leaf spot (*Cercospora arachidicola* S. Hori) and moderately efficient in iron absorption efficiency (Motagi *et al.* 2000b).

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Iron-chlorosis Tolerant Groundnut Line

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PBS-24004 (INGR No. 01032, IC 296811)

PBS 24004, is a high yielding elite groundnut, *Arachis hypogaea* L. subsp. *hypogaea* var. *hypogaea* germplasm line with tolerance to lime induced iron-deficiency. Screening for iron-chlorosis tolerance along with resistant and susceptible checks in calcareous soil having soil pH of 7.9, 29.6 per cent calcium carbonate, 6 ppm available P and 1.35 ppm available Fe at National Research Centre for Groundnut, Junagadh during summer 1999 resulted in identification of PBS 24004. The comparative data on visual chlorotic rating (VCR) on a 1 to 5 scale (1=tolerant and 5=susceptible) is given in the Table.

It was developed from a cross between Latur 33 and Tifrun, using combination of pedigree and bulk method. Tifrun (ICG 9937) is a released variety from USA belonging to *A. hypogaea* L. subsp. *hypogaea* var. *hypogaea*. Early generation were handled through pedigree selection and later generations through bulk method. From F_5 bulk, green plants were tagged, grouped and bulked based on similar plant type, pod, maturity and reaction to iron chlorosis. In subsequent generations similar process was followed until F_8 resulting in development of a stable, uniform advanced breeding culture, PBS 24004.

PBS 24004 has a decumbent–3 growth habit (IBPGR and ICRISAT 1992), alternate branching, with medium-sized, oblong, dark green leaves with acute leaf tip and moderate pubescence. It has six primary and 6-8 secondary branches. It matures in 115-120 days in the rainy season and 110-115 days in summer season. The pods are slightly reticulated, constricted and beaked. The average length and width of pod was 25 and 11 mm, respectively. The pods are mostly two-seeded with

Table 1. Visual chlorotic rating (VCR), chlorophyll a (Chl a) and total chlorophyll content (mg/g on dry weight basis) and pod yield of PBS 24004 compared checks

Culture name	VCR	Chl a (mg/g dwt)	Total chl (mg/g dwt)	Pod yield (g/plant)
PBS 24004	1.25	6.42	8.55	11.26
I_1 (tolerant check)	1.00	7.67	9.86	9.31
VRI 3 (susceptible check)	3.16	4.06	5.24	6.79

it has four primary and two secondary branches and matures between 100-110 days. It has medium sized pods (22.3 and 8.9 mm average pod length and width) with slight reticulation and beak, and moderate constriction. The majority of pods are two-seeded with few one-seeded with an average shelling out-turn of 76%. The seeds are tan in colour with 100 seed weight of 42 g. The seeds contain 48% oil with a 1.76 oleic/ linoleic acid ratio (Motagi et al. 2000c). In trials conducted at three locations in northern transitional tract of Karnataka during the 1998, 1999 and 2000, crop seasons, GPBD 4 out-yielded the national check variety JL 24 for pod (16.0%), kernel (18.0%), oil (18.75%) and fodder (19.2%) yield (Motagi et al. 2001 and 2000a).

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National Research Centre for Groundnut, Ivnagar Road, P. O. Box. 5, Junagadh-362 001 (Gujarat)

PBS-24004 (INGR No. 01032, IC 296811)

PBS 24004, is a high yielding elite groundnut, *Arachis hypogaea* L. subsp. *hypogaea* var. *hypogaea* germplasm line with tolerance to lime induced iron-deficiency. Screening for iron-chlorosis tolerance along with resistant and susceptible checks in calcareous soil having soil pH of 7.9, 29.6 per cent calcium carbonate, 6 ppm available P and 1.35 ppm available Fe at National Research Centre for Groundnut, Junagadh during summer 1999 resulted in identification of PBS 24004. The comparative data on visual chlorotic rating (VCR) on a 1 to 5 scale (1=tolerant and 5=susceptible) is given in the Table.

It was developed from a cross between Latur 33 and Tifrun, using combination of pedigree and bulk method. Tifrun (ICG 9937) is a released variety from USA belonging to *A. hypogaea* L. subsp. *hypogaea* var. *hypogaea*. Early generation were handled through pedigree selection and later generations through bulk method. From F_5 bulk, green plants were tagged, grouped and bulked based on similar plant type, pod, maturity and reaction to iron chlorosis. In subsequent generations similar process was followed until F_8 resulting in development of a stable, uniform advanced breeding culture, PBS 24004.

PBS 24004 has a decumbent–3 growth habit (IBPGR and ICRISAT 1992), alternate branching, with medium-sized, oblong, dark green leaves with acute leaf tip and moderate pubescence. It has six primary and 6-8 secondary branches. It matures in 115-120 days in the rainy season and 110-115 days in summer season. The pods are slightly reticulated, constricted and beaked. The average length and width of pod was 25 and 11 mm, respectively. The pods are mostly two-seeded with

Table 1. Visual chlorotic rating (VCR), chlorophyll a (Chl a) and total chlorophyll content (mg/g on dry weight basis) and pod yield of PBS 24004 compared checks

Culture name	VCR	Chl a (mg/g dwt)	Total chl (mg/g dwt)	Pod yield (g/plant)
PBS 24004	1.25	6.42	8.55	11.26
I_1 (tolerant check)	1.00	7.67	9.86	9.31
VRI 3 (susceptible check)	3.16	4.06	5.24	6.79

average shelling of 67%. The average length and width of seed was 13.3 and 7.6 mm, respectively. The seeds are tan coloured with average 100-seed weight of 67g. The seeds contain 49.6% oil and 18.2% protein.

Also, PBS 24004 is moderately resistant to early leaf spot (*Cercospora arachidicola* Hori) and rust (*Puccinia arachidis* Spegazzini) and scores 5.0 and 5.1 respectively on 1-9 scale under field conditions.

References

IBPGR and ICRISAT (1992) Descriptors for groundnut, IBPGR, Rome, Italy and ICRISAT, Patancheru, India 22p.

Narrow Leaf Mutant of Groundnut

RK Mathur, P Manivel, MY Samdur and A Bandyopadhyay
National Research Centre for Groundnut, Ivnagar Road, P.O. Box 5, Junagadh-362 001 (Gujarat)

Girnar 1 nlm (INGR No. 01033, IC 296812)

Girnar 1 nlm (PBS 30008) is a small narrow leaved groundnut, *Arachis hypogaea* L. ssp. *hypogaea* var. *hypogaea* mutant. This mutant was identified in M_2 generation of ethyl methane sulphonate (EMS) and diethyl sulphonate (DES) treated Spanish bunch groundnut cultivar, Girnar 1, *Arachis hypogaea* sub-species *fastigiata* var. *vulgaris* at National Research Centre for Groundnut, Junagadh. The mutant bred true in subsquent M_3 and M_4 generations and was designated as Girnar 1 nlm. The first four leaves are normal and the narrow leaflet character is manifested at fifth or sixth leaf stage of initial growth.

The genetics of narrow leaf trait was studied in F_1 and F_2 of the cross between Girnar 1 nlm and Girnar 1. In F_1 generation, all plants were similar to Girnar 1. In F_2 generation 189 plants had normal leaf and 66 had narrow leaf, fitting in the segregation ratio of 3 normal: 1 narrow leaf (c^2 value = 0.11 with P value ranging between 0.7 and 0.8). This indicated that a single recessive gene governs the narrow leaf character. The gene symbols for this character could be $\mathbf{I^N I^N}$ for normal leaf and $\mathbf{I^n I^n}$ for narrow leaf.

Girnar 1 nlm has erect growth habit (IBPGR and ICRISAT, 1992), alternate branching, and small sized linear lanceolate leaves with moderate pubescence. It has 5-6 primary and 6-8 secondary branches. It matures in 90-95 days in the rainy season in Junagadh, Gujarat, India. The pods are mostly three-seeded with shelling out turn of 64%. The pods have slight constriction, moderate reticulation and medium beak. The seeds are tan coloured with 100 seed weight 20 g, containing 49.6% oil. Compared to the parent, the narrow leaf mutant is dwarf with shorter internodes and more branching and peculiar small, narrow and pointed leaflets. Girnar 1 has Spanish, *Arachis hypogaea* ssp *fastigiata* var. *vulgaris* growth habit, while the mutant has a shift towards Virginia bunch growth habit, *Arachis hypogaea* ssp. *hypogaea* var. *hypogaea* (Table). The mutant is early in maturing, has low specific leaf area (SLA) and is moderately resistant to rust (*Puccinia arachidis*).

References

IBPGR and ICRISAT 1992. Descriptors for Groundnut, IBPGR, Rome Italy, and ICRISAT, Patancheru, India.

Table 1. Salient features of the Girnar 1 nlm mutant and its parent Girnar 1

Salient Characteristics	Girnar 1 nlm	Girnar 1
Growth habit	Virginia bunch	Spanish
Flowering habit	Alternate	Sequential
Height of main axis (cm)	9.30	15.30
Maximum branch height (cm)	10.90	20.30
Number of primary branches	4.00	4.07
Number of secondary branches	7.00	1.30
Number of nodes on main axis	9.90	9.90
Number of leaves per plant	80.00	43.00
Inter-nodal length (cm)	0.94	1.55
Leaflet length (cm)	2.00	3.50
Leaflet width (cm)	0.73	1.70
Petiole length (cm)	2.20	4.40
Specific leaf area (cm^2)	53.18	96.38
Days to maturity	90 days	100 days
Number of pods/plant	7.00	15.33
Number of seeds/plant	10.13	28.47
Pod length (cm)	1.20	3.20
Pod weight/plant (g)	2.86	10.39
Seed weight/plant (g)	1.77	6.05
100 seed weight (g)	20.00	29.00
Shelling out turn (%)	64.00	68.00

Registration of Chickpea Germplasm, H 96-99 (INGR No. 02003; IC 296887)

VS Lather[1], RS Waldia[2], Ram Kumar Yadav[1], IS Solanki[1], RK Choudhary[1] and BS Dahiya[1]
[1]*Chaudhary Charan Singh, Haryana Agricultural University, Hisar-125004 (Haryana)*
[2]*KVK Jagdishpur, Sonepat (Haryana)*

The ideotype approach has been suggested to overcome genetic limits of productivity in chickpea (*Cicer arietinum*). Based on this concept, a spontaneous brachytic mutant with erectness and compactness for higher plant density suited to rice-chickpea or cotton-chickpea sequential cropping system has been identified at Chaudhary Charan Singh Haryana Agricultural University, Hisar. The mutants are erect and compact in growth habit (for higher plant density), with strong and reasonably tall stem (for better competition with weeds and resistance to lodging), few but erect secondary and later order branches (for better interception of light). H 96-99 is one of these lines recording comparable seed yield against check varieties at normal density, while showing significant seed yield superiority under high density planting of 50 plants/ m^2 (Table 1). This chickpea ideotype is also found suitable for mechanical harvesting as the fruiting zone starts at about 20 cm from the base.

References

Lather VS (2000) Promising chickpea ideotype for higher plant density. *International Chickpea Newslet.* **7**: 26.

Table 1. Performance of lines developed on ideotype approach for higher density planting

	Genotype				
Character	H96-99	H96-26	C 235 (Ch)	H86-18 (Ch)	CD at 5%
Plant height (cm)	81.13	69.93	46.98	68.87	
Number of primary branches	5.33	5.27	4.07	5.02	
Number of secondary branches	9.98	9,87	14.86	12.72	
Canopy spread (cm)	19.67	16.27	29.89	25.32	
Initiation of fruiting nod (cm)	22.60	23.47	28.87	27.97	
Number of pods/plant	69.92	63.27	58.82	52.56	
Number of seeds/pod	1.26	1.22	1.34	1.28	
Seed yield (kg/ha) normal density	2627.00	2421.00	2659.00	2460.00	261.52
Seed yield (kg/ha) higher density	3843.00	3981.00	3033.00	2870.00	197.48

CD (5%) for comparing seed yield means of plant densities x genotypes: 792.91 kg/ha

Registration of Chickpea Germplasm, E100y (M) (INGR No. 02004; IC 296886)

BS Dahiya, VS Lather, IS Solanki and Ram Kumar
Department of Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar-125 004(Haryana)

The spontaneous mutant, E100Y (m) in chickpea (*Cicer arietinum*) with compact and erect plant type, resistance to *Ascochyta* blight and Grey mould diseases was identified at the Department of Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar.

E100Y (m) is a late germinator and takes 15-16 days for emergence as compared to 7-8 days by the parental line under field conditions. It has a thick and stout stem with thick and bluish green leaflets. Seeds are bold (32 g/100 seeds) and brown in colour. The length of stigma is also reduced compared to the parental line. Inheritance studies showed that a single recessive gene with pleiotropic effect governs the mutation. Other characteristics of E100Y (m) have been summarized in Table 1. This mutant has been found very useful in recombination breeding, particularly for transfer of compact plant type and resistance to *Ascochyta* blight to high yielding but susceptible cultivars, such as H208 and L550. The segregants from these crosses have been advanced to F_5 generation and those from the cross L550 x E100Y (m) having bold Kabuli seeds and resistance to blight, appear promising.

Table 1. Characteristic features of E100Y (m)

Character	E100Y (m)
Height (cm)	40.0
Primary branches	3
Secondary branches	10
Internode length (cm)	2.0
Leaf colour	Bluish green
Leaf area (sq. cm.)	31.8
Leaf surface	Glossy
Pod length (cm)	2.9
Pod breadth (cm)	1.3
Seeds/pod	1.0
Seed colour	Brown

Reference

Dahiya BS, VS Lather, IS Solanki and Ram Kumar (1984) Useful spontaneous mutants in chickpea (*Cicer arietinum* L.). *Curr. Sci.* **53**: 1210-1211.

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average shelling of 67%. The average length and width of seed was 13.3 and 7.6 mm, respectively. The seeds are tan coloured with average 100-seed weight of 67g. The seeds contain 49.6% oil and 18.2% protein.

Also, PBS 24004 is moderately resistant to early leaf spot (*Cercospora arachidicola* Hori) and rust (*Puccinia arachidis* Spegazzini) and scores 5.0 and 5.1 respectively on 1-9 scale under field conditions.

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RK Mathur, P Manivel, MY Samdur and A Bandyopadhyay
National Research Centre for Groundnut, Ivnagar Road, P.O. Box 5, Junagadh-362 001 (Gujarat)

Girnar 1 nlm (INGR No. 01033, IC 296812)

Girnar 1 nlm (PBS 30008) is a small narrow leaved groundnut, *Arachis hypogaea* L. ssp. *hypogaea* var. *hypogaea* mutant. This mutant was identified in M_2 generation of ethyl methane sulphonate (EMS) and diethyl sulphonate (DES) treated Spanish bunch groundnut cultivar, Girnar 1, *Arachis hypogaea* sub-species *fastigiata* var. *vulgaris* at National Research Centre for Groundnut, Junagadh. The mutant bred true in subsquent M_3 and M_4 generations and was designated as Girnar 1 nlm. The first four leaves are normal and the narrow leaflet character is manifested at fifth or sixth leaf stage of initial growth.

The genetics of narrow leaf trait was studied in F_1 and F_2 of the cross between Girnar 1 nlm and Girnar 1. In F_1 generation, all plants were similar to Girnar 1. In F_2 generation 189 plants had normal leaf and 66 had narrow leaf, fitting in the segregation ratio of 3 normal: 1 narrow leaf (c^2 value = 0.11 with P value ranging between 0.7 and 0.8). This indicated that a single recessive gene governs the narrow leaf character. The gene symbols for this character could be $\mathbf{I^N I^N}$ for normal leaf and $\mathbf{I^n I^n}$ for narrow leaf.

Girnar 1 nlm has erect growth habit (IBPGR and ICRISAT, 1992), alternate branching, and small sized linear lanceolate leaves with moderate pubescence. It has 5-6 primary and 6-8 secondary branches. It matures in 90-95 days in the rainy season in Junagadh, Gujarat, India. The pods are mostly three-seeded with shelling out turn of 64%. The pods have slight constriction, moderate reticulation and medium beak. The seeds are tan coloured with 100 seed weight 20 g, containing 49.6% oil. Compared to the parent, the narrow leaf mutant is dwarf with shorter internodes and more branching and peculiar small, narrow and pointed leaflets. Girnar 1 has Spanish, *Arachis hypogaea* ssp *fastigiata* var. *vulgaris* growth habit, while the mutant has a shift towards Virginia bunch growth habit, *Arachis hypogaea* ssp. *hypogaea* var. *hypogaea* (Table). The mutant is early in maturing, has low specific leaf area (SLA) and is moderately resistant to rust (*Puccinia arachidis*).

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Flowering habit	Alternate	Sequential
Height of main axis (cm)	9.30	15.30
Maximum branch height (cm)	10.90	20.30
Number of primary branches	4.00	4.07
Number of secondary branches	7.00	1.30
Number of nodes on main axis	9.90	9.90
Number of leaves per plant	80.00	43.00
Inter-nodal length (cm)	0.94	1.55
Leaflet length (cm)	2.00	3.50
Leaflet width (cm)	0.73	1.70
Petiole length (cm)	2.20	4.40
Specific leaf area (cm^2)	53.18	96.38
Days to maturity	90 days	100 days
Number of pods/plant	7.00	15.33
Number of seeds/plant	10.13	28.47
Pod length (cm)	1.20	3.20
Pod weight/plant (g)	2.86	10.39
Seed weight/plant (g)	1.77	6.05
100 seed weight (g)	20.00	29.00
Shelling out turn (%)	64.00	68.00

Registration of Lentil Germplasm

IS Solanki, RS Waldia and VP Singh
Department of Plant Breeding, Pulse Section, Chaudhary Charan Singh Haryana Agricultural University, Hisar-125 004 (Haryana)

LH 90-54 (INGR No. 02005; IC 296884)

LH-90-54 is a high-yielding, medium maturing, extra bold-seeded and disease resistant line of lentil (*Lens culinaris*) developed from the cross, K75 x L4076 through pedigree method of selection at the Department of Plant Breeding, Pulse Section, Chaudhary Charan Singh Haryana Agricultural University, Hisar. The plants of this line possess bright dark green coloured foliage and pinkish-red stem at the base. Its leaves are larger in size and the stem is thicker and stouter, making it resistant to lodging. It has large seeds that are light pale-green in colour with small black dots. The seeds possess 22.7% protein. Its hydration and swelling capacities are also higher providing better cooking quality.

LH-90-54 was evaluated in 11 coordinated varietal trials from 1993-94 to 1995-96 in North-west Plain Zone, where it recorded yield superiority of 10.9% over L4076 (check). The genotype is resistant to rust, root rot, *Botrytis* grey mould and *Ascochyta* blight, whereas it is tolerant to wilt. It is resistant to both the species of nematode *i.e. Meloidogyne incognita* and *M. javanica* and is tolerant to lentil pod borer. It is recommended for normal sown conditions, *i.e.* from 15 to 30th November for whole Haryana, except for southern districts. It is highly suitable for growing after paddy or cotton. It matures within 136 days.

LH-92-27 (INGR No. 02006; IC 296883)

LH-92-27 is an early maturing and high-yielding genotype of lentil (*Lens culinaris*) possessing multiple resistance to diseases and insect-pests. This genotype was developed from the cross, Ranjan x K75 through pedigree method of selection at the Department of Plant Breeding, Pulse Section, Chaudhary Charan Singh Haryana Agricultural University, Hisar. The plants of this genotype are tall (46 cm), semi-erect, possess dull green foliage and are tolerant to lodging. Its seeds are round with thickness at the centre. LH-92-27 has been evaluated in 12 coordinated varietal trials from 1994-95 to 1996-97 in North-west Plain Zone, recording yield superiority of 7.0% over DPL 15 (the best check), 8.0% over LH-84–8 and 17.0% over L 4076.

LH-92-27 is either at par or better than the existing checks in its reaction to different diseases like, rust, wilt and blight. It is resistant to both the species of nematode, *Meloidogyne incognita* and *M. javanica* and lentil pod borer. It matures in 132 days and may be suitable for growing in cotton/paddy-wheat rotation where its sowing can be done even up to December 15.

Registration of Wild Horsegram Germplasm (INGR No. 02007; IC 212722)

KS Negi[1], S Yadav[2], S Mandal[2] and DC Bhandari[1]
[1]*National Bureau of Plant Genetic Resources, Regional Station, Bhowali-236 132, Nainital (Uttranchal)*
[2]*National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012*

Horsegram, (*Macrotyloma uniflorum*) locally known as 'kulath', 'kulthi' or 'gahat' is cultivated in whole of the Uttranchal during rainy season. The related species *Macrotyloma sar-garhwalensis* (IC 212722) investigated in the present study is not yet consumed as a pulse. It grows in tropical and sub-temperate conditions of the Uttranchal on exposed grassy slopes, along the edge of crop fields associated with species of *Desmodium* and *Alysicarpus* as well as other shrubs.

The seeds of this species were procured from Prof. RD Gaur, Head, Department of Botany, HNB Garhwal University, Srinagar, Uttranchal, with collector number of GN-1882. This collection was made from village Sara, District Pauri, Uttranchal, at an altitude of 700 m and was multiplied at NBPGR Regional Station, Bhowali, for further characterization.

The species is an annual, erect, non-twining herb, 50-60 cm tall; leaves imparipinnate, pentafoliate, lanceolate with 6.5 cm long, sessile or sub-sessile and oblong leaflets; stipules large, 4-12 mm long and hairy on both surfaces; inflorescence axillary with short peduncle; flowers 1-2, 6-8 mm long; bracts obovate to lanceolate with acute apex; corolla blue included within the calyx, 5-7 mm long; stamens diadelphous (9+1), 5 mm long; pods compressed, shortly beaked, straw coloured becoming brown on ripening, 3.0-4.7 cm x 0.3 -0.7 cm in size,

Lemon Yellow Colour Leaf Mutant of Groundnut

RK Mathur, P Manivel, MY Samdur and A Bandyopadhyay
National Research Centre for Groundnut, P.O. Box 5, Junagadh-362 001 (Gujarat)

Girnar 1 Lym (INGR No. 01034, IC 296813)

Girnar 1 lym (PBS 30017), *Arachis hypogaea* L. spp. *hypogaea* var. *vulgaris* is a lemon yellow colour leaf groundnut mutant. This mutant was identified in M_2 generation progeny of a Spanish bunch groundnut cultivar, Girnar 1, whose seeds were treated with 0.10% ethyl methane sulphonate (EMS) at National Research Centre for Groundnut, Junagadh. The mutant bred true in subsequent M_3 and M_4 generations and was designated as Girnar 1 lym. The lemon yellow colour leaf started expressing from fourth to fifth leaf stage onwards and continued till maturity, resulting in lemon yellow appearance of the plant.

Based on F_2 generation segregation of the cross between Girnar 1 lym and Girnar 1, this trait appears to be governed by a monogenic recessive gene (Table 1). The gene symbols proposed are **Ly** for green and **ly** for lemon yellow.

Girnar 1 lym has erect growth habit (NBPGR and ICRISAT, 1992), sequential branching, and medium sized wide elliptic lemon yellow colour leaves. It has 6 primary and occasionally 1-2 secondary branches. It matures in 95 days in the rainy season at Junagadh, Gujarat, India. The pods are mostly three-seeded, with shelling out turn of 75%. The pods have slight constriction, moderate reticulation and medium beak. The seeds are tan colour with 100 seed weight of 37g and contain 47% oil and 13% protein. Based on field screening during two rainy seasons, Girnar 1 lym is moderately resistant/tolerant to early leaf-spot, late leaf-spot, and rust scoring 5 on 1-9 scale.

Table 1. F_2 segregation of lemon yellow leaf trait in cross, Girnar 1 lym x Girnar 1

Families	Number of F_2 phenotypes*			χ^2 (3:1 ratio)	Probability
	Normal green	Lemon yellow	Total		
1.	58	15	73	0.7717	0.5-0.3
2.	47	13	60	0.3556	0.7-0.5
3.	76	20	96	0.8889	0.5-0.3
4.	60	19	79	0.3890	0.9-0.8
5.	30	11	41	0.0732	0.8-0.7
6.	52	17	69	0.0048	0.95-0.9
Pooled	323	95	418	1.1515	0.3-0.2
Hetero-geneity	–	–		0.9806	0.95-0.90

*F_1 had normal green leaves like male parent, Girnar 1

Vegetable Type Soybean

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

P-1366 (INGR No. 01035, IC 296814)

P-1366 is a vegetable type bold seeded soybean, *Glycine max* L. Merr. collected during 1988 by Mr. KC Pant, NBPGR, Regional Station, Bhowali from Pithoragarh district of Uttar Pradesh (Now Uttaranchal). P-1366 has determinate growth habit with thick dark green leaves. The plant height is 30-35 cm at Bhowali and 35-40 cm at Akola. It has tawny pubescence with normal density and white flowers. It flowers between 32-34 days at Bhowali and 30-32 at Akola and matures between 105-108 days. It has thick brown pods containing 2-3 seeds/pod. The seeds are creamish yellow with black hilum and contain 20.13% oil and 40.20% protein on dry weight basis. It was evaluated at NBPGR, Regional Station, Akola, Maharashtra (1991-1997) and at Bhowali (1988-2000) for agronomic features. Grain yields of 18-22 q/ha with bold seeds were recorded. The seeds are sweet in taste and have no beany flavour during pod filling stage. Hundred seed weight is 44-46 g at Akola and 36-38 g at Bhowali.

Registration of Lentil Germplasm

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LH 90-54 (INGR No. 02005; IC 296884)

LH-90-54 is a high-yielding, medium maturing, extra bold-seeded and disease resistant line of lentil (*Lens culinaris*) developed from the cross, K75 x L4076 through pedigree method of selection at the Department of Plant Breeding, Pulse Section, Chaudhary Charan Singh Haryana Agricultural University, Hisar. The plants of this line possess bright dark green coloured foliage and pinkish-red stem at the base. Its leaves are larger in size and the stem is thicker and stouter, making it resistant to lodging. It has large seeds that are light pale-green in colour with small black dots. The seeds possess 22.7% protein. Its hydration and swelling capacities are also higher providing better cooking quality.

LH-90-54 was evaluated in 11 coordinated varietal trials from 1993-94 to 1995-96 in North-west Plain Zone, where it recorded yield superiority of 10.9% over L4076 (check). The genotype is resistant to rust, root rot, *Botrytis* grey mould and *Ascochyta* blight, whereas it is tolerant to wilt. It is resistant to both the species of nematode *i.e. Meloidogyne incognita* and *M. javanica* and is tolerant to lentil pod borer. It is recommended for normal sown conditions, *i.e.* from 15 to 30th November for whole Haryana, except for southern districts. It is highly suitable for growing after paddy or cotton. It matures within 136 days.

LH-92-27 (INGR No. 02006; IC 296883)

LH-92-27 is an early maturing and high-yielding genotype of lentil (*Lens culinaris*) possessing multiple resistance to diseases and insect-pests. This genotype was developed from the cross, Ranjan x K75 through pedigree method of selection at the Department of Plant Breeding, Pulse Section, Chaudhary Charan Singh Haryana Agricultural University, Hisar. The plants of this genotype are tall (46 cm), semi-erect, possess dull green foliage and are tolerant to lodging. Its seeds are round with thickness at the centre. LH-92-27 has been evaluated in 12 coordinated varietal trials from 1994-95 to 1996-97 in North-west Plain Zone, recording yield superiority of 7.0% over DPL 15 (the best check), 8.0% over LH-84–8 and 17.0% over L 4076.

LH-92-27 is either at par or better than the existing checks in its reaction to different diseases like, rust, wilt and blight. It is resistant to both the species of nematode, *Meloidogyne incognita* and *M. javanica* and lentil pod borer. It matures in 132 days and may be suitable for growing in cotton/paddy-wheat rotation where its sowing can be done even up to December 15.

Registration of Wild Horsegram Germplasm (INGR No. 02007; IC 212722)

KS Negi[1], S Yadav[2], S Mandal[2] and DC Bhandari[1]
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Horsegram, (*Macrotyloma uniflorum*) locally known as 'kulath', 'kulthi' or 'gahat' is cultivated in whole of the Uttranchal during rainy season. The related species *Macrotyloma sar-garhwalensis* (IC 212722) investigated in the present study is not yet consumed as a pulse. It grows in tropical and sub-temperate conditions of the Uttranchal on exposed grassy slopes, along the edge of crop fields associated with species of *Desmodium* and *Alysicarpus* as well as other shrubs.

The seeds of this species were procured from Prof. RD Gaur, Head, Department of Botany, HNB Garhwal University, Srinagar, Uttranchal, with collector number of GN-1882. This collection was made from village Sara, District Pauri, Uttranchal, at an altitude of 700 m and was multiplied at NBPGR Regional Station, Bhowali, for further characterization.

The species is an annual, erect, non-twining herb, 50-60 cm tall; leaves imparipinnate, pentafoliate, lanceolate with 6.5 cm long, sessile or sub-sessile and oblong leaflets; stipules large, 4-12 mm long and hairy on both surfaces; inflorescence axillary with short peduncle; flowers 1-2, 6-8 mm long; bracts obovate to lanceolate with acute apex; corolla blue included within the calyx, 5-7 mm long; stamens diadelphous (9+1), 5 mm long; pods compressed, shortly beaked, straw coloured becoming brown on ripening, 3.0-4.7 cm x 0.3 -0.7 cm in size,

minutely hairy on both sides; 4-5 seeds in each pod, which are compressed, flat, squarish-round, 4 mm long and broad, shining brownish-black, wrinkled and mottled. Flowering and fruiting occurs between August to November. Fifty per cent flowering occurs in 90 days and seeds mature within 175 days. Number of pods/plant is 35-45 and 100-seed weight is 2.63 g. The average seed yield/plant is around 50 g, while grain yield 4-6 q/h.

Seed samples analysed 4-5 times in Ujeltac Auto Analyzer were found with 38.35 ± 1.35 per cent protein content which is more than cultivated check varieties of horsegram, such as SK 2001 (21.09%), VLG-1 (21.06%) and Raipur local (22.80%). Also, it has higher protein content than that (16.87% to 30.36%) recorded in kulthi germplasm (434 accessions) maintained at NBPGR Regional Station, Akola.

Registration of Urdbean Germplasm, Amp 36–13 (INGR No 02008; IC 296878)

Kushal Pal Singh, SK Sharma and RK Yadav

Department of Genetics, Chaudhary Charan Singh Haryana Agricultural University, Hisar-125 004 (Haryana)

Wide hybridization among *Vigna* species has been advocated to broaden the genetic base. Amphidiploids have been produced between *Vigna* species overcoming sterility problem of hybrids. During the last 20 years, inter-specific derivatives involving a large number of amphidiploids from crosses of *V. radiata* x *V. mungo* and different urdbean varieties have been produced at the Department of Genetics, Chaudhary Charan Singh Haryana Agricultural University, Hisar, generating a wide spectrum of genetic variability. The amphidiploids in C2-C3 generation reverted back to parental types, with high frequency towards mungbean, but with some genomic exchange. In subsequent generations, the progenies segregated into mungbean and urdbean types on the basis of grain colour and other features. These progenies were evaluated in two separate experiments for three years resulting in identification of three urdbean promising lines, Amp 36, Amp 56 and Amp 62 (Singh *et al.*, 1986; Singh *et al.*, 1988). The genotype, Amp 36 of urdbean (*Vigna mungo*) was also involved in inter-specific hybridization and was found to be a good donor for plant and seed traits (Singh and Singh, 1998). However, cryptic genomic variability was released in advance generations for morphological and seed traits. Therefore, selections from such cryptic variations were made in populations of Amp 36, Amp 56 and Amp 62. Selected progenies were evaluated for variability in morphological and grain traits (Sharma and Singh, 2002). From Amp 36 population of inter-specific hybrid, K 851 X MCK-2, Amp 36-13 expressing novel morphological characters and good agronomic traits was isolated.

Amp 36-13 is dwarf and erect type with compact growth habit, determinate growth pattern, short peduncle length, erect attachment of pods to peduncle, more number of pods per plant and high grain yield. Some distinct morphological and agronomical features compared to the check are listed in Table 1.

Table 1. Distinct morphological and agronomical features of Amp 36-13

Character	Genotype	
	Amp 36-13	**T-9**
Growth habit	Erect compact	Semi-erect
Growth pattern	Determinate	Indeterminate
Petiole length	Short	Long
1st pod bearing node	2nd	4th
Peduncle length	Short (2-3cm.)	Long
Raceme position	Intermediate	Pods not visible
Attachment of mature pod to peduncle	Erect	Sub-erect
Position of pods with axil	Compressed along axil	Loose on peduncle
No. of pods/plant	65.1	46.4
100-seed weight (g)	4.53	4.80
Yield/plant (g)	12.73	9.50
Protein content (%)	23.2	22.6
Plant height (cm)	43.3	68.4

References

Sharma Hem Lata and KP Singh (2002) Variability studies in selected polymorphs of amphidiploid derivative of *Vigna radiata* x *Vigna mungo*. Proc. Second International Conference on Sustainable Agriculture for Food, Energy and Industry, Sept 8-13, 2002, Institute of Botany, Chinese Academy of Sciences, Beijing, pp 788-791.

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Singh KP, SK Sharma, RK Singh and DR Sood (1986) Performance of amphidiploid derivatives of greengram x blackgram crosses. *Indian J. Agric. Sci.* **56:** 390-392.

Singh Phool, DP Singh, A Kumar, BD Chaudhary and SK Thakral (1988) Response of mungbean x blackgram hybrids under water stress conditions. Proc. II International symposium on mungbean, AVRDC, Taiwan, pp 263-271.

Lemon Yellow Colour Leaf Mutant of Groundnut

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Girnar 1 Lym (INGR No. 01034, IC 296813)

Girnar 1 lym (PBS 30017), *Arachis hypogaea* L. spp. *hypogaea* var. *vulgaris* is a lemon yellow colour leaf groundnut mutant. This mutant was identified in M_2 generation progeny of a Spanish bunch groundnut cultivar, Girnar 1, whose seeds were treated with 0.10% ethyl methane sulphonate (EMS) at National Research Centre for Groundnut, Junagadh. The mutant bred true in subsequent M_3 and M_4 generations and was designated as Girnar 1 lym. The lemon yellow colour leaf started expressing from fourth to fifth leaf stage onwards and continued till maturity, resulting in lemon yellow appearance of the plant.

Based on F_2 generation segregation of the cross between Girnar 1 lym and Girnar 1, this trait appears to be governed by a monogenic recessive gene (Table 1). The gene symbols proposed are **Ly** for green and **ly** for lemon yellow.

Girnar 1 lym has erect growth habit (NBPGR and ICRISAT, 1992), sequential branching, and medium sized wide elliptic lemon yellow colour leaves. It has 6 primary and occasionally 1-2 secondary branches. It matures in 95 days in the rainy season at Junagadh, Gujarat, India. The pods are mostly three-seeded, with shelling out turn of 75%. The pods have slight constriction, moderate reticulation and medium beak. The seeds are tan colour with 100 seed weight of 37g and contain 47% oil and 13% protein. Based on field screening during two rainy seasons, Girnar 1 lym is moderately resistant/tolerant to early leaf-spot, late leaf-spot, and rust scoring 5 on 1-9 scale.

Table 1. F_2 segregation of lemon yellow leaf trait in cross, Girnar 1 lym x Girnar 1

Families	Number of F_2 phenotypes*			χ^2 (3:1 ratio)	Probability
	Normal green	Lemon yellow	Total		
1.	58	15	73	0.7717	0.5-0.3
2.	47	13	60	0.3556	0.7-0.5
3.	76	20	96	0.8889	0.5-0.3
4.	60	19	79	0.3890	0.9-0.8
5.	30	11	41	0.0732	0.8-0.7
6.	52	17	69	0.0048	0.95-0.9
Pooled	323	95	418	1.1515	0.3-0.2
Hetero-geneity	–	–		0.9806	0.95-0.90

*F_1 had normal green leaves like male parent, Girnar 1

Vegetable Type Soybean

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

P-1366 (INGR No. 01035, IC 296814)

P-1366 is a vegetable type bold seeded soybean, *Glycine max* L. Merr. collected during 1988 by Mr. KC Pant, NBPGR, Regional Station, Bhowali from Pithoragarh district of Uttar Pradesh (Now Uttaranchal). P-1366 has determinate growth habit with thick dark green leaves. The plant height is 30-35 cm at Bhowali and 35-40 cm at Akola. It has tawny pubescence with normal density and white flowers. It flowers between 32-34 days at Bhowali and 30-32 at Akola and matures between 105-108 days. It has thick brown pods containing 2-3 seeds/pod. The seeds are creamish yellow with black hilum and contain 20.13% oil and 40.20% protein on dry weight basis. It was evaluated at NBPGR, Regional Station, Akola, Maharashtra (1991-1997) and at Bhowali (1988-2000) for agronomic features. Grain yields of 18-22 q/ha with bold seeds were recorded. The seeds are sweet in taste and have no beany flavour during pod filling stage. Hundred seed weight is 44-46 g at Akola and 36-38 g at Bhowali.

P-1366 is resistant to yellow mosaic virus and moderately resistant to bacterial pustules (*Xanthomonas campestris*), but susceptible to pod blight (*Colletotrichum dematium*). Being bold seeded it has poor seed storability.

Table 1. Nutritional profile of P1336 compared with nationally released varieties

Cultivars	100-seed weight (g)	Oil (%)	Protein (%)	Major fatty acids				
				Palmitic	Stearic	Oleic	Linoleic	Linolenic
PK-416	10.20	20.88	41.60	10.88	4.13	23.85	52.80	6.98
Pusa 16	12.50	19.45	41.68	11.20	3.60	19.58	54.57	7.82
P 1336	36.38	20.13	40.20	10.29	3.33	24.89	50.75	8.12

Crotolaria Germplasm

N R Das, N Ghosh, S Mitramajumdar and D Panda
Agronomy/Seed Science & Technology Department, Faculty of Agriculture, Bidhan Chandra Krishi Viswavidyalaya (BCKV), Mohanpur-741 252 (West Bengal)

Bidhan Shan (INGR No. 01036, IC 296815)

Bidhan Shan is an improved self-compatible sunnhemp, *Crotolaria juncea* L. germplasm developed at Bidhan Chandra Krishi Viswavidyalaya, West Bengal. It was selected from the bulk seed obtained from local market (Chinsurah, West Bengal) and was further improved and fixed by the repeated bulk selection method (1998-99 and 1999-2000).

In April/May planting, the stem height of Bidhan Shan is 3.3 m with less branches and flowers, while in rabi planting, the stem height is about 1 m with higher number of branches and more number of flowers per branch. It requires 60 days for green manure and 120 days for fibre production in summer planting, while 125-130 days in *rabi* planting for seed production. It possesses kidney shaped glossy blackish coloured seeds, with 1000-seed weight of about 25-30 g. It can smother the weeds in field. In yield trials conducted at BCKV Farm, Kalyani (1997-98) Bidhan Shan out yielded ST 55, by nearly 200% with an average seed yield of 6.2 quintal and stover yield of 33.3 q/ha.

This germplasm is highly resistant to diseases and pests and could be cultivated as a *paira/utera* crop in rice-fallows. Also, it can be utilized as annual bast fibre, fodder and green manure crop in the drier areas.

Watermelon Germplasm

JP Luthra and VS Yadav
Melon Scheme, Department of Horticulture, Agriculture Research Station, Durgapura, Jaipur-18 (Rajasthan)

Yellow Flesh Watermelon, RW 187-2 (INGR No. 01037, IC 296816)

Watermelon 'RW 187-2' has been selected from the local germplasm material available at Agriculture Research Station, Durgapura, Jaipur. Individual plant progenies were advanced to establish the pure line. The vines are 2.5-3 meters long. It takes 105-110 days for first picking. The fruits are oval, light green with dark linings on rind, with yellow/saffron colour flesh and white colour medium sized seeds. Sweetness is 9-11 per cent and average fruit weight is 3-5 kg. Fruit yield is 350-500 q/ha, 56.10 per cent higher than the best checks, Sugarbaby (local check) and Arkamanik (national check) in trials conducted under All India Co-ordinated Vegetable Improvement Project (Table). RW 187-2 is suited to well drain sandy loam soil. RW 187-2 is moderately resistant to powdery mildew and blight under field conditions.

minutely hairy on both sides; 4-5 seeds in each pod, which are compressed, flat, squarish-round, 4 mm long and broad, shining brownish-black, wrinkled and mottled. Flowering and fruiting occurs between August to November. Fifty per cent flowering occurs in 90 days and seeds mature within 175 days. Number of pods/plant is 35-45 and 100-seed weight is 2.63 g. The average seed yield/plant is around 50 g, while grain yield 4-6 q/h.

Seed samples analysed 4-5 times in Ujeltac Auto Analyzer were found with 38.35 ± 1.35 per cent protein content which is more than cultivated check varieties of horsegram, such as SK 2001 (21.09%), VLG-1 (21.06%) and Raipur local (22.80%). Also, it has higher protein content than that (16.87% to 30.36%) recorded in kulthi germplasm (434 accessions) maintained at NBPGR Regional Station, Akola.

Registration of Urdbean Germplasm, Amp 36–13 (INGR No 02008; IC 296878)

Kushal Pal Singh, SK Sharma and RK Yadav

Department of Genetics, Chaudhary Charan Singh Haryana Agricultural University, Hisar-125 004 (Haryana)

Wide hybridization among *Vigna* species has been advocated to broaden the genetic base. Amphidiploids have been produced between *Vigna* species overcoming sterility problem of hybrids. During the last 20 years, inter-specific derivatives involving a large number of amphidiploids from crosses of *V. radiata* x *V. mungo* and different urdbean varieties have been produced at the Department of Genetics, Chaudhary Charan Singh Haryana Agricultural University, Hisar, generating a wide spectrum of genetic variability. The amphidiploids in C2-C3 generation reverted back to parental types, with high frequency towards mungbean, but with some genomic exchange. In subsequent generations, the progenies segregated into mungbean and urdbean types on the basis of grain colour and other features. These progenies were evaluated in two separate experiments for three years resulting in identification of three urdbean promising lines, Amp 36, Amp 56 and Amp 62 (Singh *et al.*, 1986; Singh *et al.*, 1988). The genotype, Amp 36 of urdbean (*Vigna mungo*) was also involved in inter-specific hybridization and was found to be a good donor for plant and seed traits (Singh and Singh, 1998). However, cryptic genomic variability was released in advance generations for morphological and seed traits. Therefore, selections from such cryptic variations were made in populations of Amp 36, Amp 56 and Amp 62. Selected progenies were evaluated for variability in morphological and grain traits (Sharma and Singh, 2002). From Amp 36 population of inter-specific hybrid, K 851 X MCK-2, Amp 36-13 expressing novel morphological characters and good agronomic traits was isolated.

Amp 36-13 is dwarf and erect type with compact growth habit, determinate growth pattern, short peduncle length, erect attachment of pods to peduncle, more number of pods per plant and high grain yield. Some distinct morphological and agronomical features compared to the check are listed in Table 1.

Table 1. Distinct morphological and agronomical features of Amp 36-13

Character	Genotype	
	Amp 36-13	**T-9**
Growth habit	Erect compact	Semi-erect
Growth pattern	Determinate	Indeterminate
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1st pod bearing node	2nd	4th
Peduncle length	Short (2-3cm.)	Long
Raceme position	Intermediate	Pods not visible
Attachment of mature pod to peduncle	Erect	Sub-erect
Position of pods with axil	Compressed along axil	Loose on peduncle
No. of pods/plant	65.1	46.4
100-seed weight (g)	4.53	4.80
Yield/plant (g)	12.73	9.50
Protein content (%)	23.2	22.6
Plant height (cm)	43.3	68.4

References

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P-1366 is resistant to yellow mosaic virus and moderately resistant to bacterial pustules (*Xanthomonas campestris*), but susceptible to pod blight (*Colletotrichum dematium*). Being bold seeded it has poor seed storability.

Table 1. Nutritional profile of P1336 compared with nationally released varieties

Cultivars	100-seed weight (g)	Oil (%)	Protein (%)	Major fatty acids				
				Palmitic	Stearic	Oleic	Linoleic	Linolenic
PK-416	10.20	20.88	41.60	10.88	4.13	23.85	52.80	6.98
Pusa 16	12.50	19.45	41.68	11.20	3.60	19.58	54.57	7.82
P 1336	36.38	20.13	40.20	10.29	3.33	24.89	50.75	8.12

Crotolaria Germplasm

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Bidhan Shan (INGR No. 01036, IC 296815)

Bidhan Shan is an improved self-compatible sunnhemp, *Crotolaria juncea* L. germplasm developed at Bidhan Chandra Krishi Viswavidyalaya, West Bengal. It was selected from the bulk seed obtained from local market (Chinsurah, West Bengal) and was further improved and fixed by the repeated bulk selection method (1998-99 and 1999-2000).

In April/May planting, the stem height of Bidhan Shan is 3.3 m with less branches and flowers, while in rabi planting, the stem height is about 1 m with higher number of branches and more number of flowers per branch. It requires 60 days for green manure and 120 days for fibre production in summer planting, while 125-130 days in *rabi* planting for seed production. It possesses kidney shaped glossy blackish coloured seeds, with 1000-seed weight of about 25-30 g. It can smother the weeds in field. In yield trials conducted at BCKV Farm, Kalyani (1997-98) Bidhan Shan out yielded ST 55, by nearly 200% with an average seed yield of 6.2 quintal and stover yield of 33.3 q/ha.

This germplasm is highly resistant to diseases and pests and could be cultivated as a *paira/utera* crop in rice-fallows. Also, it can be utilized as annual bast fibre, fodder and green manure crop in the drier areas.

Watermelon Germplasm

JP Luthra and VS Yadav
Melon Scheme, Department of Horticulture, Agriculture Research Station, Durgapura, Jaipur-18 (Rajasthan)

Yellow Flesh Watermelon, RW 187-2 (INGR No. 01037, IC 296816)

Watermelon 'RW 187-2' has been selected from the local germplasm material available at Agriculture Research Station, Durgapura, Jaipur. Individual plant progenies were advanced to establish the pure line. The vines are 2.5-3 meters long. It takes 105-110 days for first picking. The fruits are oval, light green with dark linings on rind, with yellow/saffron colour flesh and white colour medium sized seeds. Sweetness is 9-11 per cent and average fruit weight is 3-5 kg. Fruit yield is 350-500 q/ha, 56.10 per cent higher than the best checks, Sugarbaby (local check) and Arkamanik (national check) in trials conducted under All India Co-ordinated Vegetable Improvement Project (Table). RW 187-2 is suited to well drain sandy loam soil. RW 187-2 is moderately resistant to powdery mildew and blight under field conditions.

P-1366 is resistant to yellow mosaic virus and moderately resistant to bacterial pustules (*Xanthomonas campestris*), but susceptible to pod blight (*Colletotrichum dematium*). Being bold seeded it has poor seed storability.

Table 1. Nutritional profile of P1336 compared with nationally released varieties

Cultivars	100-seed weight (g)	Oil (%)	Protein (%)	Major fatty acids				
				Palmitic	Stearic	Oleic	Linoleic	Linolenic
PK-416	10.20	20.88	41.60	10.88	4.13	23.85	52.80	6.98
Pusa 16	12.50	19.45	41.68	11.20	3.60	19.58	54.57	7.82
P 1336	36.38	20.13	40.20	10.29	3.33	24.89	50.75	8.12

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Bidhan Shan (INGR No. 01036, IC 296815)

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In April/May planting, the stem height of Bidhan Shan is 3.3 m with less branches and flowers, while in rabi planting, the stem height is about 1 m with higher number of branches and more number of flowers per branch. It requires 60 days for green manure and 120 days for fibre production in summer planting, while 125-130 days in *rabi* planting for seed production. It possesses kidney shaped glossy blackish coloured seeds, with 1000-seed weight of about 25-30 g. It can smother the weeds in field. In yield trials conducted at BCKV Farm, Kalyani (1997-98) Bidhan Shan out yielded ST 55, by nearly 200% with an average seed yield of 6.2 quintal and stover yield of 33.3 q/ha.

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Watermelon Germplasm

JP Luthra and VS Yadav
Melon Scheme, Department of Horticulture, Agriculture Research Station, Durgapura, Jaipur-18 (Rajasthan)

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Watermelon 'RW 187-2' has been selected from the local germplasm material available at Agriculture Research Station, Durgapura, Jaipur. Individual plant progenies were advanced to establish the pure line. The vines are 2.5-3 meters long. It takes 105-110 days for first picking. The fruits are oval, light green with dark linings on rind, with yellow/saffron colour flesh and white colour medium sized seeds. Sweetness is 9-11 per cent and average fruit weight is 3-5 kg. Fruit yield is 350-500 q/ha, 56.10 per cent higher than the best checks, Sugarbaby (local check) and Arkamanik (national check) in trials conducted under All India Co-ordinated Vegetable Improvement Project (Table). RW 187-2 is suited to well drain sandy loam soil. RW 187-2 is moderately resistant to powdery mildew and blight under field conditions.

Table 1. Performance of RW 187-2 in station (1989-95) and in coordinated (1992-96) trials

S. No	Selected entries	Station trials (1989-91, 95)	Co-ordinated trials (1992-96)	Pooled	Per cent increase in trials				
					Station	Co-ordinated	Pooled mean		Average
1	RW-187-2	401.09 (4)	271.48 (15)	336.28	116.65	18.26	23.56	56.1	53.06
2	Sugarbaby	185.13 (4)	229.50 (15)	215.43	00.00	0.00	-	00.0	-
3	Arkamanik	-	219.71 (15)	219.71	-	-	00.00	-	00.0

Figures in parenthesis are number of locations

Simple Un-lobed Leaf Watermelon, RW 177-3 (INGR No. 01038, IC 296817)

Watermelon RW 177-3 (Durgapura Lal), was a selection from segregating population of a cross between Sugarbaby and K-3566, a Russian culture at A.R.S. Durgapura, Jaipur. The vines are 3.0–3.5 meters long. The leaves are simple and un-lobed unlike other varieties. The fruits are round, dark green with darker linings and thin and hard skin. The flesh is dark red in colour with 10–11% sugar. The fruit size is medium, weighing 4 to 5 Kg and easy to transport. It takes 110 days for first picking. The seeds are less in number, small and brown in colour with black spots. The 1000 seed weight is 44g. Fruit yield is 350-450 q/ha, 27 per cent higher over the best national check, Arkamanik and 41 per cent over the local check, Sugarbaby (Table). The portion of fruit that touches the ground turns pale yellow on maturity. It is suitable for irrigated areas.

Table 1. Performance of watermelon culture RW-177-3 in station trials

S. No.	Cultures	Yield (q/ha) 1995	Pooled Mean 1996	1997	1998	2001	Percent Increase over Sugarbaby	Arkamanik	
1	RW-177-3	381.94 (8.5)	355.55 (11.0)	327.77 (11.00)	462.47 (10.5)	369.75 (11.0)	379.50 (10.40)	40.94	26.72
2	Sugarbaby (Local check)	236.11 (9.0)	224.00 (9.0)	224.07 (9.5)	338.87 (9.5)	323.30 (10.50)	269.27 (9.50)	-	-
3	Arkamanik (National check)	222.03 (8.0)	327.78 (9.0)	214.81 (9.0)	433.30 (9.5)		299.40 (8.67)	-	-
	CD at 5%	47.57	62.25	37.65	20.22	27.54			
	CV (%)	12.01	11.86	8.36	3.22	6.28			

Figures in parenthesis are total soluble sugar in per cent.

Hybrid Coffee Germplasm

RL Narasimhaswamy and S Vishveshwara, M Ramchandran and VB Suresh Kumar
Central Coffee Research Institute, Coffee Research Station, Post 577 177, Chikmagalur District (Kerala)

Genus *Coffea* of the family Rubiaceae contains about 100 species of which two are commercially cultivated namely *Coffea arabica* L. (arabica coffee) and *C. canephora* Pierre ex Froehner (robusta coffee). Most of the species are native of Africa. *C. arabica* was introduced to India in 1600 A.D. and *C. canephora* in about 1900 A.D. Arabica is the only allotetraploid in this genus with 2n=44 and is predominantly self-pollinated, while *C. canephora* is diploid (2n=22) and an obligate cross-pollinator. After the establishment of Central Coffee Research Institute (CCRI) in 1925 near Chikmagalur in Karnataka, organised research on coffee breeding was undertaken and several new genotypes of arabica and robusta were developed and established through inter-specific hybridisation. The seeds of these genotypes were distributed for cultivation.

A Compact Hybrid of Coffee, Congensis x Robusta (INGR No. 01039, IC 296818)

It is an interspecific hybrid between *Coffea congensis*, Froehner and *C. canephora* cv. S-274 robusta, developed by back crossing to *C. canephora* followed by pedigree selection and sib-mating. It is compact, bush type with shorter internodes than robusta and drooping to semi-

Registration of Cytoplasmic Male Sterile Line in Cotton (INGR No. 02011; IC No. 296907)

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Cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri-413 722 (Maharashtra)

Several cytoplasmic and genetic male sterile genotypes have been identified in cotton (*Gossypium hirsutum*) ranging from partial to complete male sterility (Meyer, 1969; Bowman *et al.*, 1978). At the Cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, a cytoplasmic male sterile line (CMS) along with its fertility restorer line was identified from a survey of germplasm of *G. hirsutum.*

In the summer of 1976 in the germplasm accession GH: 572/76, a peculiar plant was noticed. The plant was okra-leaved in an otherwise entire-leaved *G. hirsutum* line. It produced non-dehiscent anthers without any pollen. Cytological studies indicated that pollen mother cells (PMCs) are not formed due to persistent tapetum layer, which was confirmed by histological studies, where cross sections of 8-12 mm thickness of anthers stained with Heidenhain's iron-alum haematoxyline showed that anther wall remained intact without degeneration of tapetal cells. In the male sterile anthers extensive vacuolation was observed resulting in empty anther sac.

CMS nature of this plant was confirmed on the basis of similar observation made by Murthi and Weaver (1974) who observed the male sterile line with *G. harknessii* cytoplasm. On this plant a large number of bolls were set through natural cross-pollination. Later pollen from 15 different cotton varieties were transferred to this male sterile plant during the same crop season. The boll and seed setting was about 70% indicating considerable female fertility. One of the 15 pollinators produced fertile segregates from a known genetic male sterile source. These fertile segregates produced normal PMCs and good fertile pollen. These fertile segregates were selfed and also mated with their male sterile sibs.

The cytoplasmic male sterility from this line has been successfully transferred into several lines, such as CMS Laxmi, CMS LRA-5166, CMS 76 IH-20, CMS SRT-1, which have been found to be highly promising female parents. This has also led to development of CMS-based hybrids, MSRHH 23, MSRHH 25, MSRHH 28 (Mehetre *et al.*, 1996).

Reference

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Murthi AN and JR Weaver (1974) Histological studies on five male sterile strains of upland cotton. *Crop Sci.* **14:** 658-663.

Registration of Genetic Male Sterile Line of Cotton, LRA 5166 GMS (INGR No 02012; IC 296905)

Suman Bala Singh, Jyoti Hebbar and Shine John
Central Institute for Cotton Research, Post Bag No. 2, Shankarnagar P. O., Nagpur-440 010 (Maharashtra)

In cotton (*Gossypium hirsutum)* both genetic and cytoplasmic genic male sterility have been used in hybrid breeding. The pollen sterility, which is caused by nuclear genes, is referred to as genetic male sterility. The first case of GMS was reported by Justus and Lienweber (1960) in upland cotton (*G. hirsutum*). Both recessive and dominant genes have been reported to govern male sterility. In all, 16 genes in tetraploid and two genes in diploid cotton have been identified. The Gregg male sterile lines governed by two recessive genes (ms_5, ms_6) are the most stable and commonly used in breeding programme. In order to generate variability for male sterility, a released variety LRA 5166 from Central Institute for Cotton Research (CICR), Regional Station, Coimbatore, was selected. This variety is a three way cross derivative, Laxmi x (Reba B 50 x AC 122) and has wider adaptability, higher yield and good fibre properties. LRA 5166 GMS line (*Gossypium hirsutum*) was developed using exotic Gregg as male sterility source in backcross breeding programme.

Table 1. Performance of RW 187-2 in station (1989-95) and in coordinated (1992-96) trials

S. No	Selected entries	Station trials (1989-91, 95)	Co-ordinated trials (1992-96)	Pooled	Per cent increase in trials				
					Station	Co-ordinated	Pooled mean		Average
1	RW-187-2	401.09 (4)	271.48 (15)	336.28	116.65	18.26	23.56	56.1	53.06
2	Sugarbaby	185.13 (4)	229.50 (15)	215.43	00.00	0.00	-	00.0	-
3	Arkamanik	-	219.71 (15)	219.71	-	-	00.00	-	00.0

Figures in parenthesis are number of locations

Simple Un-lobed Leaf Watermelon, RW 177-3 (INGR No. 01038, IC 296817)

Watermelon RW 177-3 (Durgapura Lal), was a selection from segregating population of a cross between Sugarbaby and K-3566, a Russian culture at A.R.S. Durgapura, Jaipur. The vines are 3.0–3.5 meters long. The leaves are simple and un-lobed unlike other varieties. The fruits are round, dark green with darker linings and thin and hard skin. The flesh is dark red in colour with 10–11% sugar. The fruit size is medium, weighing 4 to 5 Kg and easy to transport. It takes 110 days for first picking. The seeds are less in number, small and brown in colour with black spots. The 1000 seed weight is 44g. Fruit yield is 350-450 q/ha, 27 per cent higher over the best national check, Arkamanik and 41 per cent over the local check, Sugarbaby (Table). The portion of fruit that touches the ground turns pale yellow on maturity. It is suitable for irrigated areas.

Table 1. Performance of watermelon culture RW-177-3 in station trials

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drooping branches. Thirty to 50 fruits occur at each node in tight clusters, which are orange to crimson red in colour with prominent and projected nanel. The fruits are bold in size with protruding honey disc. Seeds are bold giving 60 per cent 'A' type grade (retained on 6.65 mm screen). Cup quality is superior to robusta with soft neutral and light acidity, which is normally absent in other robustas. It is cross-pollinated and seeds are produced by inducing blossom through irrigation in seed blocks. Most of the plants are resistant to leaf rust with tolerance to drought.

Leaf Rust Resistant Arabica Coffee Selections

RL Narasimhaswamy and S Vishveshwara
Central Coffee Research Institute, Coffee Research Station, Post 577 177, Chikmagalur District (Kerala)

S.795 (INGR 01040, IC 296819)

S. 795, is a selection from the F_2 progenies of a cross between S. 288 and Kent's arabica, both of which have originated in India. Majority of plants show resistance to common races I and II of leaf rust caused by *Hemileia vastatrix*. S 795 is characterised by vigorous growth, spreading habit and profuse cropping wood. The internodes are short being 1.5 – 3.5 inches long. Leaves are linear-oblong, thick and leathery, dark green and shining with prominent wavy margin, and longish acuminate apex. Fruits are borne in thick clusters. Seeds are oblong, bold with small to broad navel and 60-65 per cent 'A' grade. Yields vary from 1000 to 2000 kg/ha with an all India average of 975 Kg/ha. It is predominantly self-pollinated.

Leaf Rust Resistant Arabica Selections, 5B (INGR No. 01041, IC 296820)

5B (S. 2931 & S. 4422), is a selection identified from a cross between S 333 and Devamachy hybrid. Devamachy is a spontaneous Indian hybrid originated from a cross, robusta x arabica. For development of this genotype pedigree method was practised from F_2 to F_5 and progenies showing uniformity for bush, vigour and resistance to leaf rust caused by *Hemileia vastatrix* was selected. The bush has medium internodes, spreading primaries with dark green broad elliptic leaves, and bronze apex. Fruits are medium bold, squarish with flush and small honey disc. Seeds are medium bold. Yield potential is 1500 Kg/ha. Pollination is predominantly autogamous.

Self-Pollinating Hybrid, Selection 6 (INGR No. 01042, IC 296821)

Selection 6 is a hybrid selected from an interspecific cross between between *C.canephora* cv. S 274 (robusta) and *C. arabica* Kent. backcrossed twice with arabica. The third generation progeny from BC_2 showed better uniformity for bush size and vigour; with high resistance to leaf rust caused by *Hemileia vastatrix*, with yield, bean size and cup quality similar to arabica. Chromosome number is 2n=44. Yield potential is 1000 to 1500 Kg/ha and pollination is predominantly autogamous.

Drought Tolerant Selection 7.3 (INGR No. 01043, IC 296822)

The selection 7.3, is an interspecific hybrid evolved out of step by step crossing first between San Ramon (dwarf mutant of arabica isolated in Colombia and introduced into India from Guatemala in 1953) and S.795, followed by crosses with Agaro and Hibrido-de-Timor in subsequent steps to improve leaf rust resistance. It is tolerant to drought. It segregated into 70 per cent dwarfs and 30 per cent tall. Dwarfs can be used for closer planting (1.5 x 1.5 m). The plant height is 2 m, internodes are extremely short with lateral branches of reduced length, and leaves are wide elliptic and dark green. Also, it is resistant to drought and produces fruits with delayed ripening. Suited to low rainfall areas, its yield potential 1000-1500 Kg/ha.

Drought Tolerant Selection 9 (INGR No. 01044, IC 296823)

The selection has evolved out of cross between Hibrido-de-Timor (a natural hybrid of robusta x arabica from Timor, introduced to India from Portugal in 1967) and Tafarikela, an Ethiopian arabica. This was an F_3 progeny showing high uniformity. The plants are tall, vigorous with drooping to spreading branches. Internodal distance is more in spreading type. Fruits are bold with often persistent calyx. It is an early ripening variety and

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Registration of Genetic Male Sterile Line of Cotton, LRA 5166 GMS (INGR No 02012; IC 296905)

Suman Bala Singh, Jyoti Hebbar and Shine John
Central Institute for Cotton Research, Post Bag No. 2, Shankarnagar P. O., Nagpur-440 010 (Maharashtra)

In cotton (*Gossypium hirsutum)* both genetic and cytoplasmic genic male sterility have been used in hybrid breeding. The pollen sterility, which is caused by nuclear genes, is referred to as genetic male sterility. The first case of GMS was reported by Justus and Lienweber (1960) in upland cotton (*G. hirsutum*). Both recessive and dominant genes have been reported to govern male sterility. In all, 16 genes in tetraploid and two genes in diploid cotton have been identified. The Gregg male sterile lines governed by two recessive genes (ms_5, ms_6) are the most stable and commonly used in breeding programme. In order to generate variability for male sterility, a released variety LRA 5166 from Central Institute for Cotton Research (CICR), Regional Station, Coimbatore, was selected. This variety is a three way cross derivative, Laxmi x (Reba B 50 x AC 122) and has wider adaptability, higher yield and good fibre properties. LRA 5166 GMS line (*Gossypium hirsutum*) was developed using exotic Gregg as male sterility source in backcross breeding programme.

The newly developed GMS line has plant height ranging from 100 to 120 cm with short internodes and open canopy. Leaves are light green in colour, medium in size and possess one-nectar gland on mid rib. Flowers are creamy with light yellow claw and nectaries at the base of all the five petals, but nectaries are absent on the calyx. Three bracts with deep or medium deep notch surround corolla. Bracteoles may or may not contain nectaries. In general, 0-3 nectaries were recorded. They possess 8-10 serrations and are separated by U-shaped notch. Stamen number varies from 75-102 with yellow pollen colour and staminal length of 0.95 cm. Total ovary length is 0.8 cm, which is oval-shaped and medium in size. Boll weight is 4 to 4.5 g. LRA 5166 GMS line has desirable fibre properties (24.4 mm, 2.5% span length with bundle strength 20.5 g/tex 1/ 8 mm gauge), uniformity ratio of 48 and micronaire value of 3.2 (10^{-6} g/in). The line has good general combining ability and it is expected to produce high heterotic potential hybrids. The converted lines have been put to use in hybrid development programme.

Reference

Justus NJ and CL Lienweber (1960) A heritable partial male sterile character in cotton. *J. Heredity* **51:** 191-192.

Registration of Cotton Germplasm, 30838 (INGR No. 02020; IC 296857)

Punit Mohan, PM Mukewar, VV Singh and CD Mayee

Central Institute for Cotton Research, Post Bag No. 2, Shankar Nagar, P.O. Nagpur-440 010 (Maharashtra)

The grey mildew/areolate mildew disease of cotton caused by *Ramularia areola* Atk., has become a very important disease in India affecting cultivation of all the four commercially cultivated *Gossypium* species. The disease has been recorded in epidemic form in Central India during the years 1958, 1988 and 1993 (Mukewar *et al.*, 1994). The yield losses have been recorded up to 68% under epidemic disease conditions in Maharashtra. Considering the great economic importance of the disease, a screening programme was initiated. A total of 1592 *Gossypium arboreum* germplasm lines available with Central Institute for Cotton Research (CICR), Nagpur were evaluated during the years 1985 to 1989. This resulted in identification of seven immune lines, Bangladesh, G-135-49 belonging to *Gossypium arboreum* race *bengalense* and 30305, 30814, 30826, 30838 and 30856 belonging to *Gossypium arboreum* race *cernuum* (Mukewar *et al.*, 1995). The resistance potential was further confirmed by subjecting to immunity performance in glasshouse and field conditions with artificial inoculations during 1989 to 1992. The basis of resistance among these lines was studied by conducting morphological and anatomical studies (Punit Mohan *et al.*, 1997) and biochemical analysis of factors governing resistance (Chakrabarty *et al.*, 2002). For assessment of commercial value, these lines were evaluated for fibre characteristics and other economic parameters (Punit Mohan *et al.*, 2001).

Of these lines, line 30838 is being registered for immunity against grey mildew/areolate mildew disease of cotton. It has five-lobed narrow elongated leaf with long stalk (up to 8 inches long), reticulate and palmate divergent venation and sparsely hairy surface. Flowers are yellow with long pedicle, short claw, and petal blotch red, anthers yellow with long filaments. It has three-large and broad bracteoles with serrated margin at apex and 2-3 teeth. Capsules are big, trilocular and elongated with tapering ends with long peduncle. Capsule surface is densely pitted. Staple length is 20.3 mm at 2.5% span length, uniformity ratio of 50%, fineness-micronaire above scale at 10^{-6} g/m micronaire, bundle strength 16.6 at bundle tenacity g/tex 3.2 mm, ginning outturn- 42.15% and seed-cotton yield/plant 44.59 g.

Reference

Chakrabarty PK, PM Mukewar, S Raj and V Sravan Kumar (2002) Biochemical factors governing resistance in diploid cotton against grey mildew. *Indian Phytopath.* **55:** 140-146.

Punit Mohan, PM Mukewar, S Raj and VV Singh (1997) Anatomy of *Gossypium arboreum* lines immune to grey mildew disease. *J. Cotton Res. Dev.* **11:** 191-195.

Punit Mohan, VV Singh and PM Mukewar (2001) Morphological and fibre characteristics of *Gossypium arboreum* L. germplasm lines immune to grey mildew (*Ramularia areola* Atk.) disease of cotton. *Indian J. Plant Genet. Resour.* **14:** 81-84.

Mukewar PM, S Raj and PK Chakrabarty (1994) Epidemic occurrence of grey mildew disease of cotton in Central India, *J. Indian Soc. Cotton Improv.* **10:** 170-172.

Mukewar PM, S Raj, VV Singh and GR Anap (1995) Screening of tree cotton (*Gossypium arboreum*) germplasm to grey mildew caused by *Ramularia areola. Indian J. Agric. Sci.*, **65:** 298-300.

drooping branches. Thirty to 50 fruits occur at each node in tight clusters, which are orange to crimson red in colour with prominent and projected nanel. The fruits are bold in size with protruding honey disc. Seeds are bold giving 60 per cent 'A' type grade (retained on 6.65 mm screen). Cup quality is superior to robusta with soft neutral and light acidity, which is normally absent in other robustas. It is cross-pollinated and seeds are produced by inducing blossom through irrigation in seed blocks. Most of the plants are resistant to leaf rust with tolerance to drought.

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Leaf Rust Resistant Arabica Selections, 5B (INGR No. 01041, IC 296820)

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Self-Pollinating Hybrid, Selection 6 (INGR No. 01042, IC 296821)

Selection 6 is a hybrid selected from an interspecific cross between between *C.canephora* cv. S 274 (robusta) and *C. arabica* Kent. backcrossed twice with arabica. The third generation progeny from BC_2 showed better uniformity for bush size and vigour; with high resistance to leaf rust caused by *Hemileia vastatrix*, with yield, bean size and cup quality similar to arabica. Chromosome number is 2n=44. Yield potential is 1000 to 1500 Kg/ha and pollination is predominantly autogamous.

Drought Tolerant Selection 7.3 (INGR No. 01043, IC 296822)

The selection 7.3, is an interspecific hybrid evolved out of step by step crossing first between San Ramon (dwarf mutant of arabica isolated in Colombia and introduced into India from Guatemala in 1953) and S.795, followed by crosses with Agaro and Hibrido-de-Timor in subsequent steps to improve leaf rust resistance. It is tolerant to drought. It segregated into 70 per cent dwarfs and 30 per cent tall. Dwarfs can be used for closer planting (1.5 x 1.5 m). The plant height is 2 m, internodes are extremely short with lateral branches of reduced length, and leaves are wide elliptic and dark green. Also, it is resistant to drought and produces fruits with delayed ripening. Suited to low rainfall areas, its yield potential 1000-1500 Kg/ha.

Drought Tolerant Selection 9 (INGR No. 01044, IC 296823)

The selection has evolved out of cross between Hibrido-de-Timor (a natural hybrid of robusta x arabica from Timor, introduced to India from Portugal in 1967) and Tafarikela, an Ethiopian arabica. This was an F_3 progeny showing high uniformity. The plants are tall, vigorous with drooping to spreading branches. Internodal distance is more in spreading type. Fruits are bold with often persistent calyx. It is an early ripening variety and

produces 60 to 65 percent 'A' grade beans, which are bold in size and bettering cup quality. This selection has good drought tolerance with resistance to common races I and II of leaf rust caused by *Hemileia vastatrix* It is predominantly self-pollinated and yields 1200-1500 Kg/ha.

Novel Non-Narcotic Poppy

JR Sharma, RK Lal, AP Gupta, HO Misra and V Pant
Central Institute of Medicinal and Aromatic Plants, (Central Institute for Medicinal and Aromatic Plants (CIMAP), Lucknow-226 015 (Uttar Pradesh)

Sujata (INGR No. 01045, IC 296824)

An opium-less, alkaloid-free (non-narcotic) var. *Sujata* (LL34) of opium poppy (*Papaver somniferum*) was developed for the first time at CIMAP, Lucknow. It is a fine example of genetic conversion of a narcotic crop, like 'opium' poppy into non-narcotic 'seed' poppy. It does not exude latex (raw opium) on lancing (incision) of the capsule (Fig. 1). The straw (capsule hull) is also free from opium alkaloids, viz. morphine, codeine, thebaine and papaverine, etc.

It was developed by mutation breeding through a combined mutagenic treatment of 20 Kr gamma rays and 0.4 per cent Ethyl Methane Sulphonate on the high opium yielding parental strain, Mass-2B (var. *Sampada*). A latex-less mutant, LL34 was detected by 'ray-pluck' method (JR Sharma *et al.*, 1999) in M_2 generation, stabilized by M_7 generation and was finally re-christened as var. *Sujata*. The table summarises the morphological features of the mutant. It was evaluated for seed yield and non-latex production in initial evaluation (replicated, paired rows), bench scale (replicated, 5 x 3m plot size), and pilot scale trial (200 m^2 plot size) at Central Institute of Medicinal and Aromatic Plants for three years; giving 10-20 per cent higher seed yield (Table 1) than parent.

References

Sharma JR, RK Lal, AP Gupta, HO Misra, V Pant, NK Singh and V Pandey (1999) *Plant Breeding* (Berlin) **118**:449-452.

Sharma JR, RK Lal, HO Misra, AA Naqvi and DD Patra 1999. *Curr. Sci.* **77(12)**: 1584 -1589.

Table 1. The comparative features of *Sujata* and its parent Mass-2B

S. No.	Quali-quantitative traits	Sujata	Mass-2B
1.	Days to mid-flowering	100-105	100-104
2.	Plant height (cm)	80-100	85-110
3.	Capsule surface	Glabrous	Waxy
4.	Number of stigmatic rays per capsule	10-12	12-14
5.	Latex-flow on incision	Absent	Profuse
6.	Alkaloids in straw (capsule hulls)	Absent	Present
7.	Seed count per g of weight	3040-3310	4410-4520
8.	Seed size	Bold	Medium
9.	Estimated average seed yield (q/ha)	8-10	7-8
10.	Protein content in seeds (%)*	24.0	24.5
11.	Oil content in seeds (%)*	58.9	59.4
12.	Oleic + Linoleic fatty acids in oil (%)*	82.1	81.1
13.	Ca in seeds (mg/100g)*	1702	1213
14.	Fe in seeds (mg/100g)*	9.5	7.9
15.	Mg in seeds (mg/100g)*	405	286

*Analysed by ESAQC Lab., Central Food Technology Research Institute, Mysore

The newly developed GMS line has plant height ranging from 100 to 120 cm with short internodes and open canopy. Leaves are light green in colour, medium in size and possess one-nectar gland on mid rib. Flowers are creamy with light yellow claw and nectaries at the base of all the five petals, but nectaries are absent on the calyx. Three bracts with deep or medium deep notch surround corolla. Bracteoles may or may not contain nectaries. In general, 0-3 nectaries were recorded. They possess 8-10 serrations and are separated by U-shaped notch. Stamen number varies from 75-102 with yellow pollen colour and staminal length of 0.95 cm. Total ovary length is 0.8 cm, which is oval-shaped and medium in size. Boll weight is 4 to 4.5 g. LRA 5166 GMS line has desirable fibre properties (24.4 mm, 2.5% span length with bundle strength 20.5 g/tex 1/ 8 mm gauge), uniformity ratio of 48 and micronaire value of 3.2 (10^{-6} g/in). The line has good general combining ability and it is expected to produce high heterotic potential hybrids. The converted lines have been put to use in hybrid development programme.

Reference

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Registration of Cotton Germplasm, 30838 (INGR No. 02020; IC 296857)

Punit Mohan, PM Mukewar, VV Singh and CD Mayee

Central Institute for Cotton Research, Post Bag No. 2, Shankar Nagar, P.O. Nagpur-440 010 (Maharashtra)

The grey mildew/areolate mildew disease of cotton caused by *Ramularia areola* Atk., has become a very important disease in India affecting cultivation of all the four commercially cultivated *Gossypium* species. The disease has been recorded in epidemic form in Central India during the years 1958, 1988 and 1993 (Mukewar *et al.*, 1994). The yield losses have been recorded up to 68% under epidemic disease conditions in Maharashtra. Considering the great economic importance of the disease, a screening programme was initiated. A total of 1592 *Gossypium arboreum* germplasm lines available with Central Institute for Cotton Research (CICR), Nagpur were evaluated during the years 1985 to 1989. This resulted in identification of seven immune lines, Bangladesh, G-135-49 belonging to *Gossypium arboreum* race *bengalense* and 30305, 30814, 30826, 30838 and 30856 belonging to *Gossypium arboreum* race *cernuum* (Mukewar *et al.*, 1995). The resistance potential was further confirmed by subjecting to immunity performance in glasshouse and field conditions with artificial inoculations during 1989 to 1992. The basis of resistance among these lines was studied by conducting morphological and anatomical studies (Punit Mohan *et al.*, 1997) and biochemical analysis of factors governing resistance (Chakrabarty *et al.*, 2002). For assessment of commercial value, these lines were evaluated for fibre characteristics and other economic parameters (Punit Mohan *et al.*, 2001).

Of these lines, line 30838 is being registered for immunity against grey mildew/areolate mildew disease of cotton. It has five-lobed narrow elongated leaf with long stalk (up to 8 inches long), reticulate and palmate divergent venation and sparsely hairy surface. Flowers are yellow with long pedicle, short claw, and petal blotch red, anthers yellow with long filaments. It has three-large and broad bracteoles with serrated margin at apex and 2-3 teeth. Capsules are big, trilocular and elongated with tapering ends with long peduncle. Capsule surface is densely pitted. Staple length is 20.3 mm at 2.5% span length, uniformity ratio of 50%, fineness-micronaire above scale at 10^{-6} g/m micronaire, bundle strength 16.6 at bundle tenacity g/tex 3.2 mm, ginning outturn- 42.15% and seed-cotton yield/plant 44.59 g.

Reference

Chakrabarty PK, PM Mukewar, S Raj and V Sravan Kumar (2002) Biochemical factors governing resistance in diploid cotton against grey mildew. *Indian Phytopath.* **55:** 140-146.

Punit Mohan, PM Mukewar, S Raj and VV Singh (1997) Anatomy of *Gossypium arboreum* lines immune to grey mildew disease. *J. Cotton Res. Dev.* **11:** 191-195.

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produces 60 to 65 percent 'A' grade beans, which are bold in size and bettering cup quality. This selection has good drought tolerance with resistance to common races I and II of leaf rust caused by *Hemileia vastatrix* It is predominantly self-pollinated and yields 1200-1500 Kg/ha.

Novel Non-Narcotic Poppy

JR Sharma, RK Lal, AP Gupta, HO Misra and V Pant
Central Institute of Medicinal and Aromatic Plants, (Central Institute for Medicinal and Aromatic Plants (CIMAP), Lucknow-226 015 (Uttar Pradesh)

Sujata (INGR No. 01045, IC 296824)

An opium-less, alkaloid-free (non-narcotic) var. *Sujata* (LL34) of opium poppy (*Papaver somniferum*) was developed for the first time at CIMAP, Lucknow. It is a fine example of genetic conversion of a narcotic crop, like 'opium' poppy into non-narcotic 'seed' poppy. It does not exude latex (raw opium) on lancing (incision) of the capsule (Fig. 1). The straw (capsule hull) is also free from opium alkaloids, viz. morphine, codeine, thebaine and papaverine, etc.

It was developed by mutation breeding through a combined mutagenic treatment of 20 Kr gamma rays and 0.4 per cent Ethyl Methane Sulphonate on the high opium yielding parental strain, Mass-2B (var. *Sampada*). A latex-less mutant, LL34 was detected by 'ray-pluck' method (JR Sharma *et al.*, 1999) in M_2 generation, stabilized by M_7 generation and was finally re-christened as var. *Sujata*. The table summarises the morphological features of the mutant. It was evaluated for seed yield and non-latex production in initial evaluation (replicated, paired rows), bench scale (replicated, 5 x 3m plot size), and pilot scale trial (200 m^2 plot size) at Central Institute of Medicinal and Aromatic Plants for three years; giving 10-20 per cent higher seed yield (Table 1) than parent.

References

Sharma JR, RK Lal, AP Gupta, HO Misra, V Pant, NK Singh and V Pandey (1999) *Plant Breeding* (Berlin) **118**:449-452.

Sharma JR, RK Lal, HO Misra, AA Naqvi and DD Patra 1999. *Curr. Sci.* **77(12)**: 1584 -1589.

Table 1. The comparative features of *Sujata* and its parent Mass-2B

S. No.	Quali-quantitative traits	Sujata	Mass-2B
1.	Days to mid-flowering	100-105	100-104
2.	Plant height (cm)	80-100	85-110
3.	Capsule surface	Glabrous	Waxy
4.	Number of stigmatic rays per capsule	10-12	12-14
5.	Latex-flow on incision	Absent	Profuse
6.	Alkaloids in straw (capsule hulls)	Absent	Present
7.	Seed count per g of weight	3040-3310	4410-4520
8.	Seed size	Bold	Medium
9.	Estimated average seed yield (q/ha)	8-10	7-8
10.	Protein content in seeds (%)*	24.0	24.5
11.	Oil content in seeds (%)*	58.9	59.4
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*Analysed by ESAQC Lab., Central Food Technology Research Institute, Mysore

Registration of Cotton Germplasm Line, CNH 123 (INGR No. 02021; IC 325211)

VV Singh
Division of Crop Improvement, Central Institute for Cotton Research, Post Bag No. 2, Shankar Nagar P.O., Nagpur-440 010 (Maharashtra)

CNH 123, an upland cotton (*Gossypium hirsutum*) germplasm line was identified at Central Institute for Cotton Research, Nagpur, with resistance to Cotton Leaf Curl Virus during 2002, using mutation breeding. This is a mutant of SRT 1.

Description of morpho-agronomic characters of CNH 123 along with information on its multi-location performance for yield and yield components are summarized in Table 1.

CNH 123 has higher level of Bollworm resistance and tolerance to sucking pests. It is tolerant to moisture stress (performed well under rain-fed condition).

References

All India Coordinated Cotton Improvement Project – Annual Report for (1997-98) (North Zone) presented at Annual Workshop of AICCIP, April 26-27, 1998, held at CICR, Regional Station, Coimbatore.

Annual Report (1997-98) Natural Resource Management Central Institute for Cotton Research, Nagpur.

Table 1. Morpho-agronomic characters of CNH 123

Character	Details	Character	Details
Growth habit		**Flower characters**	
Plant type	Lanky	Bracts	Normal
Plant height (cm)	84.5	Petal colour	Cream
Monopodia/plant	2.6	Pollen colour	Cream
Sympodia/plant	21.1	Petal spot	Absent
Stem characters		**Fruit/capsule (boll) characters**	
Hairiness	Hairy	Bearing habit	Normal
Colour	Green purple	Size	Medium
Internode length (cm)	5.1-10	Shape	Round-oval
Leaf characters	Surface	Densely pitted	
Size	Small	Gossypol glands	Dense
Shape	Palmate	Capsule bearing	Normal
Lobing	Broad	Loculi/capsule	3-5
Colour	Green	**Seed characters**	
Surface	Hairy	Seeds/locule	7-9
Gossypol glands	Dense	Fuzz colour	White
Nectary/leaf	One	Seed index (g)	7.0
Yield attributes		**Fibre quality attributes**	
Capsules (boll)/plant	21.2	2.5% Span length (mm)	23.6
Seed-cotton yield/boll (g)	3.3	Uniformity ratio (%)	43.7
Seed-cotton yield/plant (g)	33.2	Micronaire value 10^{-6} g/in	3.8
Ginning outturn (%)	39.8	Maturity coefficient (%)	0.8
Lint index (G)	4.6	Tenacity (g/tex) (3.2 mm)	16.3

Registration of Sugarcane Germplasm, Co A 89085 (85 A 261) (INGR No. 02013; IC 296832)

JVR Bhupal Rao, NV Naidu, K Prasada Rao, V Rajabapa Rao, K Baghavan Dora, C Ramana Reddy, M Jayaprakash, J Papa Rao, Y Satyanarayana, A Padma Raju, LVV Prasada Rao, VSP Lalitha, KK Prasada Rao and MA Rama Rao
Regional Agricultural Research Station, Anakapalle-531 001, Visakhapatnam (Andhra Pradesh)

Co A 89085 is an early maturing sucrose-rich and red rot resistant sugarcane (*Saccharum officinarum*) clone with good ratooning. Co A 89085 was developed from a bi-parental cross Co 6806 x Co 775 followed by selection. It is suitable for cultivation under irrigated and rain-fed conditions. It comes to maturity by nine

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months and serves as an opening mill cane. It is insensitive to temperatures and, hence, can be planted from December-January to May-June. It responds to iron and zinc application both in plant and ratoon crops.

It is erect in habit with medium thick cane. Foliage is light green with medium-sized leaves and curved tips. Leaf sheath is light green with purple blotches. Exposed stalk is green with black blotches while un-exposed stalk is greenish yellow. It is non-lodging and non-flowering type. It is moderate cane yielder (95–115 t/ha), rich in sucrose (19-21%). Maximum sugar accumulation takes place from 8th month onwards up to 11 months without any deterioration. It has relatively less fibre and bagasse. The cane yield advantage over the popular standard variety, Co 6907 was 3.95%, while the CCS yield and jaggery yield were about 23.84 and 25.90%, respectively. It performed well in different locations of East Coast Zone under AICRP trials, on-farm testing and large-scale demonstrations.

It is resistant to all the three races of red rot (*Colletotricum falcatum*) *viz.*, Cf 419, Cf 997 and Cf 671 prevalent in Andhra Pradesh and suitable for crop rotation with cereal or pulse or even with commercial crops like cotton.

Registration of Coffee Germplasm, Selection 5A (INGR No. 02009; IC 2968845)

CS Srinivasan, D Ganesh and R Naidu
Central Coffee Research Institute, Chikmagalur (Karnataka)

Arabica coffee (*Coffea arabica*) shows different degrees of susceptibility to leaf rust (*Hemileia vastatrix* B. & Br.). Selection 5A was bred at Central Coffee Research Institute (CCRI), Chikmaglur, India by crossing Devamachy hybrid (a natural hybrid of *C. robusta* x *C. arabica*) with S.881 (a wild arabica strain introduced from Rume Sudan in Africa). The F_3 generation was planted in 1967, which showed high uniformity for bush size and rust resistance.

Selection 5A is characterized by spreading and drooping branches and generally smaller leaves. Young unfolding leaves are green in colour. Fruits and seeds are longish with reduced breadth giving more of "B" grade beans (retained on 6.00 mm sieve). It has recorded mean yield of 1176 kg/ha at CCRI. This selection performed well in the coffee area of Andhra Pradesh.

Selection 5A expresses high field tolerance to rust (80% plants free from rust). Seedlings tested at Coffee Rust Research Centre, Portugal, have shown high tolerance to "coffee berry disease" caused by *Colletotrichum kahawae* – a dreaded disease of coffee in Africa. It has shown cup quality at par with other arabica varieties developed in India.

Early Rice

SN Chakrabarti
Division of Genetics, Indian Agricultural Research Institute (IARI), Pusa, New Delhi-110 012

Jaldi Dhan 8 (INGR No. 01046, IC 296825)

Jaldi Dhan 8 is an extra early (80 days), medium tall upland rice, developed from cross between mutants Dular and N-22, having marked tolerance to moisture stress and coastal salinity. It is an improved plant type of medium tall stature with extra-early maturity, long glume opening period and ability to maintain cytoplasmic male sterility with wide abortiveness, making it a potential parent for hybrid rice breeding involving tropical japonica restorers. Also, it has been identified as an improved source for wide compatibility gene (WCG) to overcome sterility barriers in crosses between indica and japonica.

Table 1. Grain yield (q/ha) of Jaldi Dhan 8 under co-ordinated trials (1988-1991)

Variety	Direct seeded rainfed	Transplanted	Direct seeded irrigated
Jaldi Dhan 8	17.35 (60)*	32.29	38.19
Checks			
Sattari	12.89 (54)	24.03	–
Heera	15.93 (54)	20.59	17.51
Aditya	8.76 (68)	29.45	22.88

* days to 50% flowering

It is widely adapted to rainfed upland situation that has low inherent fertility status and frequent droughts. It possesses tolerance for Brown spot disease and pests like Gall midge biotype I, and leaf folder.

Powdery Mildew Resistant Hybrid, Hexaploid Triticale x Bread Wheat

GS Sethi and P Plaha
Biotechnology Centre, Chaudhury Saran Kumar Himachal Pradesh Krishi Vishwavidhyalaya (CSKHPKV), Palampur-176 062 (Himachal Pradesh)

RL 22 (INGR No. 01047, IC 296896)

One hundred true-breeding derivatives of triticale (X *Triticosecale* Wittmack, 2n=6x-42) x bread wheat (*Triticum aestivum* L. m. Thell, 2n=6x-42) were screened for their reaction against powdery mildew (*Erysiphe graminis* DC. Ex Merat f. sp. *tritici*), at the Himachal Pradesh Krishi Vishva Vidyalaya, Palampur and its regional research station, Kukumseri (Lahaul valley). One derivative, RL 22, was found to be free from powdery mildew. It has been maintaining its resistance since 1983.

Twenty-one diverse single-colony cultures of *Egt*, collected from North India, were used to characterize the resistance in RL 22. Seventeen lines/cultivars with known resistance genes and RL 22 was subjected to infection-typing technique. The RL 22 was resistant to all the cultures, but due to the non-differential response, the resistance gene could not be ascertained. Based upon the reaction of different cultures, it is inferred that the resistance gene in RL 22 is other than Pm 2, Pm 3a, Pm 3b, Pm 3c, Pm 4a, Pm 5, Pm 6, Pm 7, Pm 8, Pm (Ma), Pm 17 and Pm 20. All the 25 genes reported for powdery mildew resistance in wheat (McIntosh *et al.* 1998) are dominant, except Pm 5. In RL 22, the inheritance pattern of powdery mildew resistance revealed the presence of a single recessive gene governing resistance. Allelic test revealed that the resistance gene in RL 22 is different from Pm 5. Meiotic analysis of the F_1 of RL 22 with normal 42-chromosome wheat and *in situ* hybridisation pattern of mitotic metaphase chromosomes of RL 22 using labeled total genomic DNA as probe showed the presence of a pair of rye (*Secale cereale* L., 2n=2x=14) chromosomes. The C-binding analysis revealed this rye chromosome to be 6R, substituting the corresponding homoeologue 6D. This substituting rye chromosome might be imparting resistance to powdery mildew.

RL 22 is semi-spreading type with dark green, coarse leaves, pubescent glumes, late maturing, and has red and laterally compressed grains. However, considering a wide range of resistance to *Egt* isolates of northern India, RL 22, having a new resistance gene, can potentially be involved in the hybridisation programme to broaden the genetic base of wheat cultivars and impart a wide

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spectrum of resistance to powdery mildew.

The derivative was also free from the disease at the seedling stage as ascertained by inoculating with single-colony cultures of *Egt*. The triticale parent 'TL 68' of this line was free from powdery mildew, whereas, the bread wheat parent 'Shailaja' was susceptible.

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Early Maturing Gobhi Sarson

SP Landge

Botany Department, Nagpur University, Nagpur and National Dairy Development Board (NDDB), Anand, Gujarat

The exotic double zero cultivars of Gobhi sarson (*Brassica napus*) introduced in India are very late. These cultivars are not suitable for cultivation in mustard growing areas of the country. Therefore, an induced mutation-breeding programme was initiated to develop early maturing double zero genotypes suitable to agro-climatic conditions of the country.

NUDB-38 (INGR No. 01048, IC 296827)

NUDB-38 is an early maturing mutant of exotic Canadian variety Westar (*B. napus* L.) developed at the Botany Department, Nagpur University, Nagpur. Seeds of variety Westar of '00' quality (12 m moles/g seed and less than 1% erucic acid) were treated with sodium azide (pre-soaked in water for 12 hrs followed by Sodium azide, 0.06 % for 6 hrs). In M_2 generation 12 early flowering and maturing plants were isolated. They were subsequently tested for breeding behaviour. In M_3 generation, selection NUDB-38 was isolated from one of the mutants with early maturity (Table 1).

NUDB-38 has ovate dark green leaves, glabrous white coating, and undulate margin and dentations. Petiole is grooved with leafy wings at the base. Seed coat colour is blackish dark brown. Scanning Electron Microscopy showed two types of reticulation i.e., primary and secondary and pits shallow and circular in shape. It has shown early maturity across the locations. The '00' quality characters are similar to that of the parent variety 'Westar' (0 erucic acid with glucosinolate about 9.4 m moles/g of seed). Under multi-location trial in 1988-99 it gave an average yield of 1815 kg/ha as against 1319 kg/ha of HPN-3 and 1838 kg/ha of Pusa Bold and 1940 kg/ha of Varuna (Table 2).

Table 1. Salient characteristics of NUDB-38 compared to its parent

Genotype	Height (cm)	50% flowering (days)	Maturity (days)	1000-seed weight (g)	Reaction to disease
NUDB-38	109.6± 2.2	49.0± 2.0	110.0± 3.0	4.0 ± 0.39	Resistant to white rust
Westar	129.0 ± 2.2	75.0 ± 3.0	169.0± 3.0	4.2 ± 0.22	Resistant to white rust

Table 2. Yield data of NUDB-38 under multi-location trial

Line	Salon	Mehsana	Nagpur	Bharatpur-I	Bharatpur-II	Chandigarh	Anand	Gwalior	Delhi	Average
NUDB-38	1765	1760	936	1212	1904	1892	2209	2863	1797	1815
Varuna	1067	2132	908	1616	1942	1164	3246	3305	2082	1940
Pusa Bold	1032	1662	1080	1122	2079	1235	3304	3051	1980	1838
HPN-3	680	555	515	755	1887	1649	1894	1960	1976	1319

NUDB-42 (INGR No. 01049, IC 01050)

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spectrum of resistance to powdery mildew.

The derivative was also free from the disease at the seedling stage as ascertained by inoculating with single-colony cultures of *Egt*. The triticale parent 'TL 68' of this line was free from powdery mildew, whereas, the bread wheat parent 'Shailaja' was susceptible.

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Early Maturing Gobhi Sarson

SP Landge

Botany Department, Nagpur University, Nagpur and National Dairy Development Board (NDDB), Anand, Gujarat

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maturity from one of the mutants (Table 1).

NUDB-42 has ovate, dark green leaves with glabrous white coating, margin is undulate with dentation and petiole is grooved with leafy wings at the base. Seed coat colour is blackish dark brown and Scanning Electron Microscopy observations indicate primary and secondary reticulation and pits shallow and circular in shape. It has shown early maturity across the locations as compared to parent. The '00' quality characters of NUDB-42 are similar to that of the parent variety 'Westar' with zero erucic acid in oil and about 11.1 m moles of glucosinolate in per gram of seed. Under multi-location trials conducted by NUDB during 1988-99, the NUDB-42 yielded 1758 kg/ha as against 1319 kg/ha of HPN-3, 1838 kg/ha of Pusa Bold and 1940 kg/ha of Varuna (Table 2).

Table 1. Some characteristic features of NUDB-42

Genotype	Height (cm)	50% flowering (days)	Maturity (days)	1000 seed weight(g)	Reaction of disease
NUDB-42	102.1± 3.6	44.0± 2.0	100.0 ± 3.0	3.7 ± 0.37	Resistant to white rust
Westar	129.0 ± 2.2	75.0 ± 3.0	169.0 ± 3.0	4.2 ± 0.22	Resistant to white rust

Table 2. Yield evaluation of NUDB-42 under multi-location trial

Line	Salon	Mehsana	Nagpur	Bharatpur-I	Bharatpur-II	Chandigarh	Anand	Gwalior	Delhi	Average
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Yellow Seeded Indian Mustard

GG Nayar
Anantham, N. Paravur-683513, Ernakulam Dist., Kerala

TM-1 (INGR No. 01050, IC 296829)

Mustard (*Brassica juncea*) is being grown in our country from times immemorial for the seeds and oil that are used for various purposes, in medicine, food, industry etc. It is a seasonal crop and cultivated primarily during *Rabi* season. All the varieties of Indian mustard under cultivation possess black or blackish brown seeds. A mutant TM-1 having yellow seeds was developed for the first time in the country following irradiation of the seeds of a popular black seeded variety, Rai-5 of West Bengal. The mutant is identified for yellow seeds as a source for breeding yellow mustard that can restrict adulteration of mustard with similar looking seed of other crops. The features characterising the genotype are presented in Table 1.

Table 1. Characteristic features of Yellow Seeded Indian Mustard, TM-1

Pedigree	An artificially induced mutant from mustard variety Rai-5 of West Bengal
Plant type	Medium
Stem	Moderately branched, hairy
Leaves	Alternate, petiolate and hairy. Tender leaves are taken as a vegetable
Flowering	30-35 days after planting
Flowers	In raceme, bisexual, self-compatible. Sepals and petals-4, yellow in colour, hypogynous
Pods	Siliqua, beaked
Seeds	One seriate, yellow, seed coat reticulate, non-mucilaginous in water
Oil	25 to 30 per cent, golden yellow in colour
Maturity	100-110 days after planting
Pests and diseases	Moderately resistant to aphids, *Alternaria* blight and droughts
Chromosome number	2n=36

maturity from one of the mutants (Table 1).

NUDB-42 has ovate, dark green leaves with glabrous white coating, margin is undulate with dentation and petiole is grooved with leafy wings at the base. Seed coat colour is blackish dark brown and Scanning Electron Microscopy observations indicate primary and secondary reticulation and pits shallow and circular in shape. It has shown early maturity across the locations as compared to parent. The '00' quality characters of NUDB-42 are similar to that of the parent variety 'Westar' with zero erucic acid in oil and about 11.1 m moles of glucosinolate in per gram of seed. Under multi-location trials conducted by NUDB during 1988-99, the NUDB-42 yielded 1758 kg/ha as against 1319 kg/ha of HPN-3, 1838 kg/ha of Pusa Bold and 1940 kg/ha of Varuna (Table 2).

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