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Genetic Divergence in Chickpea (*Cicer arietinum* L.)

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Genetic divergence as measured by D^2 technique was studied for seed yield and its components in 60 chickpea germplasm accessions. The analysis of variance revealed significant differences among the genotypes for each character under study. The genotypes were grouped into 6 clusters and the maximum intra-cluster distance was observed in cluster I comprising 14 genotypes. Cluster III and VI were identified as genetically divergent. Considering the cluster means and cluster distances, IG 327, IG 326, IG 323, IG 311, IG 314 of cluster V; ICCV 89243, ICCV 91020, ICCV 91024, ICCV 91007, IG 313 of cluster VI; ICCV 91004, ICCV 91003, ICCV 89228 of cluster III; ICCV 91008, ICCV 91012, ICCV 89224 of cluster I were the most promising genotypes. They may be utilized in future breeding programme to obtain high heterotic effect or to develop desirable recombinants.

Key Words: Chickpea, *Cicer arietinum* L., Genetic divergence

Chickpea being the most important among pulse crops can change the scenario of pulse production in the country if improved cultivars of high and stable seed yield along with disease and pest resistance to biotic and abiotic stresses are developed. Determination of the nature and magnitude of genetic diversity and variability for the character under improvement is a prerequisite for any breeding programme. The present study was aimed at determining the grouping pattern of genotypes and identifying genetically diverse and agronomically desirable parents to be used in breeding programme for high seed yield.

Materials and Methods

The material for the study consisted of 60 chickpea germplasm accessions. Forty were received from International Crop Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh (ICRISAT) and 20 accessions were locally collected from Chhattisgarh. The material was grown in a Randomized Complete Block Design with two replications at Research Farm, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur. Each accession was grown in plots of 3 rows of 2 m length at spacing of 30 cm between rows and 10 cm between plants in a row. The nutrients (N:P:K) were applied @ 20 : 50 : 20 kg/ha as DAP and muriate of potash. Two sprays of monocrotophos 40 EC @ 750 ml/ha were applied to protect the crop from *Heliothis armigera*. Observations were recorded on five randomly selected plants per replication for seed yield (g) and its components *viz.*, days to 50% flowering, plant height (cm), number of secondary branches per plant, number of pods per plant, number of seeds per pod, number of seeds per plant and 100-seed weight (g). The data were subjected to the Mahalanobis (1936) D^2 statistics to measure the genetic divergence. The varieties were grouped into a number of clusters by Tocher's method as described by Rao (1952). The criterion was that any two varieties on an average showing lower D^2 values were grouped into the same cluster while those showing high D^2 values were grouped into different clusters.

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for each character, indicating the existence of variability among the genotypes for the characters studied. Based on the relative magnitude of D^2 values 60 genotypes were grouped into 6 clusters (Table 1). Maximum number of 14 genotypes were accommodated in cluster I followed by 12 in cluster II, 11 each in clusters IV and VI, 7 in cluster V and 5 genotypes in cluster III (Table 2). The maximum intra-cluster distance (D = 2.242) was observed in cluster I followed by cluster III (D = 2.009) and cluster VI (D = 1.789). The minimum intra-cluster value (D = 1.553) exhibited by cluster II indicated limited genetic divergence among the 12 genotypes.

The relative divergence of each cluster from other clusters (inter-cluster distances) indicated greater divergence between clusters III and VI (D = 4.116) followed by clusters II and III (D = 3.942) and clusters III and IV (D = 3.865). The selection of divergent genotypes from above clusters would produce a broad spectrum of variability for yield components studied, which may enable further selection and improvement in seed yield. The hybrids developed from the selected genotypes within limits of compatibility of these clusters may produce high magnitude of heterosis or desirable

Table 1. Clustering of 60 genotypes based on D^2 statistic

Cluster	No. of genotypes	Genotypes
I	14	ICCV 89224, ICCV 89238, ICCV 91001, ICCV 91006, ICCV 91008, ICCV 91012, ICCV 91013, ICCV 91014, ICCV 91016, ICCV 91017, ICCV 91018, ICCV 91130, ICCV 89205, ICCV 89220
II	12	IG 316, IG 322, IG 324, ICCV 91129, ICCV 89214, ICCV 89302, ICCV 89303, ICCV 89304, ICCV 89308, ICCV 89311, JG 74(C), ICCV 89325
III	5	ICCV 89215, ICCV 89216, ICCV 89228, ICCV 91003, ICCV 91004,
IV	11	IG 315, IG 317, IG 318, IG 319,s IG 321, IG 325, IG 328, IG 329, ICCV 89213, ICCV 89305, ICCV 89310
V	7	ICC 4918, IG 311, IG 314, IG 320, IG 323, IG 326, IG 327
VI	11	ICCV 89222, ICCV 91007, ICCV 91020, ICCV 91024, IG 312, IG 313, ICCV 91128, ICCV 89204S, ICCV 89209, ICCV 89240, ICCV 89243

Table 2. Mean intra-cluster (diagonal and bold) and inter-cluster distances among six clusters

Clusters	1	2	3	4	5	6
1	**5.027**	13.757	10.208	11.290	14.669	7.231
	(2.242)	(3.709)	(3.195)	(3.360)	(3.830)	(2.689)
2		**2.412**	15.539	2.849	13.513	5.527
		(1.553)	(3.942)	(1.688)	(3.676)	(2.351)
3			**4.036**	14.938	12.076	16.941
			(2.009)	(3.865)	(3.475)	(4.116)
4				**2.856**	8.387	5.396
				(1.690)	(2.896)	(2.323)
5					**2.921**	9.474
					(1.709)	(3.078)
6						**3.201**
						(1.789)

Note : D values given in parenthesis and D^2 values above in the diagonal and non-diagonal

transgressive segregants, which would be rewarding in chickpea improvement programme. Arora and Tripathi (1991), Kumar *et al.* (1998), Sirohi *et al.* (1999) and Yadav *et al.* (2000) also found similar degree of diversity in chickpea.

The cluster mean value for seed yield and its components are furnished in Table 3. There was a wide range of variation in cluster mean values for most of the traits except days to 50% flowering and secondary branches per plant. The average cluster-wise mean for different characters showed that the genotypes included in cluster V, such as IG 327, IG 326, IG 323 and IG 311 had maximum seed yield per plant. Genotypes IG 327, IG 314 and IG 326 of cluster V exhibited maximum number of pods per plant. The genotypes ICCV 89243, ICCV 91020, ICCV 91024, ICCV 91007 and IG 313 forming separate cluster (VI) had maximum 100-seed weight. ICCV 91004, ICCV 91003 and ICCV 89228 in cluster III had maximum number of seeds per plant. Genotypes ICCV 91016, ICCV 91008 and ICCV 91018 of cluster I flowered earlier while ICCV 91012, ICCV 89224, ICCV 91008 possessed maximum plant height. Of the cluster I genotypes ICCV 91008, ICCV 91012 and ICCV 89224 had maximum number of secondary branches per plant.

Crosses among the parents having genetic divergence are likely to yield desirable combinations. Therefore, a crossing programme should be initiated between the genotypes belonging to different clusters. In the present investigation hybridization among the genotypes IC 327, IG 326, IG 323, IG 311, IG 314 of cluster V (for seed yield per plant and pods per plant), ICCV 89243, ICCV 91020, ICCV 91024, ICCV 91007, IG 313 of cluster VI (for 100-seed weight), ICCV 91004, ICCV 91003, ICCV 89228 of cluster III (for seeds per plant), ICCV 91008, ICCV 91012 and ICCV 89224 of cluster I (for earliness, plant height, secondary branches)

Table 3. Cluster means for different characters

Cluster	No. of genotypes	D/F 50%	Plant height (cm)	Branches/ plant	Pods/ plant	Seeds/ plant	Seeds/ pod	100-seed wt(g)	Seed yield/ plant
I	14	55.35	54.29	3.27	59.35	1.42	74.09	21.93	5.60
II	12	60.75	45.29	2.43	46.25	1.19	50.44	17.41	6.22
III	5	56.84	44.20	2.68	70.40	1.64	101.58	19.79	5.40
IV	11	62.39	47.15	2.95	48.39	1.28	58.54	14.22	7.96
V	7	60.94	45.41	3.04	73.21	1.21	84.06	17.13	12.73
VI	11	60.60	50.63	2.91	51.08	1.15	56.85	24.00	9.14
MEAN		59.46	48.64	2.90	55.74	1.29	66.80	19.25	7.62
RANGE	MIN.	51.95	39.15	2.13	31.60	1.09	36.05	11.93	2.75
	MAX.	67.05	59.75	4.34	85.20	1.04	113.90	31.91	17.89
CV(%)		2.19	2.84	4.96	2.51	11.51	2.15	3.98	5.97

(Table 4) are expected to give promising and desirable recombinants in segregating generations because they possess desirable features as seen from their cluster means.

Table 4. Promising genotypes for different characters

S.No.	Characters	Genotypes
1	Seed yield	IG 327, IG 326, IG 323, IG 311
2	100-seed weight	ICCV 89243, ICCV 91020, ICCV 91024, ICCV 91007, IG 313
3	Pods per plant	IG 327, IG 314, IG 326
4	Seeds per plant	ICCV 91004, ICCV 91003, ICCV 89228
5	Days to 50 % flowering	ICCV 91016, ICCV 91008, ICCV 91018
6	No. of branches	ICCV 91008, ICCV 91012, ICCV 89224
7	Plant height	ICCV 91012, ICCV 89224, ICCV 91008

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Estimation of Genetic Divergence in Apple (*Malus* x *domestica* Borkh.)

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Genetic diversity was assessed in twenty-five apple genotypes on the basis of twenty characters. These genotypes were grouped into four clusters on the basis of relative magnitude of D^2 values using Tocher's method. Cluster I was the largest with twenty genotypes followed by cluster II consisting of three genotypes. The inter-cluster D value was maximum between cluster III and IV (55.46) followed by cluster I and IV (46.59). The maximum intra-cluster distance was in cluster II (19.10). Crossing between the genotypes belonging to cluster III and IV as well as cluster I and IV is expected to give maximum heterosis.

Key Words: Apple, Diversity, Mahalanobis

Genetic diversity is the result of evolution, including domestication and plant breeding. The process of natural evolution resulted in a build up of genetic diversity in natural population (Hintum, 1995). In order to understand the usable variability, grouping or classification of genetic stocks based on suitable scale is quite imperative. The choice of genetically divergent parents for hybridization under transgressive breeding programme is dependent upon categorization of breeding materials on the basis of appropriate criteria (Sharma, 1998). The information about the extent of genetic divergence is critical for the improvement of any crop in order to have high heterotic response and desirable segregants (George, 1976; Valsalakumari *et al.*, 1985). Though clonally propagated, significant variation is observed among apple cultivars and the estimation of genetic divergence in this fruit crop has not been done so far in detail. Apple being an important temperate fruit crop, high yielding, disease resistant and delicious apple varieties with good keeping quality are needed to be developed for the benefit of the apple cultivators.

Materials and Methods

The present investigation was carried out during 1999 using Randomized Block Design with three replications on twenty-five apple genotypes planted at a spacing of 5m x 3.5 m. The genotypes are listed in Table 1. The experimental site was located at 1250 meters above mean sea level and situated at 31^0 N latitude and 77^0 E longitude with an average annual rainfall of about 1200 mm. Three plants for each genotype were taken into consideration for recording observations on twenty characters. Ten fruits were taken randomly from each tree for recording data on mean fruit weight, length and breadth. The genetic divergence among the entries were estimated by Mahalanobis D^2 statistic as suggested by Rao (1952), Chaudhary and Singh (1975) and George (1976). All the genotypes were grouped into clusters according to Tocher's method as described by Rao (1952).

Results and Discussion

The assessment of genetic divergence among the genotypes showed the presence of appreciable amount of divergence. The genotypes were grouped into four clusters (Table 1). It was found that the early cultivars like Scab Resistant, Stark Red Rome, Paragon and Sweet Semi Red, mid cultivars Red Baron, Hardeman and Top Red, and late cultivars Skyline Supreme, Maayan and McIntosh were grouped in cluster I. The earliest cultivar, Early McIntosh and very late cultivar, Aziza fell into cluster III and II, respectively. Similar trend of clustering pattern was reported by Dwivedi and Mitra (1995) in litchi.

The average intra-cluster distance (Table 1) was maximum (19.10) in cluster II followed by cluster I (16.76). Highest inter-cluster distance was obtained between cluster III and IV (55.46) followed by cluster I and IV (46.59). Crossing between the genotypes Tropical Beauty and Early McIntosh falling in the most distant clusters IV and III, respectively, should result in maximum hybrid vigour and eventually desirable segregants leading to the development of useful genetic stocks. Cultivars Sweet Semi Red, Maayan, Red Baron, Spur Type Red Delicious, Skyline Supreme and Top Red from cluster I can be crossed with Tropical Beauty (cluster IV), as the earlier cultivars exhibited higher mean values for the yield contributing characters

Table 1. Clustering pattern of 25 genotypes and their average intra- and inter-cluster distance

Clusters	Genotypes	I	II	III	IV
I	McIntosh, Spur Type Red Delicious, Emperor, Top Red, Morspur, Red Royal, Skyline Supreme, Hardeman, Stoyanova Krasavista, Mollie's Delicious, Nemared Delicious, Maayan, Red Baron, Idared, Paragon, Stark Summer Gold, Alkane, Sweet Semi Red, Scab Resistant, Stark Red Rome	16.76	33.34	27.29	46.59
II	Cox's Orange Pippin, Parlin's Beauty, Aziza		19.10	43.58	29.78
III	Early McIntosh			0.00	55.46
IV	Tropical Beauty				0.00

and are likely to show desirable transgressive segregants.

The average cluster means (Table 2) showed that for the traits stem girth (72.33 cm), plant height (6.87 m), leaf area (264.77 cm^2), tree volume (132.73 m^3), days to full bloom (22.00 days), days between date of petal fall and date of commencement of June drop (89.67 days), fruit set 20 days after full bloom (41.73%) fruit set 40 days after full bloom (26.54%), final fruit before harvesting (24.67%), yield per plant (25.00 kg), mean fruit weight (188.33 g), mean fruit length (6.10 cm), mean fruit breadth (7.92 cm) and fruit yield per unit shoot length (1783.33g), cluster IV had the highest values. Cluster III was superior in respect of days to full bloom (22.00 days) and number of flowers per unit shoot length (24.42). Cluster II showed the maximum value for the traits like mean tree spread (6.02 m), total duration of flowering (18.20 days), days after full bloom (131.33 days) and number of fruits per unit shoot length (8.23). The character, days between date of commencement of June drop and date of harvesting possessed highest value (40.15 days) in cluster I. Thus, by involving the genotypes of outstanding mean performance from these clusters as potential parents in crosses, hybrids with high yield and quality can be developed.

The most important trait contributing maximum genetic divergence was yield per plant (22.00%, 1618) followed by mean fruit length (21.33 %, 1687) as per cent contribution and rank total, respectively. The minimum contribution towards genetic divergence was made by tree volume (0.00%, 4847) followed by stem girth (0.00%, 4605) and plant height (0.00%, 4425). The characters contributing maximum divergence can be given more emphasis for the purpose of fixing priority of parents in hybridization programme. It is suggested to effect crosses between cultivars selected from most distant clusters with high mean performance to get desirable transgressive segregants.

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Table 2. Cluster means for the characters among 25 genotypes and their contribution towards divergence

Traits	Clusters				Per cent	Rank
	I	II	III	IV	contribution	Total
Stem girth (cm)	45.22	55.89	31.67	72.33	0.00	4605
Plant height (m)	5.39	4.61	3.40	6.87	0.00	4425
Mean tree spread (m)	4.32	6.02	2.60	5.78	0.00	3976
Leaf area (cm^2)	176.65	194.36	138.73	264.77	0.00	3617
Tree volume (m^3)	58.33	80.45	13.93	132.73	0.00	4847
Days to full bloom	20.15	19.67	22.00	22.00	0.33	3909
Total duration of flowering	13.88	18.20	14.67	15.30	0.33	3073
Days after full bloom	121.33	131.33	101.00	126.67	20.33	1959
Days between petal fall and commencement of June drop	76.97	88.78	77.33	89.67	10.00	2305
Days between commencement of June drop and harvesting	40.15	37.78	19.33	32.33	0.67	3137
No. of flowers/unit shoot length	10.93	22.12	24.42	15.72	1.33	2819
No. of fruits/unit shoot length	5.86	8.23	5.67	7.67	3.67	2924
Fruit set 20 days after full bloom (%)	24.38	35.14	28.15	41.73	0.00	3581
Fruit set 40 days after full bloom (%)	15.65	22.18	22.33	26.54	1.33	2732
Final fruit before harvesting (%)	13.25	17.12	20.65	24.67	0.00	4141
Yield per plant (kg)	4.71	18.56	4.33	25.00	20.00	1618
Mean fruit weight (g)	113.85	99.22	107.00	188.33	14.33	2014
Mean fruit length (cm)	5.65	4.66	5.18	6.10	21.33	1687
Mean fruit breadth (cm)	6.75	5.21	6.61	7.92	1.00	2837
Fruit yield/unit shoot length (g)	764.43	1002.67	1068.67	1783.33	3.33	2794

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Characterization and Evaluation of White Clover Collections

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Seventy-seven lines of white clover, a temperate forage species, comprising sixty local collections made from different altitudes in Himachal Pradesh and seventeen exotic accessions procured from IGER, UK, were evaluated for twenty morphological parameters. Most of the characters exhibited variability both within and between populations. Based on overall morphology, the populations were grouped into eight groups. The populations with desirable traits were identified for further use in white clover improvement.

Key Words: Persistence, *Trifolium repens*, Variability, White Clover

White clover (*Trifolium repens*) is a sub-temperate – temperate forage species found where soil moisture is adequate for growth. It is the predominant legume sown in most grazed pastures, improving forage quality and providing upto 400kg N/ha in swards annually through N-fixation (Crush, 1987). The stoloniferous growth and phenotypic plasticity make it an ideal companion legume in most grass swards and enable it to withstand severe defoliation (Woodfield and Caradus, 1994). Despite these advantages, it is not popular among farmers in Himachal Pradesh and other sub-temperate and temperate regions in India, although it constitutes predominant component of flora of these regions. This calls for its improvement so that farmers can adopt it. Phenotypic recurrent selection within adapted germplasm pools has been by far the most common means of population improvement in white clover (Williams, 1987). In the present study seventy-seven collections of white clover were evaluated for identification of superior lines which can be used for its improvement.

Material and Methods

Sixty populations of white clover were collected from various altitudes in Himachal Pradesh and seventeen exotic lines were procured from IGER, UK. All the collections were raised in experimental plots measuring 2m x 1m in Randomised Block Design in three replicates during 1999-2000. The data were recorded on twenty one morphological characters (Table 1). The observations were made on five mature plants each of three replicates of all populations. For cyanogenesis, picrate paper test was used. The herbage was oven dried at 60° C to calculate dry matter yield. The collections were grouped on the basis of morphological data.

Results and Discussion

The range, mean values, S.D. and CV% for the twenty one characters recorded, are given in Table 1. The plant height ranged from 1.65 cm to 13.9 cm. Most of the local collections and exotic lines were dwarf- or medium-sized. Only six collections, namely RRCP-L-53, RRCP-L-55, RRCP-L-56, RRCP-L-111, RRCP-L-117 and RRCP-L-123 were classified as tall having height more than 10 cm. Five collections (RRCP-L-5, RRCP-L-10, RRCP-L-11, RRCP-L-12, RRCP-L-19) were identified as spreading. The number of stolon branches and growing points ranged between 2.1-11.62 and 2.5-11.0 respectively. The number of roots per stolon branch ranged from

Table 1. Morphological variability in white clover collections

Character	Range	Mean±S.D.	CV%
Plant height (cm)	1.65-13.90	5.91±2.71	45.67
Mid leaflet (mm)	3.20-8.60	4.63±2.37	51.33
Petiole length (cm)	1.28-13.60	5.48±2.66	48.45
Stolon branch (cm)	2.08-11.62	6.39±1.63	25.54
Stolon diameter (mm)	0.10-0.38	0.22±0.05	22.12
No. of stolon branches	2.00-16.00	6.35±2.05	32.23
Nodes/stolon branch	1.40-8.80	4.98±1.47	29.54
No. of growing points	2.50-11.00	5.89±1.71	29.03
Root length(cm)	2.53-13.87	6.63±3.09	46.64
No. of roots	3.00-46.00	11.02±7.57	68.72
Nodules/root	1.53-17.00	4.98±2.60	52.18
Heads/plant	27.00-153.00	90.85±33.24	36.59
Floret/head	17.50-62.00	41.72±10.52	25.21
Seed/floret	0.00-3.80	2.26±0.84	36.96
Seed/head	0.00-191.00	93.47±47.84	51.19
1000-seed weight (g)	0.53-0.56	0.54±0.01	1.11
Peduncle length (cm)	2.56-15.30	8.52±3.18	37.35
Peduncle diameter (mm)	0.10-0.20	0.12±0.03	26.45
Seed yield (t/ha)	0.05-0.80	0.22±0.14	64.22
Herbage (t/ha)	0.10-78.75	7.88±6.38	80.96
Cyanogenesis	0.00-4.83	1.65±1.51	91.92

3 to 46 and nodules per root from 1.43 to 17.0. Only three collections namely, RRCP-L-11, RRCP-L-15 and RRCP-L-65 had more than 10 nodules/root. There were two peaks for flowering in white clover. The first one was from March to May and second one from July to August. The populations came into flowering in March and continued till May. Fourteen populations were classified as early bloomers. All exotic and eight local populations were late flowering where flowering started during last week of April or first week of May. All the collections were self-incompatible. The seed set per floret ranged from 0 to 3.8. Only five populations i.e. RRCP-L-10, RRCP-L-17, RRCP-L-45, RRCP-L-52 and RRCP-L-58 set more than three seeds per floret.

Considerable variation was recorded for presence or absence of crescent in leaflets and cyanogenesis score. Thity-seven populations were classified as acyanogenic, having cyanogenesis score less than one, while 15 populations were classified as cyanogenic having cyanogenesis score more than three.

The present study reveals that white clover exhibits considerable variability for most of the morphological traits. Phenotypic plasticity is well known in white clover; High levels of genetic variability are typically detected both within and between white clover populations for most traits (Caradus *et al.*, 1989; Williams, 1987). Based on overall morphology and quality, the populations were grouped into eight groups (Table 2). Group I consisted of two populations where plants were large leaved, prostrate with lesser growing points and smaller stolons, cyanogenic, low in yield and nodulation and average in flower abundance. Group II had medium leaved, erect, persistent, cyanogenic, medium in yield and nodulation, late and average flowering. Group III consisted of medium leaved, erect, persistent, acyanogenic, medium in yield and nodulation, late and abundant flowering. Group IV consisted of medium leaved, prostrate, non-persistent, acyanogenic, medium in yield but low in nodulation, late and average flowering. Group V had small leaved, prostrate, persistent, acyanogenic, medium in yield and nodulation and abundant flowering. Group VI was similar to Group V except the populations had high incidence of cyanogenesis and average flowering. Group VII consisted of small leaved, prostrate, non-persistent, acyanogenic, medium in yield and less flowering. Group VIII differed from Group VII in having cyanogenic populations and abundant flowering. Groups III, V and VII had 30, 15 and 14 populations respectively.

Table 2. Grouping of white clover collections

Group	Characteristics	No. of populations
I	Large leaved, prostrate, non-persistent, cyanogenic, low in yield and nodulation and average in flower abundance	2
II	Medium leaved, erect, persistent, cyanogenic, medium in yield and nodulation, late and average flowering.	2
III	Medium leaved, erect, persistent, acyanogenic, medium in yield and nodulation, late and abundant flowering	30
IV	Medium leaved, prostrate, non-persistent, acyanogenic, medium in yield but low in nodulation, late and average flowering.	3
V	Small leaved, prostrate, persistent, acyanogenic, medium in yield and nodulation, abundant flowering.	15
VI	Small leaved, prostrate, persistent, cyanogenic, medium in yield and nodulation, average flowering.	3
VII	Small leaved, prostrate, non-persistent, acyanogenic, medium in yield and less flowering.	14
VIII	Small leaved, prostrate, non-persistent, cyanogenic, medium in yield and abundant flowering.	8

The uncertainty of persistence is the most important problem in white clover. The white clover types which are strongly stoloniferous will have better potential persistence than less stoloniferous types (Davies and Young, 1967). At the same time, it is considered that the prostrate small leaved varieties are less vulnerable to loss of their tap root system and therefore, their persistence is enhanced (Frame and Newbould, 1986). However the ideotype of white clover should bear large leaves as well as they should be persistent. The present

Table 3. Promising white clover collections

Character	Collection no.
Plant height	RRCP-L-123
Large leaves	RRCP-L-119
Long stolons	RRCP-L-17
Nodes/stolon branch	RRCP-L-11, RRCP-L-12
Growing points	RRCP-L-12
Nodules/root	RRCP-L-15
Flowering abundance	RRCP-L-19, RRCP-L-62
Seed/floret	RRCP-L-10, RRCP-L-52
Herbage yield	RRCP-L-23
Seed yield	RRCP-L-21
Acyanogenic	RRCP-L-11, RRCP-L-14, RRCP-L-17, RRCP-L-28, RRCP-L-41, RRCP-L-48, RRCP-L-49, RRCP-L-52, RRCP-L-59

study helped in identification of populations bearing particular desirable traits (Table 3) for improvement of white clover.

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

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Fifty-eight sunflower genotypes along with three checks were evaluated for obtaining information regarding genetic divergence through Mahalanobis' D^2 statistic. The analysis of variance revealed significant differences among the genotypes for all the traits. The 61 genotypes were grouped into 19 clusters, where cluster I accommodated maximum number of entries (29). The inter-cluster distance was maximum between cluster XIV and XIX followed by cluster V and XIX and cluster XVIII and XIX. Based on inter-cluster distance and *per se* performance of genotypes, four entries *viz.*, EC 376211, EC 399318, RHA 344 and BLC-P6 were selected which could be intercrossed to obtain high heterotic crosses and also to recover desirable transgressive segregants.

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

In order to develop genotypes with desirable traits, the breeder would like to choose genetically distant parents. Genetic diversity plays an important role in plant breeding because hybrids derived from the lines of diverse origin generally display a greater heterosis than those between closely related strains. In addition to the identification of diverse parent material, assessment of genetic divergence also helps in downsizing the core collections to be maintained based on diversity. Several methods have been developed to study the extent of genetic divergence in the genotypes among which Mahalanobis' generalized distance (D^2) (Mahalanobis, 1936) is frequently used. In sunflower several inbred lines have been recently developed from different source materials. In order to utilize the material for further improvement, it is imperative to know the extent of diversity among the inbreds. Keeping this in view, the present investigation was carried out to know the magnitude of diversity present in newly developed inbreds and to select diverse parents with an aim to obtain heterotic crosses and wide array of recombinants.

Materials and Methods

The material for the present study comprised 58 sunflower inbreds and three checks viz., KBSH 1, MSFH 17 and Surya. The experiment was conducted at Directorate of Oilseeds Research, Hyderabad during *kharif*, 1999. Each genotype was sown in two rows of 5 m length spaced at 60 cm with interplant distance of 30 cm. The experiment was laid in Randomized Block Design with three replications. In each entry, five plants were randomly tagged and utilized to collect data on yield and its component characters. The characters considered were days to 50% flowering, days to maturity, plant height (cm), head diameter (cm), 100-seed weight (g), seed yield plant^{-1} (g) and oil content (%). The data were subjected to statistical analysis using Mahalanobis' D^2 statistic (Mahalanobis, 1936). Treating D^2 as a generalized statistical distance, the criterion used by Tocher (Rao, 1952) was applied for determining the group constellation. The character-wise rank totals were used to calculate the percent contribution of each character to the total divergence. Average intra and inter-cluster distances were estimated as per the method given by Singh and Chaudhary (1977).

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the traits studied, indicating the scope for developing high yielding genotypes. Based on D^2 statistic, the 61 genotypes were grouped into 19 clusters with variable number of entries (Table 1) revealing the presence of considerable amount of genetic diversity in the material. Cluster I had the maximum number of 29 genotypes followed by cluster II with 7 genotypes and cluster III with 5 genotypes. These three clusters together accounted for most number of genotypes (41) reflecting narrow genetic diversity among them. The similarity in the base material from which they had been evolved might be the cause of genetic uniformity. Further, clusters IV, XIII and XV had two genotypes in each, while rest of the clusters were solitary entry clusters. However, lines derived from the same source of parentage were grouped in different clusters demonstrating the impact of selection pressure in increasing genetic diversity. The checks Surya, KBSH 1 and MSFH 17 were included in clusters III, X and XI, indicating their distinctness from the inbreds with respect to traits considered. Similar results were reported by Teklewold *et al.* (2000).

Table 1. Grouping of 61 sunflower genotypes into 19 clusters

Cluster	Number of genotypes	Genotypes
I	29	852B, RHA341, RHA348, 345B, ACC1439-1, M924, ACC664-1, NDOL-2, ACC1149, ACC179, ACC916-1, ACC1228-1, ACC914-1, ACC136, ACC1149-1, M1018, ACC916, ACC1139-1, EC399453, ACC1142, ACC 1585, ACC916, ACC1485, ACC64, ACC914, M-1008, ACC1385, M 1017, M1005 and M 1024
II	7	ACC1426, ACC1262, RHA298, 349B, M-1014, M-19-5, RHA345
III	5	ACC1464, M-1001, ACC1439, EC376240, SURYA
IV	2	EC399464, HA341
V	1	343B
VI	1	RHA 346
VII	1	ACC1254
VIII	1	350B
IX	1	ACC1168
X	1	KBSH-1
XI	1	MSFH-17
XII	1	M1026
XIII	2	378B, ACC1376
XIV	1	RHA344
XV	2	No.1874-1, ACC1174
XVI	1	RHA 6D-1
XVII	1	EC399318
XVIII	1	BLC-P_6
XIX	1	EC376211

The intra and inter-cluster D values are calculated and presented in Table 2. Cluster II recorded maximum intra cluster distance followed by clusters I, indicating similarities among the genotypes in respective clusters for the traits considered together. The members, of clusters XIV and XIX exhibited maximum divergence followed by clusters VI and XIX and clusters XVIII and XIX, indicating greater diversity between genotypes belonging to respective pairs of clusters, whereas clusters VI and XIV were closest with minimum genetic distance.

The cluster means for all the characters are presented in Table 3. Perusal of the data revealed considerable differences among the clusters for most of the characters studied. The cluster XVII (EC 399318) recorded highest seed yield per plant, days to maturity and low oil content, whereas cluster X (KBSH 1) had highest oil content. However, cluster XIX (EC 376211) had maximum head diameter, days to 50% flowering and 100-seed weight, while cluster XIV (RHA 344) recorded minimum head diameter and 100-seed weight. Further, cluster XVIII (BLC-P_6) recorded lowest plant height, days to maturity and high oil content. The contribution of each character towards divergence is also presented in Table 2. Among the seven characters studied, 100-seed weight contributed the most to divergence of genotypes, whereas the oil content contributed the least.

The data on inter-cluster distances and *per se* performance of genotypes were used to select genetically diverse and agronomically superior genotypes. The genotypes, exceptionally good with respect to one or more characters were deemed desirable. On this basis, four inbreds *viz.*, EC 376211, EC 399318, RHA 344 and BLC P_6 were selected. Intercrossing of divergent groups would lead to greater opportunity for crossing over, which releases hidden variability by breaking linkage (Thoday, 1960). Progenies derived from such diverse crosses are expected to show wide spectrum of genetic variability, providing a greater scope for isolating transgressive segregants in the advanced

Table 2. Average intra- and inter- cluster D values among the 19 clusters in sunflower

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX
I	**9.45**	14.79	12.94	17.75	14.27	20.26	11.37	12.28	14.38	13.30	17.42	15.13	18.90	24.76	15.26	17.12	17.73	22.91	23.24
II		**9.58**	22.67	22.90	16.96	13.43	16.84	17.59	17.91	19.19	27.14	15.11	18.92	15.93	14.77	12.20	24.78	17.63	34.34
III			**8.02**	12.76	19.43	27.67	12.70	12.16	14.62	14.90	11.17	18.16	22.70	32.23	20.29	25.70	17.01	27.97	14.98
IV				**9.19**	24.35	33.69	19.05	14.20	19.18	23.54	15.90	23.87	27.29	38.32	26.86	30.29	20.02	33.54	13.77
V					**0.00**	16.29	14.01	21.47	24.37	11.26	25.50	19.80	19.28	23.98	12.23	13.05	25.40	25.08	29.85
VI						**0.00**	18.49	24.12	24.13	19.13	33.40	15.83	18.07	8.41	10.91	14.16	32.26	13.40	40.59
VII							**0.00**	11.95	14.72	12.72	19.81	9.92	11.87	23.35	11.90	20.96	22.07	19.94	25.15
VIII								**0.00**	6.93	19.63	17.20	11.67	19.25	26.92	19.03	24.34	19.74	21.46	22.09
IX									**0.00**	19.99	17.30	11.45	21.54	25.37	20.04	25.14	20.01	19.83	24.50
X										**0.00**	18.64	17.96	21.09	24.94	12.79	17.11	21.09	24.05	25.16
XI											**0.00**	24.40	28.53	36.83	26.05	29.51	10.77	32.58	11.04
XII												**0.00**	14.11	17.96	12.90	22.36	26.48	12.29	30.92
XIII													**8.30**	20.91	14.75	23.51	27.61	18.76	34.37
XIV														**0.00**	16.57	19.02	34.93	10.95	45.18
XV															**9.16**	16.24	26.36	15.43	32.57
XVI																**0.00**	26.03	23.99	36.33
XVII																	**0.00**	32.56	18.82
XVIII																		**0.00**	40.23
XIX																			**0.00**

Bold values represent intra cluster D values

Table 3. Cluster means and percent contribution of characters towards divergence in sunflower

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	100 seed weight (g)	Seed yield/ plant (g)	Oil content (%)
I	55.87	87.51	129.92	12.41	5.52	20.59	30.20
II	55.05	84.86	103.81	9.18	4.03	12.05	29.92
III	55.47	87.60	145.93	15.01	7.20	27.68	30.05
IV	58.00	91.11	132.67	17.86	7.73	13.16	29.32
V	54.00	87.67	162.67	12.07	3.83	13.80	29.20
VI	49.67	80.00	123.33	8.43	2.93	11.50	24.03
VII	49.67	85.67	135.67	11.97	6.33	18.97	32.17
VIII	54.33	85.33	105.67	13.83	7.10	14.23	29.10
IX	54.67	82.67	100.33	12.30	7.13	24.20	26.03
X	54.00	84.67	168.33	12.30	4.80	34.63	38.93
XI	58.33	89.33	140.33	16.57	7.03	45.67	31.20
XII	49.00	80.33	111.00	10.83	6.25	14.77	32.17
XIII	44.33	86.50	109.17	10.63	5.35	14.63	32.75
XIV	48.33	77.67	95.33	6.83	2.67	15.53	23.17
XV	49.50	82.17	136.17	11.87	3.93	19.13	30.03
XVI	58.00	87.33	130.00	8.77	2.43	15.33	34.33
XVII	59.33	93.33	115.00	15.50	5.37	46.33	28.17
XVIII	46.67	75.67	90.00	11.23	3.93	16.10	34.37
XIX	60.00	92.00	159.33	20.10	8.23	37.07	27.07
Percent contribution	18.96	10.55	14.54	9.45	35.03	11.42	0.05

generations. Hence, these genotypes might be used in a multiple crossing programme to recover transgressive segregants.

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Characterisation and Evaluation of an Indigenous Collection of Greater Yam (*Dioscorea alata* L.)

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The germplasm holding of *Dioscorea alata* L. at National Bureau of Plant Genetic Resources, Regional Station, Thrissur, consisting of 182 accessions collected from different agro-ecological situations of peninsular India was subjected to characterisation and preliminary evaluation during May to January 1999-2001. Data recorded for 43 qualitative and 23 quantitative traits were analysed for frequency distribution, range, mean, standard deviation and coefficient of variation. The results showed wide range of variability in leaf length (9.77 – 23.83 cm), petiole length (5.43 – 20.0 cm), bulbil length (0.38 – 11.95 cm), number of bulbils per plant (0.66 – 268.33), tuber length (10.33 – 45.0 cm) and tuber yield per plant (0.33 – 4.40 kg). The bulbils produced by different accessions varied from very small amorphous callus-like ones to very large oblong ones. The shape of the tuber and the tuber flesh colour showed maximum range of variability. The graphical representation of variance for 20 different leaf, bulbil and tuber quantitative traits indicated large variability in leaf traits, bulbil production, tuber length and tuber perimeter. Observations on flowering indicated erratic female flowering and non-synchronisation of male and female phases. Studies on correlation between different quantitative traits showed maximum correlation coefficient of 0.9187 between basal wing length and leaf breadth. Path coefficient analysis showed maximum direct effect of 0.8296 of individual tuber weight on yield.

Key Words: Correlation, *Dioscorea alata*, Morphotypes, Path Analysis, Variability

Introduction

Dioscorea alata L. (Dioscoreaceae) is a crop of considerable importance under the subsistence farming system in the tropics. It is usually cultivated as a rainfed crop in Kerala, coastal regions of Karnataka, Maharashtra, parts of Orissa and Bihar, West Bengal, North-eastern and North-western states. The plant behaves as an annual under cultivation but can perennate through the underground storage tuber.

Considerable variability of this species occurs in India (Muralidharan *et al.*, 1985; Velayudhan *et al.*, 1991) and both morphological and biometrical techniques have been used for classification of existing variability by various workers (Burkill, 1917; Gooding, 1960; Rhodes and Martin, 1972). The cultivation of this crop is on the decline and its genetic resources are being eroded. Hence this work has been carried out with a view to characterise, evaluate and document an indigenous germplasm collection from different agro-ecological situations under the rainfed condition in humid tropics and to identify the potential lines.

Materials and Methods

On the basis of the subjective morphotypic classification of *D. alata* L. (Velayudhan *et al.*, 1991), 182 different accessions collected from different agro-ecological situations of Peninsular India were grown at the experimental farm of National Bureau of Plant Genetic Resources, Regional Station, Thrissur at 10.5° N latitude and 76.5° E longitude during the cropping seasons of 1999-2001, extending from May to January. The experimental plants were raised in augmented design with three controls and the package of practices as recommended by Kerala Agricultural University was followed (Anonymous, 1996).

The data on various qualitative and quantitative vegetative characters of leaves, bulbils, and flowers were recorded at the maximum vegetative growth period during September to October and the post harvest tuber traits after harvesting during January. Data on 43 qualitative and 23 quantitative traits were recorded on 3 different plants per accession. Frequency distribution of various qualitative characteristics was computed. Range, mean, standard deviation and coefficient of variation were worked out for the quantitative traits and simple correlation and path coefficient analysis were carried out based on Dewey and Lu (1959). The existence of variability in 20 different quantitative traits were analysed by computing variance and a graphical representation has also been made. Incidence of Anthracnose blotch disease in these collections was already reported (Asha and Nair, 2001).

Results and Discussion

1. *Variability in Leaf Traits*

The foliar traits in *D. alata* showed wide variation in leaf shape between ovate, round, cordate, elongated sub-hastate and oblong sub-hastate ones and setting of basal wings from very wide to close overlapping ones through medium wide and wide ones. Leaf margin colour varied between light green and purple through green to dark green, very light purple and light purple. Petiole top and base colour varied from light purple to dark purple. Variation in waviness and colour of the petiole wing were distinct and the former varied between less waviness to very high waviness and the latter between very light green to dark purple through light purple and purple.

The range of variability recorded in quantitative leaf traits are given in Table 1. The percentage coefficient of variation was more for the distance between basal wings (74.05%) followed by depth of sinus of leaves (30.177%). This indicates that range of variability was more in these traits compared to leaf length, breadth and petiole length. The distinct variability in setting up of basal wings of leaves contributes more towards the shapes of leaves and in turn results in the variation of sinus depth of individual leaves. The variability of leaf traits as given in Fig. 1 represents the occurrence of distinct variation in leaf length, breadth and petiole length. The frequency distribution of these traits showed the occurrence of limited numbers of accessions in higher levels of leaf measurements.

2. *Variability in Aerial Bulbil Traits*

Being a vegetatively propagated species, production of aerial bulbils is one of the means of propagation in *D. alata.* Profuse bulbil production of individual accessions coincided with absence of flowering and can be an indication of degeneration of sexuality in this dioecious species. Of the 182 accessions under consideration, 156 accessions bore aerial bulbils and profuse bulbil production was recorded in TCR 265 (IC 87422). The days taken for bulbil initiation ranged between 75 (IC 136850) and 159 days (IC 87398). Variability observed in size and shape of aerial bulbils were so distinct that it varied from very small amorphous

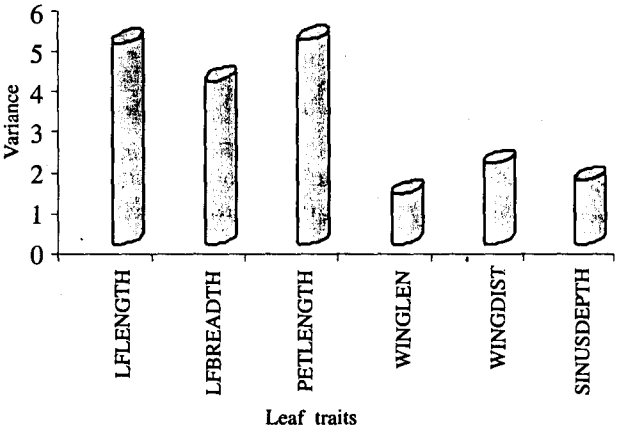

Fig. 1. Variability in leaf traits

Table I. Variability in quantitative traits in *D. alata*

S. No.	Quantitative traits	Accessions (no.)	Range	Mean	SD	% CV
1	Leaf length	182	9.77 - 23.83 cm	16.749	2.226	13.29
2	Leaf breadth	182	6.87 - 16.93 cm	11.995	2.004	16.706
3	Petiole length	182	5.43 - 20.00 cm	10.960	2.246	20.492
4	Basal wing length	182	3.17 - 9.57 cm	6.216	1.104	17.76
5	Dist. between basal wings	182	0.27 - 6.13 cm	1.90	1.407	74.05
6	Sinus depth of leaf	182	1.00 - 6.67 cm	4.119	1.243	30.177
7	Bulbil length	156	0.38 - 11.95 cm	5.395	2.495	46.246
8	Bulbil thickness	156	0.56 - 6.83 cm	3.444	1.196	34.727
9	Bulbil weight	156	0.20 - 124.50 g	33.564	23.809	70.936
10	Total no. of bulbils	156	2.00 - 805.00	139.827	135.194	96.686
11	Bulbils per plant	156	0.66 - 268.33	45.238	45.075	99.639
12	Bulbil yield	156	0.001 - 3.79 kg	0.821	0.835	101.70
13	No. of tubers	182	1.00 - 9.33	2.900	1.722	59.379
14	Individual tuber weight	182	0.30 - 2.63 g	1.158	0.498	43.005
15	Tuber length	182	10.33 - 45.00 cm	20.653	6.292	30.465
16	Tuber perimeter	182	22.67 - 55.67 cm	39.972	6.566	16.426
17	No. of branches of tuber	182	0.00 - 10.00	3.456	1.663	48.119
18	Neck length of tuber	182	0.00 - 10.00 cm	3.186	2.124	66.67
19	Yield per plant	182	0.33 - 4.40 kg	1.788	0.723	40.436
20	Total yield	182	1.00 - 13.20 kg	5.372	2.167	40.338

callus-like ones (IC 266647) to very large oblong ones TCR 266 (IC 87423) through medium to large spherical, irregular and digitate ones. The cortex colour of bulbils varied between light green, green, yellowish purple, purple and dark purple and the flesh colour between light yellow, light purple, white, purplish white, yellow and dark purple. About 50% of the accessions were with bulbil spines and the other 50% without spines on bulbils. The variability recorded in quantitative bulbil traits were summarised in Table I. The percentage coefficient of variation calculated for bulbil traits were more for bulbil yield, bulbils/plant and total number of bulbils (Fig. 2). This considerable diversity probably may be due to polymorphism and adaptation to different cultural conditions.

3. *Variability in Tuber Traits*

The tuber traits in the germplasm showed variation in both qualitative and quantitative characteristics. The shape of the tuber varied between digitate to cylindrical oblong through spherical and irregular ones. Rootiness varied from very low to highly rooted ones, the cortex colour between light green, light purple, purple and dark purple and the tuber flesh colour from pure white to very dark purple one through very light purple tint, light yellow, orange yellow, and yellow.

The variability observed in quantitative tuber traits is also summarised in Table 1. The number of tubers present in individual accessions ranged from 1 to 9.33 and the individual tuber weight between 0.30 kg to 2.63 kg. The yield per plant ranged between 0.33 kg to 4.40 kg and total yield from 1 kg (IC 87422) to 13.20 kg (IC 266655). Of the various tuber traits, the coefficient of variation was more for neck length of tuber (66.67%) followed by number of tubers (59.39%) and number of branches of tuber (48.12%). The frequency distribution curves drawn for the major tuber traits showed discontinuous variation. This highlights the fact that the indigenous germplasm has very few promising lines in the yield-related components. Fig. 3 represents the variation present in tuber traits; it was found maximum in tuber length and tuber perimeter.

4. *Flowering Behaviour*

Observations on flowering deficiencies and fertility status of this dioecious species have earlier been reported (Abraham, 1997). In the present study also, complementary observations were obtained regarding differential flowering behaviour of different accessions. Out of 182 accessions under observation, 90 flowered, of which 6 were female and rest were male. The female accessions include IC numbers 87372, 87389 B and 266653 of M6 and IC numbers 46067, 87339 B, and 87342 A of M16. Female flowering was erratic and significantly lower than the males. Distinctly different flowering periods of the two sexes resulted in the non-synchronisation of the male and female phases. Moreover, flower production of the sexes showed a greater disparity in number, the females producing far fewer flowers than the males and the female flowering commenced only in a later phase against the early male flowers. Withering of inflorescence, non-maturing of buds and non-opening of mature buds were common in female ones in contrast to males.

Analysis of Correlation

The analysis of simple correlation was carried out in 153 different combinations involving 18 traits in 156

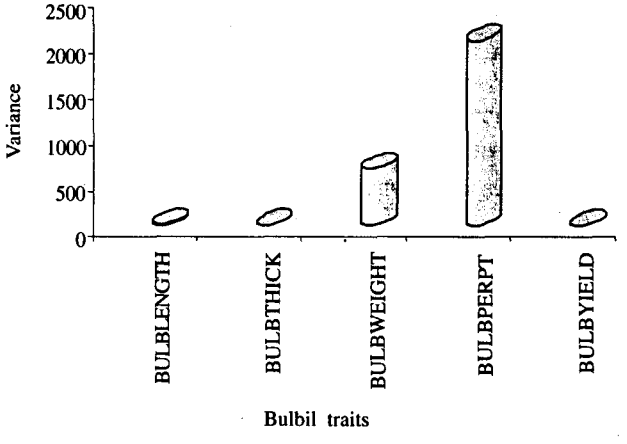

Fig. 2. Variability in bulbil traits

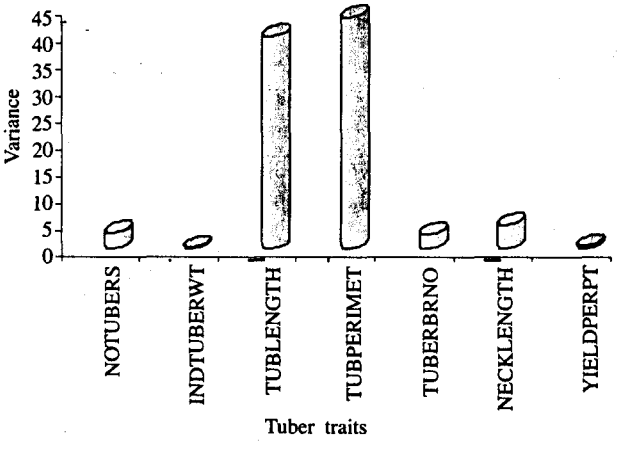

Fig. 3. Variability in tuber traits

accessions. The result in Table 2 revealed maximum correlation between leaf breadth and basal wing length followed by bulbils per plant, bulbil yield, bulbil thickness and bulbil weight, individual tuber weight and yield per plant and leaf breadth and petiole length. Correlation between yield per plant and bulbil traits were negative indicating the fact that more the production of aerial vegetative bulbils less will be the tuber yield.

Analysis of Direct and Indirect Effects

Path coefficient analysis (Table 3) revealed that individual tuber weight had maximum direct effect (0.8296) on yield followed by number of tubers (0.4809) suggesting more value to these traits in selection. Direct effects were negative for leaf length, basal wing length, distance between basal wings, bulbil weight, bulbil yield, neck length and number of branches of tuber.

Maximum positive indirect effect (0.5256) was exerted by individual tuber weight and tuber perimeter followed by tuber weight and tuber length (0.4938). The low residual effect of 0.2132 obtained in the study indicates the adequacy and legitimacy of the characters used.

Promising Lines

Based on the number of tubers produced, individual tuber weight and yield per plant, IC numbers 266649 and 266655 were found more productive giving more than 4 kg/plant. The earlier releases of Central Tuber Crops Research Institute, Trivandrum namely Sree Keerti,

Table 2. Correlation matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	1.000																	
2	0.4609	1.000																
3	0.2070	0.7517	1.000															
4	0.4770	0.9187	0.6935	1.000														
5	0.1926	-0.2879	-0.3328	-0.1832	1.000													
6	0.0016	0.5068	0.5440	0.4461	-0.5928	1.000												
7	-0.2884	0.2811	0.3986	0.1673	-0.4455	0.3051	1.000											
8	0.0211	0.1879	0.2237	0.2163	-0.3280	0.1547	0.3534	1.000										
9	-0.0878	0.1501	0.2118	0.1462	-0.3673	0.1734	0.6242	0.8409	1.000									
10	-0.1454	-0.0185	0.0813	-0.0592	-0.2753	0.0245	0.3726	0.4446	0.4761	1.000								
11	-0.1729	0.0724	0.1859	0.0528	-0.2819	0.0689	0.4901	0.6095	0.6855	0.8907	1.000							
12	0.0476	-0.3200	-0.3407	-0.3276	0.5768	-0.3294	-0.4347	-0.4071	-0.4154	-0.3316	-0.3983	1.000						
13	-0.1835	0.3296	0.5058	0.3420	-0.3120	0.3763	0.2054	0.1312	0.1240	-0.0679	0.0852	-0.3454	1.000					
14	-0.4433	0.1115	0.3816	0.0681	-0.2495	0.2791	0.4496	0.0162	0.1036	-0.0478	0.1073	-0.1737	0.5952	1.000				
15	0.0900	0.1773	0.1347	0.2897	0.0262	0.0969	-0.2400	0.1390	0.0152	-0.2162	-0.0838	-0.1293	0.6335	-0.0424	1.000			
16	0.1236	0.0301	0.0197	0.0799	0.2808	0.0217	-0.2587	-0.0827	-0.1835	-0.1764	-0.1291	0.2444	0.2285	0.0401	0.4198	1.000		
17	0.0990	-0.3391	-0.4225	-0.2376	0.3729	-0.4432	-0.3222	-0.0999	-0.1102	-0.0893	-0.1421	0.2670	-0.2791	-0.3099	-0.0008	-0.0929	1.000	
18	-0.1791	0.2673	0.4469	0.2361	-0.1754	0.3513	0.1311	-0.0078	-0.0382	-0.0857	-0.0011	0.0451	0.7834	0.5375	0.4450	0.2677	-0.2839	1.000

Table 3. Matrix of direct and indirect effects

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	Corr. value
1	**-0.0108**	0.0181	0.0097	-0.0119	-0.0069	0.0001	-0.0394	0.0032	0.0215	-0.0266	0.0130	0.0229	-0.1522	-0.0145	0.0027	-0.0028	-0.0053	-0.1791
2	-0.0050	**0.0393**	0.0353	-0.0230	0.0103	0.0430	0.0384	0.0287	-0.0368	-0.0034	-0.0054	-0.1539	0.2734	0.0036	0.0053	-0.0007	0.0181	0.2673
3	-0.0022	0.0296	**0.0470**	-0.0173	0.0119	0.0462	0.0544	0.0342	-0.0520	0.0149	-0.0139	-0.1639	0.4196	0.0125	0.0040	-0.0004	0.0225	0.4469
4	-0.0052	0.0361	0.0326	**-0.0250**	0.0065	0.0379	0.0229	0.0330	-0.0359	-0.0108	-0.0040	-0.1576	0.2837	0.0022	0.0086	-0.0018	0.0127	0.2361
5	-0.0021	-0.0113	-0.0157	0.0046	**-0.0356**	-0.0503	-0.0609	-0.0501	0.0902	-0.0503	0.0211	0.2774	-0.2588	-0.0082	0.0008	-0.0063	-0.0199	-0.1754
6	0.0000	0.0199	0.0256	-0.0112	0.0211	**0.0849**	0.0417	0.0236	-0.0426	0.0045	-0.0052	-0.1584	0.3122	0.0091	0.0029	-0.0065	0.0236	0.3513
7	0.0031	0.0111	0.0187	-0.0042	0.0159	0.0259	**0.1366**	0.0540	-0.1532	0.0681	-0.0367	-0.2091	0.1704	0.0147	-0.0071	0.0058	0.0172	0.1311
8	-0.0002	0.0074	0.0105	-0.0054	0.0117	0.0131	0.0483	**0.1527**	-0.2064	0.0813	-0.0457	-0.1958	0.1089	0.0005	0.0041	0.0019	0.0053	-0.0078
9	0.0009	0.0059	0.0100	-0.0037	0.0131	0.0147	0.0853	0.1284	**-0.2455**	0.0870	-0.0514	-0.1998	0.1029	0.0034	0.0005	0.0041	0.0059	-0.0382
10	0.0016	-0.0007	0.0038	0.0015	0.0098	0.0021	0.0509	0.0679	-0.1168	**0.1828**	-0.0670	-0.1599	-0.0571	-0.0015	-0.0066	0.0041	0.0054	-0.0857
11	0.0019	0.0028	0.0087	-0.0013	0.0100	0.0058	0.0670	0.0931	-0.1683	0.1635	**-0.0750**	-0.1916	0.0706	0.0035	-0.0025	0.0029	0.0076	-0.0011
12	-0.0005	-0.0126	-0.0160	0.0082	-0.0206	-0.0280	-0.0594	-0.0622	0.1020	-0.0608	0.0299	**0.4809**	-0.2866	-0.0057	-0.0038	-0.0055	-0.0142	0.0451
13	0.0020	0.0130	0.0238	-0.0086	0.0111	0.0319	0.0281	0.0200	-0.0304	-0.0126	-0.0064	-0.1661	**0.8296**	0.0194	0.0189	-0.0051	0.0149	0.7834
14	0.0048	0.0044	0.0179	-0.0017	0.0089	0.0237	0.0614	0.0025	-0.0254	-0.0082	-0.0080	-0.0835	0.4938	**0.0327**	-0.0013	-0.0009	0.0165	0.5375
15	-0.0010	0.0070	0.0063	-0.0072	-0.0009	0.0082	-0.0328	0.0212	-0.0037	-0.0408	0.0063	-0.0622	0.5256	-0.0014	**0.0298**	-0.0094	0.0000	0.4450
16	-0.0013	0.0012	0.0009	-0.0020	-0.0100	0.0018	-0.0353	-0.0126	0.0450	-0.0330	0.0097	0.1175	0.1896	0.0013	0.0125	**-0.0225**	0.0050	0.2677
17	-0.0011	-0.0133	-0.0199	0.0059	-0.0133	-0.0376	-0.0440	-0.0153	0.0270	-0.0186	0.0107	0.1284	-0.2315	-0.0101	0.0000	0.0021	**-0.0534**	-0.2839

Residual = 0.2132

1. Leaf length 2. Leaf breadth, 3. Petiole length, 4. Basal wing length 5. Distance between basal wings 6. Sinus depth of leaf 7. Bulbil length 8. Bulbil thickness 9. Bulbil weight 10. Bulbils per plant 11. Bulbil yield 12. No. of tubers 13. Individual tuber weight 14. Tuber length 15. Tuber perimeter 16. Number branches of tuber 17. Neck length of tuber 18. Yield per plant

Sree Roopa (25-30 t/ha) and Sree Shilpa (28-40 t/ha) has been compared with the promising lines and it has been found that the IC Nos. 87393, 266657, 87389B (35-40 t/ha) were superior, which can be considered for varietal release.

Conclusion

The characterisation and evaluation of the germplasm revealed that there exists distinct variation in qualitative and quantitative traits. Moreover the production of more vegetative aerial bulbils results in decrease of underground tuber production.

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Characterization and Evaluation of Mungbean (*Vigna radiata* L. Wilczek) Germplasm from Andhra Pradesh, India

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The results of preliminary characterization and evaluation of 89 accessions of mungbean germplasm collected from Andhra Pradesh under the National Agricultural Technology Project (Plant Biodiversity) have been presented in this paper. A total of 26 agro-morphological characters was studied. The accessions exhibited good variability in both qualitative and quantitative traits. Among the qualitative traits studied, maximum diversity was observed in leaf colour, leafiness, pod colour and seed colour. Variability observed in quantitative traits was in days to flowering (40-60 days), plant height (15.6 – 49.8 cm), number of clusters per plant (2.2 – 13.3), number of pods/plant (5 – 35.3), 100-seed weight (2.28 – 6.6 g). The protein content ranged from 12.6 to 25.9%. Correlation coefficients of the quantitative traits have been analysed.

Key Words: Characterization, Evaluation, Germplasm, Mungbean

Greengram, also known as Mungbean, is the most widely grown pulse crop in the Indian sub-continent. This crop having originated in India has a good record of domestication from ancient times (De Candolle 1884; Vavilov 1926; Zhukovsky 1950). The maximum diversity occurs in greengram (*Vigna radiata*) which is distributed throughout India across length and breadth of the country.

National Bureau of Plant Genetic Resources (NBPGR), New Delhi has been endeavouring to build up the genetic resources in greengram and other major and minor pulse germplasm and has acquired about 37,000 germplasm samples of 20 grain legumes of major and minor importance (Kawalkar *et al.*, 1996). Andhra Pradesh stands fifth in acreage among the states growing mungbean. Good phenotypic diversity is reported in cultivated greengram landraces.

Even though sizeable number of accessions have been collected from this region earlier, to salvage the landrace diversity from unsurveyed and undersurveyed areas, two surveys were undertaken during 1999-2000 in Telangana and Rayalaseema under the National Agricultural Technology Project (Plant Biodiversity). A total of 89 accessions could be acquired by the NBPGR Regional Station, Hyderabad.

Characterization and evaluation of germplasm is required to analyze and utilize the diversity in the germplasm collections. Hence, an attempt has been made to evaluate the greengram collections from the state to assess variability and identify the promising accessions. This also supplements the information already published earlier (Kawalkar *et al.*, 1996).

Materials and Methods

The preliminary characterization and evaluation of 89 accessions of Mungbean was carried out at the NBPGR regional station, Rajendranagar, Hyderabad during summer 2001. The centre is located at 17°19' N latitude, 78°23' E longitude and at an altitude of 542 m above MSL with temperature varying from a minimum of 10° C to a maximum of 42° C during the cropping season. The soil type is of red sandy loam. The germplasm accessions were raised in an Augmented Randomized Incomplete Block Design with check varieties (K-851, Kopergaon, and LGG-504) in each block. The accessions were grown in 3 m rows with a row to row spacing of 60 cm and plant to plant spacing of 15 cm. Standard agronomic and plant protection practices were followed during the cropping season. The data on qualitative and quantitative descriptors were recorded using minimal descriptors developed by NBPGR (Mahajan *et al.*, 2000). Five representative plants in each accession were tagged for recording the qualitative and quantitative characters. Protein content of each accession was estimated from fully developed dry seeds using Lowry's method (Lowry *et al.*, 1951). All the quantitative data were analysed statistically.

Results and Discussion

The 89 accessions of greengram germplasm were characterized and evaluated for 26 agro-morphological characters. Wide range of variability was recorded

in both qualitative and quantitative characters. All the accessions possessed greenish yellow flowers, non-shattering pods, entire leaflet and showed no twining tendency, although twining growth habit is reported to be dominant (Sen and Ghosh, 1959). However, variation was observed in plant growth habit, leaf colour, branching pattern, leafiness, raceme position, pod pubescence, pod shape, mature pod colour and seed colour. The range of variability and frequency observed in qualitative traits are given in Table 1. Similar observations were also reported earlier (Kawalkar *et al.*, 1996; Arora *et al.*, 1973; Chandel 1980).

The quantitative characters also showed wide variation in the evaluated germplasm. The results of descriptive statistical analysis are presented in Table 2. The characters of plant height and pods/plant seem to be highly variable based on the variance. Days to flowering ranged from 40-60 days. It is reported in earlier studies that the earliness is due to additive gene action (Chowdhury *et al.*, 1971; Ramanujam *et al.*, 1974). However, heritability estimates were not assessed in the present study. The protein content ranged from 12.6% to 25.9%.

Table 1. Characterisation and preliminary evaluation of greengram

Character	Frequency
Early plant vigour	Poor-18
	Good-62
	Very Good-09
Plant growth habit	Erect-86
	Spreading-3
Leaf colour	Light green-10
	Intermediate green-40
	Dark green-39
Terminal leaf length	Small-89
Leaflet shape	Entire-89
Plant surface	Glabrous-84
	Pubescent-5
Branching pattern	Central-57
	Basal-26
	Top-6
Flower colour	Greenish Yellow-89
Leafiness	Sparse-25
	Intermediate-58
	Abundant-6
Flowering tendency	Asynchronous-89
Twining tendency	None-89
Raceme position	Above canopy-33
	Intermediate-56
Pod pubescence	Glabrous-2
	Sparsely pubescent-82
	Moderately pubescent-5
Pod colour (mature)	Straw-09
	Tan-35
	Brown-05
	Brownish Black-27
	Black-13
Pod shape	Straight-74
	Curved-15
Shattering habit	Absent-89
Seed colour	Light green 46
	Dark green-07
	Greenish yellow-19
	Yellow-02
	Brown-04
	Brownish green-10
	Brown mosaic-01

Correlation coefficients of yield vs. some major yield-attributing characters are summarized in Table 3. Clusters per plant and pods per plant showed high positive correlation with yield. Similar results were also reported by Shanmughasundaram and Kim (1996). Negative correlation observed in the case of seed weight with pods per plant corroborates the earlier observations by Shanmughasundaram and Kim (1996). Promising lines identified performing better than the check varieties are listed in Table 4.

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Table 2. Statistical analysis of quantitative characters

Character	Min.	Max.	Mean±SE	Std.Deviation	Sample variance
Days to 50% flowering	40	60	43.7±0.45	4.24	18.03
Plant Height (cm)	15.6	49.8	29.5±0.71	6.71	45.07
Number of Primary branches	0	4.6	1.47±0.12	1.13	1.29
Number of Clusters per plant	2.2	13.3	5.66±0.20	1.96	3.9
Number of pods/plant	5	35.3	14.02±0.69	6.55	42.9
Number of seeds/pod	4	12.0	9.58±0.16	1.57	2.47
Seed yield per plant (g)	2	20.0	10.0±0.5	4.80	23.1
100-Seed weight (g)	2.28	6.6	3.54±0.07	0.66	0.43
Protein content (%)	12.6	25.9	21.3±0.024	0.24	0.06

Table 3. Correlation coefficients of yield attributing characters

	DF	PLHT	PBR	CLP	PPP	SEP	SEYL	SEWT	PRO
DF	1.00								
PLHT	0.16	1.00							
PBR	0.33 **	0.41**	1.00						
CLP	0.19	0.62**	0.53**	1.00					
PPP	0.01	0.60**	0.35**	0.82**	1.00				
SEP	0.11	0.25*	0.18	0.07	0.01	1.00			
SEYL	-0.11	0.32**	0.21*	0.30**	0.28**	0.14	1.00		
SEWT	-0.19	0.07	-0.18	-0.18	-0.02	-0.19	0.08	1.00	
PRO	-0.20	-0.20*	-0.35	-0.29	-0.21*	0.04	-0.01	0.20	1.00

** Significant at 1% level

* Significant at 5% level

• DF=Days to 50% flowering, PLHT=Plant Height, PBR=Primary branches, CLP=Clusters/plant, PPP=Pods/Plant, SEP=Seeds/pod, SEYL=Seed Yield, SEWT= 100-seed weight, PRO= Protein

Table 4. Promising accessions of greengram identified during evaluation

Trait	Promising accessions
Days to 50% flowering (= 40 days)	IC-282065, 282066, 282072, 282119, 282120, 282131
Plant Height (>40cm)	IC-282091, 282125, 282126, 261266, 261269, 261275
Primary branches (>3)	IC-282084, 261266, 261267, 261269, 261275, 261277
Clusters/plant (>8)	IC-282096, 282099, 282125, 282126, 282127, 282136, 261266, 261267, 261269, 261275
Pods/Plant (>20)	IC-282069, 282084, 282096, 282099, 282132, 282110, 282121, 282125, 282126, 282127, 261269, 261275
100-seed weight (>4.5 g)	IC-282071, 282113, 282111, 282116, 282141
Protein content (>23%)	IC-282114, 282122, 282124, 261274

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Variability in Seed Protein of Two Cultivated Species of Barnyard Millet Through SDS-PAGE

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Seed protein variability of four barnyard millets belonging to two cultivated species viz., *Echinochloa frumentacea* and *E. crusgalli* ssp. *utilis* were examined through SDS-PAGE. Morphological traits and potentiality of high seed setting at different environments (March, April, May and June sowing) indicated that the latter showed resistance/ tolerance to cold and smut disease of grain at high altitudes (2100 m and above) of Himalayas. Differences in banding patterns and intensity in colour of bands revealed that characterization and identification of genotypes belonging to these two cultivated species is possible through analysis of protein subunits.

Key Words: Barnyard Millet, Cold Tolerance, Seed Protein, SDS-PAGE

Among different minor crops, barnyard millet (*Echinochloa* species) possesses distinct position for its cultivation and consumption in India, particularly in hills of Uttaranchal. Very little attention has, however, been paid for the genetic improvement of this crop towards augmenting its yield potential. Heterogeneity of environment and exposure to low temperature at higher elevation cause economic loss in both grain and fodder yield of barnyard millet cultivars. Moreover, in absence of wide genetic diversity among local cultivars and released varieties, the selection for adaptation to cold temperature is discouraging (Gullord *et al.*, 1975). In order to explore superior genetic potential for both grain and fodder yield, SDS-PAGE analysis of total seed protein was carried out among four genetically diverse cultivars of barnyard millet for identification, characterization (Dontsova and Pausheva, 1979; Dolinsek, 1980; Shevchuk, 1985; Hussain *et al.*, 1989; Nishiyama *et al.*, 1991; Rogl and Javornik, 1996) and tolerance to biotic and biotic stresses (Padmavathy *et al.*, 1999; Pattnaik and Kole, 2002).

Materials and Methods

Four barnyard millet genotypes belonging to two different cultivated species viz., *Echinochloa frumentacea* (Local-1) and *E. crusgalli* ssp. *utilis* (PRB 9402, PRB 9403 and PRB 9404) of Asiatic origin (Halaswamy *et al.*, 2001) were grown in March, April, May and June in two consecutive years, 1997 and 1998 in randomized block design with four replications at Hill Campus (21000 m and above), G.B Pant University of Agriculture and Technology, Ranichauri (30° 15' N latitude and 7°02' E longitude). Twenty-five morphological and yield characters were recorded for respective sowings. Mean values of two years' field observations were subjected to statistical analysis.

About 200 seeds of each genotype were milled. Total seed protein was extracted at room temperature using 0.14 M Tris-HCI sample buffer (pH 6.8), 4% SDS, 3% 2-mercaptoethanol, 20% glycerol, 0.02% bromophenol blue (Rogl and Javornik, 1996). Prior to centrifugation at 10,000 rpm for 15 minutes, 0.5 g flour with 500 µl extraction buffer was incubated in boiling water for 2-3 minutes. About 25 µl of extract containing protein concentration of 0.050, 0.054, 0.057 and 0.060 in Local-1, PRB 9403, PRB 9402 and PRB 9404, respectively were loaded in individual well for one run.

SDS-PAGE was conducted following the procedure of Laemmli (1970) with a few modifications. The final concentration of separating gel was 15% acrylamide, 0.375 M Tris-HCI (pH-8.8), 0.1% SDS and 0.8 bisacrylamide. The stacking gel contained 3% acrylamide, 0.125 M Tris-HCI (pH 6.0), 0.1% SDS and 0.8% bisacrylamide. The electrode buffer contained 0.025 M Tris-HCI, 0.192 M glycline and 0.1% SDS. Electrophoresis was carried out for 5 hours at constant current of 20 mA per gel. The gels (1.0 mm thick) were stained in 0.1% coomassie brilliant blue R staining solution with 45% methanol and 0.2% acetic acid. The intensity of bands was measured in terms of optical density (O.D.) at 660 nm with spectrophotometer. Intensity of bands was classified as dark, medium dark and light with optical density range of 1.5 to 1.8, 1.0 to 1.4 and < 1.0, respectively. Five molecular weight markers viz., phosphorylase B (97.4 kD), bovine serum allbumin (67.0 kD), egg albumin (45.0 kD), carbonic

Table I. Morphological characters and yield performance of barnyard millet genotypes

Species	Domesticated	Chromosome no. (2n)	Genotype	Special features
Echinochloa	Asia/China	36	Local-1	Plant height about 150 cm, susceptible to cold and smut disease, seed sets only in March sown, no seed setting in June sown, Yield ranges from 6 to 12 q/ha.
Echinochloa crusgali ssp. *utilis*	Asia/Japan	54	PRB-9402	Plant height about 80 cm. Medium maturing ear head small, compact and awnless, cold tolerant, seeds sets in March to June sowing, yield 12-16 q/ha. Resistant to smut disease.
			PRB-9403	Plant height about 190 cm, Medium maturing, Inflorescence large awned type club shaped, pendent to erect, cold tolerant, seed sets in March to June sown crop, resistant to smut disease, yield 28-36 q/ha.
			PRB-9404	Plant height about 190 cm, early maturing, ear head large, erect, awnless and lax type, cold tolerant, resistant to smut disease, seed sets in March to June sowing, grain yield 28-36 q/ha.

Table 2. Mean performance of different quantitative characters in four barnyard millet genotypes over four dates of sowing in two years.

Characters	Local-1	PRB 9402	PRB 9403	PRB 9404	C.D. 0.05
Plant height (cm)	98.08	80.00	118.29	104.75	15.50
Days to 50% flowering	116.00	10.3.6	105.45	93.26	9.53
Grain filling (days)	48.62	45.17	43.94	3.94	1.23
Grain yield (q/ha)	4.50	8.00	22.20	20.63	3.71
Straw yield (t/ha)	3.50	1.20	8.85	8.20	1.58
Harvest	0.11	0.40	0.19	0.20	0.26
Diseases and pests	Grain smut disease appeared	Nil	Nil		

anhydrase (29.9 kD) and ribonuclease A (14.0 kD) supplied by E-Merk (Nidna) Ltd. were used as standards for determining the molecular weight of seed protein submits.

Results and Discussion

Seed protein profiles of four barnyard millet genotypes viz., Local 1 (*Echinochloa frumentacea)* and PRB 9402, PRB-9403 and PRB0\9404 (*E. crusgalli* ssp. *utilis*) differed considerably for presence and absence of various protein subunits and intensity of colour of bands (Fig. 1). The gels could be divided into three zones viz., A, B and C. Zone A showed five protein bands (A_1, A_2, A_3, A_4 and A_5), in a range of 62.00 kD to 105.68 kD molecular weight. Zone B consisted of only one band with a molecular weight of 43.00 kD whereas, zone C had maximum 6 bands i.e., C_1, C_2, C_3, C_4, C_5 and C_6 falling in a range of molecular weight of 10.43 kD to 29.00 kD. The genotypes of two species did not show many differences in banding pattern of protein subunits at zone C except intensity of bands. This indicated that both the species possessed common protein subunits of low molecular weight while the differences existed only in high and low concentration of protein bands A_3, A_4 and A_5. A major variable protein subunit was observed in zone B. Variation in the band may be helpful in distiction between two species of barnyard millets. Some of the differences in morpho-physiological characters (Tables 1, 2) such as acclimation to cold, resistance to grain smut disease (Bandyopadhyay, 1998) and cross incompatibility (de Wet *et al.,* 1983) between two species may be governed by this protein subunit.

PRB-9402, PRB-9403 and PRB-9404 exhibited similar pattern of bands at zone A with minor differences. Dwarf genotypes PRB 9402 possessed high expression of all the subunits of seed protein depicted in profile. B and A_1 was absent in PRB 9403 while in PRB 9404 both A_1 and A_2 subunits were found missing. This leads to suggest that differences in banding pattern at zone A might be associated with identification and characterization of cultivars belonged to species *E. crusgalli* ssp. *utilis.*

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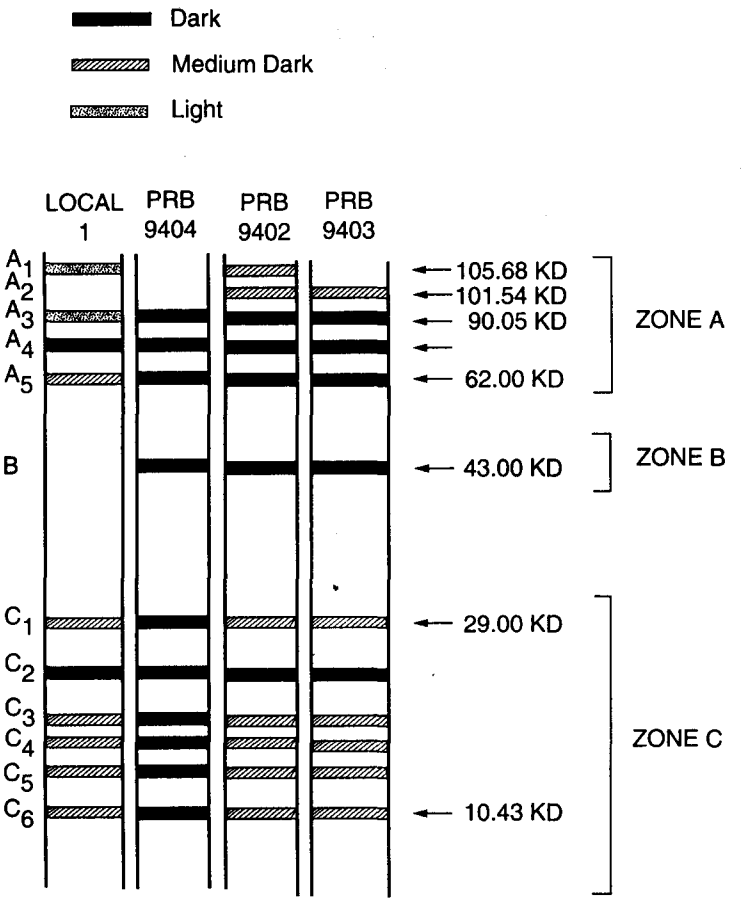

Fig. 1. Variability in seed protein subunits in barnyard millet

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Attributes of Seed Yield in Relation to Seed Size in Chickpea (*Cicer arietinum* L.)

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The present study was carried out to determine the component characters of seed yield in relation to seed size in chickpea. Fifty-three genotypes of diverse origin were grouped based on seed size as small (G I), medium (G II) and bold (G III). Significant differences were found among seed groups and genotypes. Multiple regression analysis indicated that pods per plant was found to be major contributor of seed yield among all the groups of chickpea. Days to flowering in medium seeds and days to maturity in bold seeds had shown their substantial contribution towards seed yield. Path analysis indicated that pods per plant had the highest positive direct effect on seed yield but its effect was diluted with increase in seed size. Negative indirect effect of seed weight in large seed group indicated that breeding for much larger seeds may not be helpful in increasing its productivity and greater attention should be paid on medium bold seeds. Based on *per se* performance superior genotypes like BGD 116 and BGD 115 for high number of pods, seed yield and bold seed size; H 95-25 and BGM 528 for high number of pod; Vijay, JG 74 and RSG 964 for early flowering could be considered in chickpea breeding programme

Key Words: Chickpea, Correlation, Path Analysis, Seed Size, Seed Yield

The seed yield being a complex and variable entity, is attributed to various traits. Direct selection for yield *per se* may not be very effective and it is also true that interdependency of contributing traits may affect the selection criterion. In crop like chickpea not only seed yield but seed size is also equally important in determining the value of the produce. In view of this the present study was carried out to determine the component characters of seed yield in relation to seed size in chickpea.

Materials and Methods

Fifty-three genotypes of diverse origin were grown in randomized complete block design with three replications during winter 2001-02 at Research Farm, I.G.A.U., Raipur. Each genotype was represented by 4 rows 4 m long, 30 cm apart with intra-row spacing of 10 cm. Basal application of 20 kg N and 50 kg P_2O_5 per hectare was applied at the time of sowing. Recommended package of practices was adopted to raise a good crop. Crop was sprayed twice with monocrotophos 36 EC @ 1 litre per ha. Observations were recorded on five competitive plants for plant height (cm), primary branches, pods, seed yield (g) and 100-seed weight (g). Days to first flower and maturity were recorded on plot basis. Based on test weight (100-seed weight) genotypes were grouped as small (G I), medium (G II) and bold (G III) and data were analysed using Balanced Group Design (Gomez and Gomez, 1976).

Results and Discussion

Analysis of variance (Table 1) revealed significant differences among seed groups and genotypes. A wide range of variation was observed for all the traits studied (Table 2); 44-70 for days to first flower; 97-118 for days to maturity; 39.4 – 59.4 cm for plant height;

Table 1. Analysis of variance for different characters in three seed groups of chickpea

Group	Sources of variation	d.f.	Mean Squares							
			Days to first flower	Days to maturity	Plant height	Primary branches plant^{-1}	Pods plant^{-1}	Seeds pod^{-1}	100-seed weight	Seed yield
I	Replication	2	5.500	5.031	0.047	0.025	0.051	0.019	0.084	0.052
	Genotype	21	92.545**	69.616**	60.129**	0.323**	515.567**	0.098**	7.547**	15.517**
	Error	42	0.357	0.427	0.001	0.0001	0.0005	0.0001	0.018	0.003
II	Replication	2	1.313	1.313	0.039	0.013	0.016	0.009	0.048	0.060
	Genotype	18	104.632**	27.351**	73.896**	21.524**	288.181**	0.057**	6.753**	15.166**
	Error	36	0.316	0.316	0.001	0.0001	0.001	0.0003	0.012	0.0004
III	Replication	2	0.336	0.328	0.020	0.008	0.016	0.011	2.797	0.022
	Genotype	11	38.432**	46.977**	53.195**	19.529**	513.466**	0.035**	5.814**	48.109**
	Error	22	0.151	0.152	0.001	0.028	0.0001	0.00005	2.731	0.0003

Table 2. Estimates of genetic parameters for different traits in chickpea

Characters	Mean	Range		GCV	r_g with seed
		Min.	Max.	(%)	yield
Days to first flower	58.88	44.00	70.00	9.07	0.556**
Days to maturity	104.21	97.00	118.00	3.97	-0.153
Plant height (cm)	49.67	39.40	59.40	9.76	0.210
Primary branches plant^{-1}	2.70	2.00	3.53	10.72	0.418**
Pods plant^{-1}	41.64	18.00	83.67	28.41	0.750**
Seeds pod^{-1}	1.39	1.03	1.78	12.82	-0.332**
100-seed weight (g)	20.36	13.19	31.50	24.15	0.577**
Seed yield plant^{-1} (g)	9.72	4.96	18.60	33.55	-

2-3.53 for number of primary branches; 18-84 for pods per plant; 1.03-1.78 for seeds per pod; 4.96-18.60 g for seed yield per plant and 13.19-31.50 g for 100-seed weight. Relatively high estimates of genotypic coefficient of variation (GCV) for seed yield (33.55%), pods per plant (28.41%) and 100-seed weight (24.15%) would offer better opportunities for genetic improvement of these traits. Other traits exhibited moderate to low GCV.

Relative Contribution of Attributes

Multiple Regression Analysis (MRA) presented in (Table 3) showed differential contribution of attributes towards seed yield in different seed groups. Moreover, pods per plant, invariably was found to be major contributor of seed yield in chickpea. Its relative contribution was 94.71, 63.79 and 95.46 per cent in small, medium and bold seeds, respectively. The next important contributor was seed mass especially in small (7.01%) and medium seed groups (16.64%). This was further confirmed by average yield of the genotypes obtained in each group, which clearly indicated that 15.09 and 13.21 per cent of the genotypes had seed yield above 10 gm per plant in G III and G II while only 3.77 per cent genotypes obtained this level in small seed group. Days to flowering in medium seeds and days to maturity in bold seeds had shown their substantial contribution and hence, they should be considered in selection scheme. Therefore, emphasis on genotypes with faster plant growth, early flowering and early maturity should be given. Kulkarni (2000) also reported the highest contribution of pods per plant followed by seed weight and days to flowering in rainfed chickpea.

Correlation and path analysis further confirmed the results of MRA. Significant positive association with pods per plant and days to flowering was observed in G I (Table 4). Similarly, pods per plant, days to flowering and 100-seed weight in G II and pods per plant and primary branches in G III had significant positive association with seed yield (Table 5 & 6). These findings are in agreement with the findings of Gowda and Pandya (1975) and Sarvaliya and Goyal (1994). Days to maturity had significant negative association with seed yield, emphasizing the significance of early maturity in semi-arid tropics. Setty *et al.* (1977) and Islam and Begum (1985) had also reported similar association in chickpea.

Path coefficient analysis further confirmed the results, indicating variable effects of different attributes in different seed groups (Tables 4, 5 & 6). However, pods per plant invariably had highest positive direct effect on seed yield but its effect was diluted with increase in seed size. It was highest in G I and the lowest in G III. Other important attributes were seed mass and seeds per pod in G I and II; primary branches and seeds per pod in group III. The results gave clear

Table 3. Relative contribution of individual yield components towards seed yield

Groups Characters	I	II	III
Days to first flower	-0.386	11.981	-2.343
Days to maturity	0.376	1.945	4.059
Plant height	0.161	2.800	0.005
Primary branches plant^{-1}	1.050	2.877	2.023
Pods plant^{-1}	94.714	63.788	95.457
Seeds pod^{-1}	-2.929	-0.031	-1.051
100-seed weight	7.014	16.640	1.850
Total	100.000	100.000	100.000

Table 4. Genotypic path coefficients in group I

Characters	Days to first flower	Days to maturity	Plant height	Primary branches plant^{-1}	Pods plant^{-1}	Seeds pod^{-1}	100-seed weight	r_{yi}
Days to first flower	-0.005	-0.007	0.000	0.003	0.605	-0.056	0.019	0.560**
Days to maturity	-0.001	-0.033	-0.001	0.009	-0.076	0.014	-0.022	-0.011
Plant height	0.000	-0.004	-0.005	-0.004	-0.324	0.051	-0.030	-0.316
Primary branches plant^{-1}	0.000	-0.008	0.001	0.036	0.196	-0.015	0.075	0.285
Pods plant^{-1}	-0.003	0.003	0.002	0.007	0.989	-0.083	0.000	0.914**
Seeds pod^{-1}	0.001	-0.002	-0.001	-0.002	-0.304	0.268	-0.070	-0.109
100-seed weight	0.000	0.003	0.001	0.009	0.000	-0.065	0.288	0.235

Residual effect = 0.045

Table 5. Genotypic path coefficients in group II

Characters	Days to first flower	Days to maturity	Plant height	Primary branches plant^{-1}	Pods plant^{-1}	Seeds pod^{-1}	100-seed weight	r_{yi}
Days to first flower	0.182	0.010	0.044	0.001	0.296	0.004	0.107	0.644**
Days to maturity	-0.082	-0.022	-0.033	-0.006	-0.415	-0.004	-0.025	-0.588**
Plant height	0.081	0.007	0.099	-0.017	0.045	0.047	0.008	0.269
Primary branches plant^{-1}	0.003	0.002	-0.026	0.065	0.325	-0.022	0.082	0.429
Pods plant^{-1}	0.078	0.013	0.006	0.030	0.691	-0.005	0.071	0.885**
Seeds pod^{-1}	0.005	0.001	0.031	-0.010	-0.021	0.149	-0.160	-0.005
100-seed weight	0.059	0.002	0.002	0.016	0.147	-0.072	0.330	0.485*

Residual effect = 0.044

Table 6. Genotypic path coefficients in group III

Characters	Days to first flower	Days to maturity	Plant height	Primary branches plant^{-1}	Pods plant^{-1}	Seeds pod^{-1}	100-seed weight	r_{yi}
Days to first flower	0.066	0.084	-0.004	0.045	0.315	-0.059	0.048	0.495
Days to maturity	-0.019	-0.302	0.003	-0.032	-0.300	0.001	0.045	-0.603**
Plant height	-0.010	-0.035	0.029	-0.043	-0.010	0.034	0.031	0.003
Primary branches plant^{-1}	0.007	0.022	-0.003	0.446	0.347	0.003	-0.146	0.706**
Pods plant^{-1}	0.039	0.171	-0.001	0.292	0.530	-0.033	-0.027	0.971**
Seeds pod^{-1}	-0.034	-0.003	0.009	0.013	-0.153	0.114	-0.091	-0.145
100-seed weight	-0.021	0.092	-0.007	0.347	0.096	0.069	-0.149	0.427

Residual effect = 0.039

indication that number of seeds and seed mass are the sole entities of seed yield but their contribution was hidden in group III as evidenced by its negative and negligible direct effect and non-significant positive association with seed yield. Secondly, number of seeds per pod was decreasing with increase in seed size. Hence, this should be kept in mind while formulating breeding programme for larger seeds in chickpea. In accordance to the present findings earlier workers Gowda (1972), Chand *et al.* (1975), Singh and Paroda (1986) and Dasgupta *et al.* (1992) have also reported the highest contribution of these traits in chickpea. The results further indicated that days to flowering and primary branches had indirect contribution through pods per plant. However, negative indirect effect of plant height through pods per plant indicated that increase in plant height may not be helpful in increasing seed yield in chickpea.

It is evident from the present findings that genetic relationship and relative contribution of the attributes changed little in relation to seed size. In general, higher number of effective pods with high seed mass should be included in the selection criterion for maximization of seed yield in chickpea. Katiyar (1981) had also suggested similar selection scheme for betterment of seed yield in this crop. Negative indirect effect of seed weight in G III indicates that breeding for much larger seeds may not be helpful in increasing its productivity. Hence, much attention should be paid on medium bold seeds. Days to flowering and maturity can not be ignored in sub-tropical climate, which directly influence the pod setting and proper seed development. Hence, emphasis should be on fast growing genotypes with early in flowering and maturity.

Table 7. Mean performance of seed yield and its components with source of material

Group I

Genotype	Source	D/F	D/M	Plant height (cm)	Primary branches plant^{-1}	Pods plant^{-1}	Seeds pod^{-1}	100-seed weight (g)	Seed yield (g)
H 95-122	Haryana	57	98	49.80	2.20	44.32	1.48	13.43	7.84
PBG-78	Punjab	58	107	52.50	2.13	34.67	1.59	13.24	5.58
CSJD-901	Rajasthan	53	99	43.87	2.40	31.67	1.41	13.55	4.96
GCP 9504	Rajasthan	57	106	46.27	2.40	38.00	1.57	13.59	6.72
C-235	Punjab	61	105	49.13	2.47	48.00	1.56	13.86	7.42
CSJD-869	Rajasthan	55	103	48.20	2.47	32.67	1.40	13.92	5.31
Phule G-95007	Maharashtra	54	108	53.87	2.80	43.00	1.18	13.90	6.42

FG-559	Punjab	57	105	51.67	2.67	39.33	1.78	14.22	9.29
ICCV-97017	Andhra Pradesh	52	103	49.53	2.87	46.67	1.70	14.26	8.55
FG-712	Punjab	58	102	55.00	2.60	35.00	1.77	14.82	6.96
IG-338	Madhya Pradesh	53	102	44.53	2.53	39.00	1.68	14.83	8.73
H 95-25	Haryana	70	102	44.33	3.13	83.67	1.34	15.47	14.79
ICCV-97001	Andhra Pradesh	62	103	46.80	2.80	37.00	1.65	15.51	7.42
ICCV-97031	Andhra Pradesh	49	108	39.40	2.47	51.67	1.60	15.78	9.70
PG 97-6	Uttar Pradesh	52	98	58.07	2.60	34.67	1.65	16.42	7.49
H 95-37	Haryana	69	104	44.13	2.80	68.67	1.30	16.64	12.33
ICCV-93118	Andhra Pradesh	61	109	51.73	2.73	45.00	1.30	16.76	8.60
BGD-112	Karnataka	63	118	52.93	2.67	26.33	1.61	16.83	5.97
RSG-964	Rajasthan	53	98	44.20	2.47	33.67	1.57	17.12	7.34
Vijay (C)	Maharashtra	49	105	44.67	3.53	26.33	1.37	17.17	5.72
JG-74 (C)	Madhya Pradesh	57	97	47.87	2.00	42.00	1.14	18.04	7.94
GCP-9516	Rajasthan	56	99	49.53	2.67	36.67	1.56	18.18	8.26
mean		57.09	103.60	48.55	2.61	41.73	1.51	15.34	7.88
S.Ed		0.488	0.534	0.001	0.008	0.018	0.009	0.108	0.041
CV %		1.047	0.631	0.001	0.393	0.053	0.782	0.863	0.637
$CD_{5\%}$		0.956	1.047	0.002	0.016	0.035	0.018	0.212	0.08

Group II

Genotype	Source	D/F	D/M	Plant height (cm)	Primary branches $plant^{-1}$	Pods $plant^{-1}$	Seeds pod^{-1}	100-seed weight (g)	Seed yield (g)
ICCV-97033	Andhra Pradesh	62	107	47.07	2.33	27.00	1.42	19.31	7.30
H 95-30	Haryana	67	102	48.73	2.73	56.33	1.60	19.36	12.19
BGD-109	Karnataka	56	105	49.13	2.47	46.33	1.37	19.47	8.52
GL-96047	Punjab	64	101	55.27	2.87	35.33	1.44	19.64	8.43
Phule G-93009	Maharashtra	52	107	51.80	2.47	30.33	1.48	19.66	7.08
ICCV-97038	Andhra Pradesh	44	106	40.47	3.33	44.33	1.40	20.02	8.96
ICCV-97016	Andhra Pradesh	58	109	49.07	3.00	36.33	1.14	20.10	7.99
GL-96004	Punjab	66	101	52.80	3.00	50.67	1.50	20.14	11.98
ICCV-97024	Andhra Pradesh	55	105	50.40	2.53	27.67	1.49	20.36	6.89
ICCV-97039	Andhra Pradesh	54	104	44.33	2.60	38.33	1.24	20.59	8.20
BG-391 (C)	New Delhi	65	102	50.07	2.67	50.00	1.30	21.86	12.28
ICCV-97030	Andhra Pradesh	59	103	42.93	2.93	53.33	1.25	21.84	11.45
CG-938	Chhattisgarh	59	102	39.80	2.87	35.33	1.11	22.12	8.14
GNG-1275	Rajasthan	64	104	53.13	2.87	47.33	1.19	22.60	11.01
RSG-966	Rajasthan	59	103	55.00	2.33	35.67	1.23	22.89	9.59
ICCV-97034	Andhra Pradesh	61	112	43.53	3.87	31.00	1.35	22.97	8.87
IPC 96-27	Uttar Pradesh	63	103	57.00	2.93	44.67	1.49	22.98	12.63
BGM-528	New Delhi	68	100	55.67	3.07	60.33	1.21	23.21	14.93
JSC-3 (C)	Madhya Pradesh	62	106	45.87	2.93	42.00	1.34	23.23	9.93
mean		59.895	104.316	48.793	2.779	41.701	1.345	21.177	9.809
S.Ed.		0.488	0.459	0.009	0.010	0.027	0.013	0.088	0.015
CV %		1.047	0.539	0.025	0.451	0.079	0.222	0.507	0.193
$CD_{5\%}$		0.956	0.899	0.018	0.019	0.005	0.025	0.172	0.029

Group III

Genotype	Source	D/F	D/M	Plant height (cm)	Primary branches $plant^{-1}$	Pods $plant^{-1}$	Seeds pod^{-1}	100-seed weight (g)	Seed yield (g)
BGD-72 (C)	Karnataka	63	104	50.13	2.40	46.00	1.23	23.82	12.25
GNG-469	Rajasthan	61	102	55.07	2.60	45.00	1.19	24.07	11.36
ICCV-97032	Andhra Pradesh	56	110	47.87	3.00	34.00	1.41	27.48	9.94
IPC 97-1	Uttar Pradesh	63	111	59.20	2.47	34.00	1.41	24.25	9.16
BGM-524	New Delhi	59	110	54.93	3.00	50.33	1.19	24.58	14.49
ICCV-95138	Andhra Pradesh	57	106	48.33	2.20	18.00	1.29	25.05	5.56
BG-256 (C)	New Delhi	63	103	50.07	2.73	49.33	1.28	25.33	13.92
BGD-115	Karnataka	66	101	52.13	2.93	59.67	1.27	25.71	18.01
IPC 96-46	Uttar Pradesh	58	109	59.40	2.53	26.33	1.30	25.81	8.03
BGD-116	Karnataka	65	103	51.60	2.80	62.67	1.17	26.91	18.60
KGDB-1178	Uttar Pradesh	64	105	49.13	2.87	41.67	1.27	27.39	12.54
KGDM-1181	Uttar Pradesh	56	99	58.00	2.80	49.67	1.54	27.63	16.46
mean		60.920	105.300	52.988	2.694	43.056	1.296	25.670	12.526
S.Ed.		0.320	0.320	0.030	0.137	0.001	0.006	1.349	0.014
CV %		0.640	0.370	0.071	6.209	0.001	0.572	6.438	0.141
$CD_{5\%}$		-	-	-	-	-	-	-	-

Based on *per se* performance superior genotypes like BGD-116 and BGD-115 for high number of pods, seed yield and bold seed size; H 95-25 and BGM-528 for high number of pods; Vijay, JG-74, RSG-964 for early flowering could be considered in chickpea improvement programme.

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Genetic Diversity Analysis Based on Random Amplified Polymorphic DNAs and Agro-morphological Traits in Barley

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The genetic diversity estimation of the released varieties and the improved germplasm is a prerequisite for their immediate exploitation in any crop improvement programme. Twenty two released varieties of barley in India and 14 exotic accessions including six cross derivatives of *H.vulgare* spp *spontaneum* and *H.vulgare* ssp *vulgare* were analyzed for genetic relatedness using RAPDs and the results obtained were compared with those obtained from the analysis of 17 agro- morphological traits. Four series (OPA, OPD, OPM, OPP) of random decamer primers were screened and 16 primers with polymorphic and reproducible banding pattern were selected. Four primers, namely, OPP15, OPP16, OPA7 and OPA8 together were able to identify most of the accessions. Relationships between the accessions were ascertained with the help of dendogram constructed by using UPGMA-clustering. RAPDs markers revealed high genetic diversity particularly among Indian released varieties. On the basis of RAPDs, the genotypes were clustered though loosely according to their place of breeding perhaps due to common ancestry. Morphologically, most of the Indian varieties were clustered into four groups. Clustering based on RAPDs and agro-morphological traits were incongruous. Genetic base of the Indian released varieties of barley is quite wide. The results provide valuable information on the suitability of RAPD for varietal fingerprinting of the released varieties and for the estimation of genetic diversity among accessions.

Key Words: Barley, Genetic Similarity, Genetic Diversity, *Hordeum vulgare* ssp *vulgare*, *H. vulgare ssp spontaneum*, RAPDs, Varietal Fingerprinting

Barley is one of the oldest food crops, ranking fourth in world acreage with an annual production of approximately 130 m tonnes (http://apps.fao.org/default.htm). A highly diverse gene pool is expected in barley as it is cultivated under diverse agroclimatic environment the world over. Information about the extent of genetic variation in the cultivated barley, *H. vulgare ssp vulgare*, land races of *H. vulgare* and its wild ancestors *H. vulgare* ssp *spontaneum* is essential for germplasm conservation and optimal designing of breeding programs. Assessment of genetic diversity in *Hordeum* has been carried out by a number of researchers using pedigree information (Martin *et al.*, 1991), morphological traits (Nevo *et al.*, 1979; Brown and Munday, 1982), biochemical markers (Doebley, 1989) and molecular markers (Tinker *et al.*, 1993, Melchinger *et al.*, 1994; Ordon *et al.*, 1997). The diversity analysis based on the morphological markers, pedigree record and biochemical traits have been questioned because of large unknown effects of environment (William et. al. 1997), unreliable pedigree records and unaccounted effects of selection, mutation and random genetic drift (Dweikat *et al.*, 1993) and also poor coverage of the genome, respectively. The random amplified polymorphic DNA (RAPD) has been proposed as a new source of genetic markers, which detects nucleotide sequence polymorphism by means of PCR using primer of arbitrary nucleotide sequence (William *et al.*, 1990; Welsh and McClelland 1990). It has several distinct advantages over RFLP like cost effectiveness, no use of radioactive element and requires no prior information for designing of the primers. It has proved valuable in the construction of the linkage maps, in the identification of the strains and varieties and in genomic diversity and phylogenic studies (Dawson *et al.*, 1993) in a wide array of taxa. In present study, exotic and indigenous accessions of *H.vulgare* ssp *vulgare* and the cross derivative of *H. spontaneum* and *H. vulgare* were subjected to RAPD analysis with the objectives of identification of cultivars/accessions and to estimate the extent of genetic diversity present and to group the accession on the basis of their similarity. The results were compared with those obtained on the basis of agromorphic traits.

Materials and Methods

The plant materials used in the study include accessions/lines/varieties of *H. vulgare* ssp *vulgare* and the cross derivatives of *H. spontaneum* and *H. vulgare* (Table 1). The *spontaneum* subspecies was represented by six

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Table 1. Name of the barley varieties/accessions along with their breeding center and special features

Sr. No.	Name of the varieties/ accessions	Pedigree and Origin	Key features
1.	BH 85	HAU, Hisar, India	Six rowed, released variety with medium height, medium maturity, medium dense spike with small and slender grain
2.	BCU 322	WI2291/H.spont.41-1, ICARDA, Syria	Ssp *spontaneum* type with erect seedling, medium height, medium flowering and two rowed medium dense spike
3.	BCU 344	H.spont.41-3/3/DEI RALLA06//BGS/RES1, ICARDA, Syria	Ssp *spontaneum* type with erect seedling, tall, medium flowering and six rowed
4.	BCU 383	H.spont.UNK-5, ICARDA, Syria	Ssp *spontaneum* type with spreading type of growth habit, two rowed and medium flowering.
5	BCU 768	CI 08887/CI 05761//Lignee 640, ICARDA, Syria	Exotic advance line, medium dwarf height, medium late heading, lax and six rowed.
6.	BCU2106	ATHS/LIGNEE 686, ICARDA, Syria	Exotic advance line with medium tall height , medium maturity and six rowed.
7.	Karan 741	AICBIP, Karnal, India	Released variety of medium height and medium maturity, six rowed and husk less
8	Ratna	Selection from local, IARI, New Delhi	Released six rowed non pigmented variety with tall plants and bold kernels
9	C-138	C251/T4, HAU, Hisar, India	Released six rowed non pigmented variety with lax, long ears and medium grains
10.	Manjula	K4126/Sohan, CSAUA&T, Kanpur, India	Released six rowed non pigmented variety, medium tall, early and hull less
11	Jyoti	K12/C251, CSAUA&T, Kanpur, India	Released six rowed non-pigmented variety, medium tall plant, and medium long and medium lax ears with golden grains.
12	K141	K18/IB 254, CSAUA&T, Kanpur, India	Released six rowed non pigmented variety with medium tall plants, medium lax ear and bold grains
13.	K 550	K1001/Sohan, CSAUA&T, Kanpur, India	Advance line non pigmented, medium early, medium tall and bold grains
14	BP1607	HAU, Hisar, India	Basal pigmented, spreading seedling, medium tall, medium maturity and lax spike
15.	Alfa 93	Aurora/Queen//Beka, DWR, Karnal, India	Released two rowed malt variety with basal pigmentation, medium height and late maturity
16.	Bilara-2	RS 17/C251, RAU, Durgapura, India	Released six rowed non pigmented variety, medium height, early maturity and bluish bold grains
17	DL-88	BG1/K572//K71/EB533, IARI, New Delhi, India	Released six rowed semi dwarf variety with early maturity and suitable for late sown condition.
18	RD2035	RD137/PL101, RAU, Durgapura, India	Released six rowed high yielding variety with medium height, medium maturity and medium grains
19.	RD 2052	AP1-CM-67/50-727//PL101, RAU, Durgapura, India	Released six rowed, high yielding non-pigmented variety, medium tall and yellow bold seed.
20	BCU 376	H.spont UNK-7, ICARDA, Syria	Exotic and H.spontaneum type with medium height, late flowering and two-row type, small and slender grain.
21.	RS17	Selection from local, RAU, Durgapura, India	Released six-rowed variety with tall plants, medium bold and yellow grains.
22.	BCU 1700	Shimla local, IARI, Shimla, India	Local Line, semi spreading seedling, medium tall, late in flowering, six rowed with lax spike
23.	BCU 1520	SLB 039-16, ICARDA, Syria	Improved germplasm, basal pigmentation, medium dwarf, late flowering, two rowed with lateral florets.
24.	Himani	Atlas 54/Kailash//BHS-15-88, IARI, Shimla, India	Released husk less pigmented six rowed variety with medium height and maturity with lax spike
25.	PL 56	Mutant of C164, PAU, Ludhiana, India	Released six-rowed variety with medium compact spike, medium bold grains and rough awn.
26.	BCU67	PITAYO/CAM/4/AVT/RM 150814//POR/DS/3/ CM 67/DUG2, ICARDA, Syria	Advance exotic line, spreading type seedling. Two rowed and lax spike
27	BCU 2940	Exotic introduction IARI, New Delhi, India	High lysine line, semi spreading, medium tall, medium grain with high protein content
28.	Victoria	Not known, Romania	Exotic introduction, with medium plant height and maturity and sterile tip on the spike and resistant to scald
29.	BCU369	H.spont.27-1//ER/APM, ICARDA, Syria	Interspecfic derivative, sub species spontaneum type, exotic, erect seedling, two rowed with small and slender grain.
30.	VLB-1	NP109/HBL 62, VPKAS, Almora, India	Released variety for hilly areas with dark green foliage, basal pigmentation, medium tall height and yellow grain.
31.	Rajkiran	RDB-1/Marocaine 079-CI 8334-Genesis// UUB72-282-2d-10d-7d, RAU, Durgapura, India	Released six rowed nematode resistant variety, medium early, medium height, medium dense spike and erect seedling.
32.	BHS 169	Kailash/Briggs, IARI, Shimla, India	Released six rowed variety for lower hills, non pigmented plant, medium dense spike, white awns and drooping ear heads
33.	Lakhan	K71/IB226, CSAUA&T, Kanpur, India	Released six rowed, non pigmented variety with medium tall plants, medium dense spike and bold grains
34.	Dolma	Selection from USA 115, Bhuntar, India	Released six rowed, non pigmented variety with lax spike, small, round husk less grains
35.	BCU 353	H.spont.41-3//WI2291/WI 2296, ICARDA, Syria	Exotic, interspecific derivative, non pigmented, two rowed, lax spike and slender grain
36.	BG105	C141/Montless, HAU, Hisar, India	Released six-rowed non-pigmented variety with medium height and early maturity and dense spike.

accessions which also included the cross derivatives. The 22 released indigenous varieties (both six and two row types) and 8 germplasm lines of exotic and indigenous origin maintained in Directorate of Wheat Research, Karnal's repository represented ssp *vulgare*. For each entry a random sample of 30 kernels was sown in pots under greenhouse. Leaf tissues from 18-day-old seedlings were collected and immediately processed for DNA extraction. DNA was isolated from 5-10 g of tissue by the modified CTAB procedure. The tissue was ground in liquid nitrogen and suspended in 20 ml of CTAB extraction buffer 2x (100 mM Tris, pH 8.0; 1.4 M NaCl, 20 mM EDTA, 2% 2 mercaptoethanol and 1.5% CTAB). The slurry was incubated for one hour at 60°C and extracted with an equal volume of chloroform/isoamyl alcohol (24:1). The aqueous phase was recovered after centrifuging at 17.000 rpm for 10 minutes. DNA was precipitated with an equal volume of isopropanol. The precipitated DNA was washed twice with 70% ethanol and dried under vacuum. The DNA pellets were then dissolved in the minimum of 10:1TE (10 mM Tris, 1 mM EDTA, pH 8.0). This was followed by the treatment with RNAase and extraction in phenol: chloroform: isoamyl alcohol (25:24:1) and chloroform: isoamyl alcohol (24:1). DNA was reprecipitated by adding 1/10 volume of 3M sodium acetate and 2.5 volume of chilled ethanol and then washed in 70% ethanol. DNA was again vacuum dried and dissolved in 10:1 TE buffer. The quantification of DNA was done using flourimeter with calf thymus as the standard DNA and Hoechst 33258 as the fluorescent dye and also by running an aliquot in agarose gel along with the DNA of known concentration as standard.

RAPD analysis

Decamer oligonucleotides (Operon Technologies, USA) were used as primers for the present study. PCR was carried out in 25 μl reaction volume containing 3.5 mM of $MgCl_2$, 1 unit of Taq polymerase, 30 ng of genomic DNA and 0.5 μM of primer, 200 μmoles of each of dNTPs, 50 mM KCl and 10 mM Tris-Cl (pH8.3). The amplification were carried out in a Perkin Elmer thermal cycler programmed for initial denaturation at 92°C for 3 min., followed by 40 cycles of 1min for denaturation at 94°C, 1 min for primer annealing at 35°C and 1 min for amplification at 72°C. Amplified product were resolved on 1.4% agarose gel at constant voltage. After staining the gel with ethidium bromide, amplicons were visualized and photographed with the help of an ultraviolet transilluminator.

RAPD profiles were scored visually and the data were recorded as 1 and 0, with 1 depicting the presence of band and 0 indicating the absence. The fraction of band common between two genotypes was estimated using the formula of Nei and Li (1979). Only the clearly visible and reproducible bands were taken into consideration for the analysis. Cluster analysis, based on the unweighted pair group method with arithmetic mean (UPGMA) was carried out using NTSYS software programme to produce phenogram.

Agro-morphological data

Data were recorded in the field trial during the season 1995-96 for 17 characters viz., growth habit, basal pigmentation, auricle pigmentation, plant height, days to 75% flowering, lateral florets, spike density, row type, presence or absence of awn, awn roughness, tip sterility, waxiness of stem, seed shape, seed color, hulled/husk less, seed weight and seed protein content. The observation for each character was recorded as per the standard classification in barley used by NBPGR, New Delhi and these along with the center of origin were analyzed by using the NTSYS programme.

Results and Discussion

Thirty eight primers of the four series viz., OPA, OPD, OPM and OPP (Operon) were screened for amplification. Extensive polymorphisms (2-8 polymorphic bands) among the barley lines was detected with a number of primers. Of these, 16 primers giving good polymorphic and reproducible and discernible banding pattern were selected. Details of the primers used and the amplicons obtained are presented in Table 2. A total of 117 amplified products

Table 2. List of arbitrary primers and the extent of polymorphism in barley

Primer	Total number of bands	Polymophic bands	Per cent polymorphism
OPP3	5	2	40
OPP4	7	3	42.8
OPP6	5	2	40
OPP7	7	3	42.8
OPP8	7	4	57.1
OPP9	7	5	71.4
OPP11	5	2	40
OPP12	7	5	71.4
OPP13	9	5	55.5
OPP14	8	5	62.5
OPP15	10	8	80
OPP16	9	8	88.8
OPA4	9	6	66.6
OPA7	9	7	77.7
OPA8	6	4	66.6
OPA15	7	3	42.8

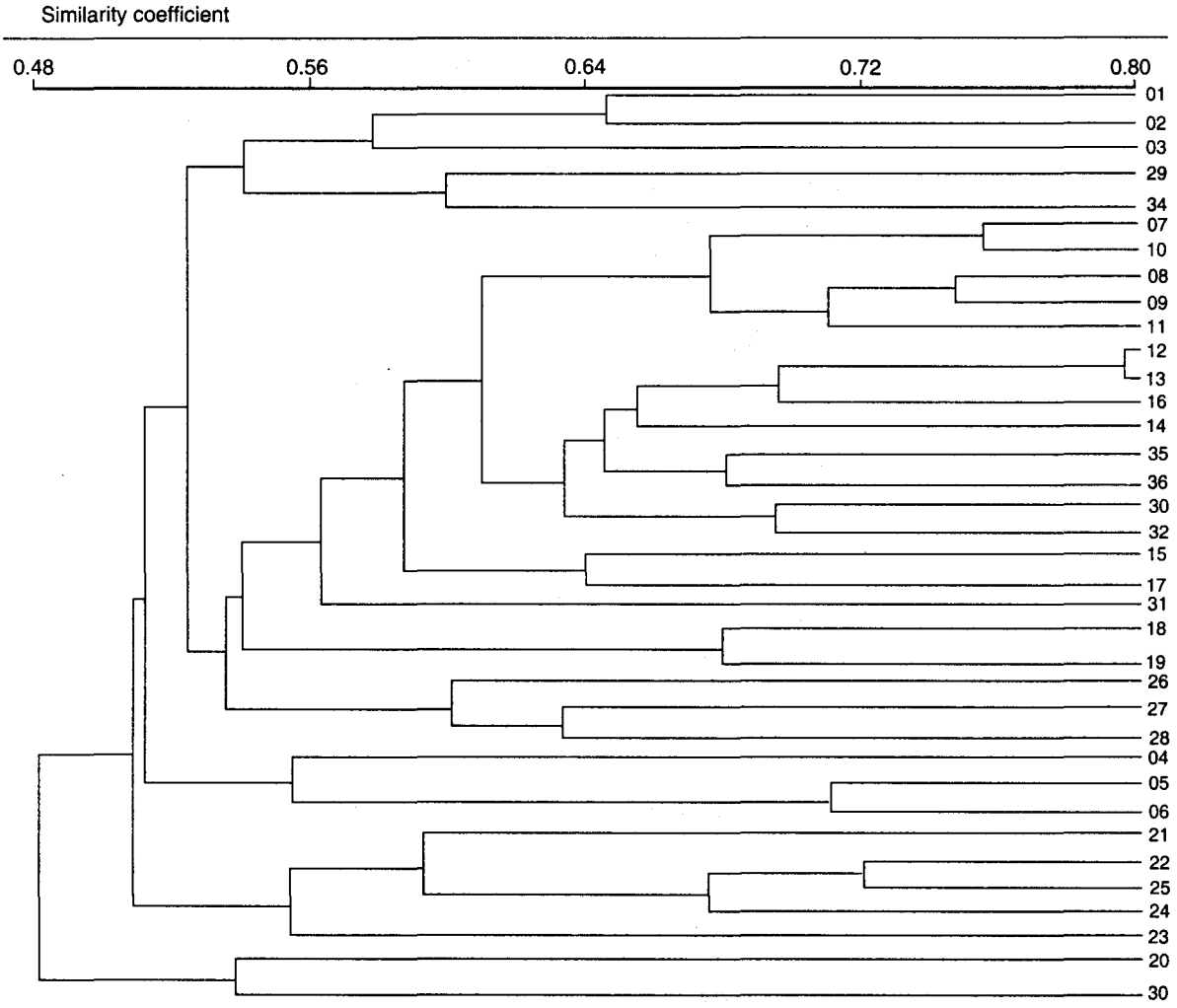

Fig. 1. Dendogram of 36 barley accessions based on RAPD markers

were obtained, of which 72 were polymorphic. Primers, OPP15, OPP16, OPA7 and OPA 8 together combination were able to identify all the varieties. Mean genetic similarity (MGS) of cultivars was estimated and presented in the Table 3. Genetic similarity estimates between the lines ranged from 0.392 to 0.796. Maximum genetic similarity was obtained between the lines K141 and K550 whereas the varieties BH85 and Lakhan showed the minimum similarity. Clustering of the lines based on UPMGA resulted in distinct groups (Fig. 1), which roughly corresponds to their center of breeding. Song and Robert (1995) also obtained broad correlation between the genetic diversity with geographic distribution. The indigenous varieties split into several groups and showed the maximum polymorphism. One group comprised Karan 741, Ratna, C-138, Manjula and Jyoti (nos 7, 8, 9, 10, 11) having the similarity value of 0.677 share more than 60% of the loci. The two varieties from Kanpur centre namely, K141 and K550 (nos. 12 and 13) though formed a separate subgroup with similarity coefficient of 0.80 but were closer in grouping with other released varieties from the Kanpur, center. The two varieties released from Durgapura center i.e. RD2035 and RD 2052 (Nos 18 and 19) are close to each other but appeared to be distinct from the rest of the released varieties of India. Maximum genetic distance was observed between an Indian released variety BH 85 and *H. spontaneum* accessions from ICARDA along with Indian released variety Lakhan and therefore, can be utilized for generating transgressive segregants. Lines like DL88, Himani, PL56 and Rajkiran were also distinct. Majority of the exotic material (nos. 2, 3, 4, 5, 6, 20, 23, 26, 27, 28, 29) did not form any separate cluster and were spread in different groups expectedly as most of the exotic lines selected for the present study were having diverse pedigree and were developed with different objectives.

Classification of the barley genotypes corresponding to row type was not revealed by the present study and it might be due to nonhomology of the primers included in the study to the site of row specific locus. The barley varieties developed and released in India have wide genetic base and it is still possible to morphologically differentiate them but the same may not be feasible in coming years with the release of more and more number of varieties and the convergence of phenotype towards a high yielding ideotype. It may, therefore, be necessary to employ newer molecular tools like STMS along with morphological traits for varietal authentication. The present study clearly indicates the value of RAPD markers in identification of the varieties. Four primers namely OPP15, OPP16, OPA7 and OPA8 could identify most of the accessions in the present study. Level of diversity revealed in the present study is quite large and was probably due to biased sampling as the varieties representing different breeding centers and accessions of species *H.vulgare* spp *spontaneum* were deliberately selected. Another interesting finding of the study is that the material developed at the Hisar Centre of India viz., nos 1, 9, 14, 36 was quite diverse whereas in the case of other breeding centres particularly Kanpur, the genetic base is quite narrow.

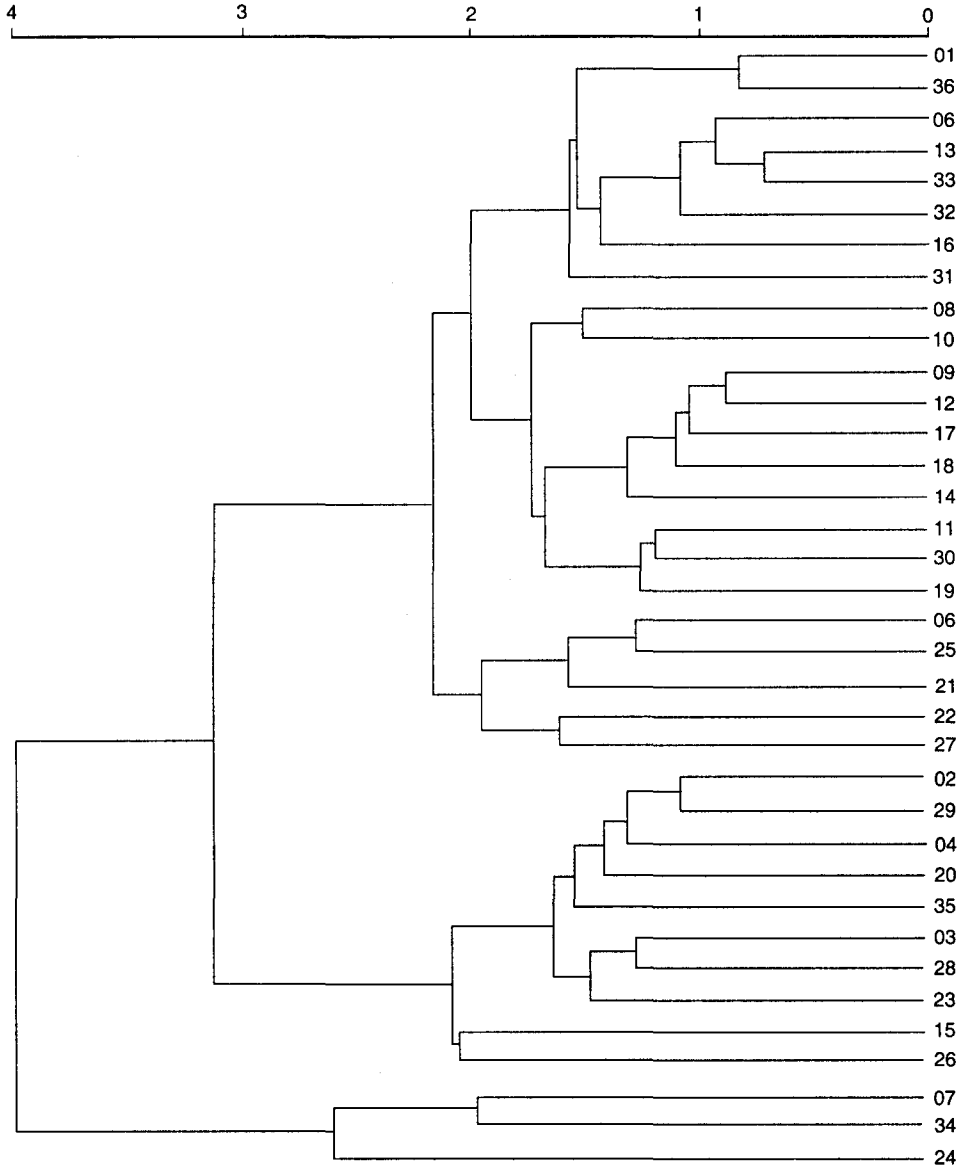

Fig. 2. Dendogram based on Euclidean distances of 36 barley accessions for agro-morphological traits

On the basis of the morphological descriptors, there were four distinct grouping (Fig. 2). The entries BH 85, BCU 2106, K550, Bilara 2, Rajkiran, BHS 169 and Lakhan (node nos., 1.6,13,16,31,32,33) were grouped under one large node. Another distinct group was of the entries Ratna, C138, Manjula, Jyoti, K141, BP1607, DL88, RD2035 and RD2052.This grouping was again more or less on the pattern of their center of development as it grouped three out of total six entries from Kanpur Centre. Third group was exclusively of the entries with exotic origin and includes mostly those developed at ICARDA. Morphologically most distinct line in the present study was BH 85 and Himani. There was not much congruence between the agromorphic data and RAPD markers but some broad link could be established between the two sets of data. BH 85 was both morphologically and on the basis of RAPDS markers the most distinct. The varieties from the Kanpur Centre form more or less a cohesive group under both sets of data. The loose parallelism between the two type of data might be due to the fact that genome fraction surveyed by the primers used in the study is random and may also involve the non coding regions of the genome and not specifically correspond to the functional part of the genomes only. Moreover, the numbers of morpho-physiological data collected in the present study were limited and not exhaustive. However, morphological and molecular survey of the released varieties in the present study indicates the genetic base of these varieties is not narrow and if used in the crossing programme along with the specific donors from the exotic sources like ICARDA in three way or double cross can still generate useful breeding material. The extent of genetic variation revealed in the indigenous material can be exploited for further improvement of barley first by selecting the parents on the basis of per se performance and then establishing their real divergent nature by DNA marker analysis. Further, this type of study will also clearly define the germplasm group and will help in assigning the line with unknown pedigree record to a particular group and thus should be of great help to the breeders in the selection of the parents. The divergent genotypes like BH 85, Lakhan, Himani DL88 and *H.spontaneum* accessions from ICARDA can be used in hybrid breeding programme too.

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Pattern of Pigmentation in Ahu Rices of Assam

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Pigmentation pattern in 142 Ahu rice genotypes/varieties of Assam showed wide range of variation in colour of 14 plant parts. Out of 142 entries 125 was pigmented in one or more parts while 17 were completely non-pigmented. Frequency of genotypes/varieties with pigmented plant part was highest for pericarp (70.42%) followed by lemma-palea at maturity (61.27%) and apiculus (33.0%). Pigmentation in leaf blade, collar, ligule and auricle was observed in very few cases. Coefficient of variation for colour was highest for apiculus (80.63%) followed by lemma-palea at maturity (75.78%), stigma (59.79) and nodal septum (58.69%). The genotypes/varieties were classified into 47 groups based on the number of parts pigmented. Correlation studies among the pigmented plant parts revealed significant and positive association of basal leaf sheath colour with colour of sheath pulvinus, clum internode, nodal septum, ligule, sterile lemma, apiculus and stigma. Positive and significant correlation of sheath pulvinus was also observed with culm internode, apiculus, stigma and lemma-palea at maturity. Except collar and paricarp colour all other plant parts were positively significantly correlated with clum internode colour. Apiculus colour was positively and correlated with all other parts under study except leaf blade, collar and lemma-palea at anthesis. Apiculus, lemma-palea at maturity and pericarp colour were positively and significantly correlated with each other.

Key Words: Ahu Rice, Pigmentation, Plant Parts

Pigmentation is one of the most important characters in rice for identification of varieties and their classification (Misro *et al.*, 1960). Assam and adjoining parts of North-East India are well known for richness in rice genetic resources. Rice germplasm of the region is not only endowed with genetic diversity but also represents a wealth of valuable genes (Sharma *et al.*, 1971). Although several reports on collection and evaluation of Assam rices are available, in the past very little attention was paid towards characterisation and evaluation of Ahu rices of Assam. Ahu rices, generally poor yielders, are grown during March/April to June/July either as dry broadcast or transplanted and are characterised by their photoinsensitivity, eary maturity and tolerance to periodic moisture stress. Detailed characterisation of these traditional rice genotypes/varieties appears to be a prerequisite for their improvement and better utilisation. As a part of detailed characterisation, the present investigation was carried out to study the pattern of pigmentation in 142 traditional Ahu rice genotypes/ varieties of Assam.

Material and Methods

The material for the present investigation comprised 142 traditional Ahu rice genotypes/varieties of Assam, procured from the Regional Rice Research Station, Titabar, Assam and B.N. College of Agriculture, Biswanath Chariali (Assam Agricultural University), Assam. The genotypes/varieties were grown in three row plots of two-meter length with a spacing of 15x20 cm during wet season of 2001. Observation on colour of 14 plant parts, *viz.* basal leaf sheath (BLS), sheath pulvinus (SP), culm internode (CI), nodal septum (NS), leaf blade (LB), collar (C), ligule (L), auricle (Ar), sterile lemma (SL), apiculus (Ap), stigma (S), lemma-palea at anthesis (LPa), lemma–palea at maturity (LPm) and pericarp (P) were recorded following Chang and Bardenos (1965) and standard evaluation system (IRRI, 1996). Modification of colour classification was done wherever standard evaluation system was not satisfied. Colours were identified with the help of colour illustrations of Hutchinson *et al.* (1938). Frequencies of genotypes/ varieties in different colour classes were worked out. Coefficient of variation in colouration was calculated for each of the plant parts based on the colour scores of different classes. Genotypes/varieties were grouped on the basis of presence or absence of pigmentation in different plant parts. Simple correlation coefficients of pigmentation pattern among the different plant parts were computed. Presence or absence of colour irrespective of intensity was scored as '1' and '0', respectively.

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Results and Discussion

A wide range of color variation was observed in the Ahu rice genotypes/varieties under study. Frequency distribution of colour classes for the 14 plant parts is presented in Table 1. The coefficient of variation for colour was highest for apiculus (80.63%) followed by lemma-palea colour at maturity (75.78%), stigma (59.79) and nodal septum (58.69%). Lowest variation was observed for collar colour (11.5%). Pigmentation in leaf blade, collar, ligule and auricle was observed in very few of the entries. Jones (1929), Nagamutu (1943), Ramiah (1945) reported that in most of the rice genotypes/varieties leaf blade and collar were non pigmented while pigmentation was present in other parts. They speculated that the preponderance of non-pigmented types for these traits may be due to presence of inhibitory gene(s) suppressing the expression of genes of pigmentation, which otherwise is/are dominant.

Based on the presence and absence of pigmentation in various plant parts the 142 genotypes/varieties were classified into 47 groups (Table 2). Similar classification was made by Hector (1922) in rice genotypes/varieties of Bengal and obtained 51 different groups based on pigmentation in 11 plant parts. Jones (1929) grouped 311 Asian rices into 48 classes while Misro *et al.* (1960) obtained 57 different pigmented classes in 796 world genetic stocks of rice. Sinha *et al.* (1988) classified 92 Gora rices of Bihar into 31 groups and observed that 8 of them were pigmented in one or the other parts. In the present investigation 78% of the genotypes/varieties had pigmentation in one or the other parts while only 12% of them were completely non-pigmented, forming the largest group (Group I) comprising 17 members. On the other hand, Rao *et al.* (2001) studied pigmentation in rice varieties of Bastar region of Chhattisgarh and observed that majority of them were non-pigmented. This indicates that the frequency of pigmentation is higher in Ahu rices than the rice varieties of Bastar. The higher tendency of pigmentation pattern is also an indication of presence of primitive types (Sinha *et al.* 1988).

Pigmentation is single plant part in the present study was observed for NS, LPm and P in 10, 1 and 12 entries, falling in group II, III and IV, respectively. Rest of the groups had pigmentation in two or more plant parts, the highest, 11 parts pigmented, being in the group XL VII. Among these groups the highest frequency was

Table 1. Frequencies of genotypes against different colour classes for 14 plant parts in Ahu rices

Plant parts/	White	Light Green	Green	Dark green	Yellowish green	Light yellow	Yellow	Pink	Brown	Red	Light purple	Purple line	Purple	Shades of purple	Dark purple	Red apex	Purple apex	Blakish brown furrow
Basal leaf sheath			132								1	8	1					
Sheath pulvinus		75		48										16			3	
Culm inernode		58	76									6	2					
Nodal septum		12		102				7			6		8		7			
Leaf blade		33	63	46														
Collar		140	2															
Ligule	98		25									19						
Auricle		136											6					
Sterile lemma	88	40						3					11					
Apiculus	77	15							2	18			22			3	5	
Stigma colour	127	5					1				3		6					
Lemma-palea (at anthesis)			100		37		3							1				1
Pericarp	42								35	64	1							
Lemma-palea (at maturity)	55	15	3	31	12	4	7	8	2	4	1							
Colour classes for Lemma-palea (at maturity)	Straw	Gold& gold furrow on straw	Brown spot on straw	Brown furrow on straw	Brown	Redish to light purple	Purple spot on on straw	Purple furrow on straw	Purple	Black	Whitish							

Table 2. Classification of Ahu rice genotypes into various groups based on pigmentation in 14 plant parts

Group No.	Pigmentation in plant parts	Number of genotypes
I.	No pigmentation	17
II.	Nodal septum	10
III.	Lemma and palea at maturity	1
IV.	Pericarp	12
V.	Sheath pulvinus, pericarp	1
VI.	Nodal septum, apiculus	1
VII.	Nodal septum, lemma and palea at anthesis	1
VIII.	Nodal septum, lemma and palea at maturity	5
IX.	Nodal septum, pericarp	9
X.	Auricle, pericarp	1
XI.	Apiculus, pericarp	7
XII.	Stigma, pericarp	2
XIII.	Lemma and palea at anthesis, lemma and palea at maturity	1
XIV.	Lemma and palea at maturity, pericarp	15
XV.	Sheath pulvinus, nodal septum and pericarp	2
XVI.	Sheath pulvinus, lemma and palea at maturity, pericarp	1
XVII.	Nodal septum, auricle, lemma and palea at maturity	1
XVIII.	Nodal septum, apiculus, pericarp	5
XIX.	Nodal septum, lemma and palea at maturity, pericarp	9
XX.	Collar, lemma and palea at maturity, pericarp	1
XXI.	Apiculus, Stigma, lemma and palea at maturity	1
XXII.	Apiculus, lemma and palea at maturity, pericarp	3
XXIII.	Stigma, lemma and palea at maturity, pericarp	1
XXIV.	Sheath pulvinus, nodal septum, lemma and palea at maturity, pericarp	1
XXV.	Nodal septum, sterile lemma, apiculus, lemma and palea at maturity	1
XXVI.	Nodal septum, sterile lemma, apiculus, pericarp	2
XXVII.	Nodal septum, apiculus, lemma and palea at maturity, pericarp	6
XXVIII.	Basal leaf sheath, nodal septum, ligule, sterile lemma, apiculus	1
XXIX.	Basal leaf sheath, nodal septum, apiculus, lemma and palea at maturity, pericarp	1
XXX.	Sheath pulvinus, culm internode, apiculus, lemma and palea at maturity, pericarp	1
XXXI.	Sheath pulvinus, nodal septum, apiculus, lemma and palea at maturity, pericarp	3
XXXII.	Sheath pulvinus, auricle, apiculus, lemma and palea at maturity, pericarp	2
XXXIII.	Culm internode, nodal septum, leaf blade, lemma and palea at maturity, pericarp	1
XXXIV.	Culm internode, nodal septum, auricle, lemma and palea at maturity, pericarp	1
XXXV.	Nodal septum, auricle, apiculus, lemma and palea at maturity, pericarp	2
XXXVI.	Nodal septum, sterile lemma, apiculus, lemma and palea at maturity, pericarp	1
XXXVII.	Nodal septum, apiculus, stigma, lemma and palea at maturity, pericarp	1
XXXVIII.	Sheath pulvinus, nodal septum, collar, apiculus, lemma and palea at maturity, pericarp	1
XXXIX.	Sheath pulvinus, nodal septum, ligule, apiculus, lemma and palea at maturity, pericarp	2
XL.	Nodal septum, sterile lemma, apiculus, stigma, lemma and palea at maturity, pericarp	1
XLI.	Basal leaf sheath, sheath pulvinus, nodal septum, apiculus, stigma, lemma and palea at maturity, pericarp	1
XLII.	Basal leaf sheath, culm internode, nodal septum, sterile lemma, apiculus, stigma, pericarp	1
XLIII.	Basal leaf sheath, sheath pulvinus, culm internode, nodal septum, leaf blade, ligule, apiculus, lemma and palea at maturity	1
XLIV.	Basal leaf sheath, sheath pulvinus, nodal septum, ligule apiculus, stigma, lemma and palea at maturity, pericarp	1
XLV.	Basal leaf sheath, culm internode, nodal septum, sterile lemma, apiculus, stigma, lemma and palea at maturity, pericarp	1
XLVI.	Basal leaf sheath, sheath pulvinus, culm internode, nodal septum, apiculus, stigma, lemma and palea at anthesis, lemma and palea at maturity, pericarp	1
XLVII.	Basal leaf sheath, sheath pulvinus, culm internode, nodal septum, leaf blade, ligule, auricle, sterile lemma, apiculus, stigma, lemma and palea at maturity, pericarp	1

observed for LPm and P (15, Group XIV) followed by NS and P (9, Group IX), NS, LPm and P (9, group XIX), Ap and P (7, Group XII), NS, Ap, LPm and P (6, Group XXVII), NS and LPm (5, Group VIII) and NS, Ap and P (5, Group XVIII).

Twenty-nine groups were represented by single genotype each, while others comprised either two or three each. Pigmentation in LPm, NS and Ap was found to occur in 32, 31 and 25 groups, respectively, indicating that these three are the pimgmented parts in most of the Ahu rices. However, Sinha *et al.* (1988) observed in Gora rices of Bihar that all the pigmented genotypes had pigmentation in apiculus (Ap). Although stigma colour (s) exhibited high CV (75.04%), pigmentation on stigma (S) was found in eight groups only, where at least four other parts were also pigmented. The wide grouping observed indicates the relevance of pigmentation pattern in varietal identification and classification in Ahu

rices. It also appears that the pigmentation in different plant parts particularly in LPm, Ap, CI and BLS has resemblance with the local names of the land races and has important bearing on varietal identification and maintenance of purity. Such resemblance was also observed in Gora rices of Bihar (Sinha *et al.*, 1988). In the present investigation no case was met with where all the parts studied were pigmented. Such observations were also reported by Misro *et al.* (1960) and other workers with the exeption of Nagamutu (1943) and Sinha *et al.* (1988) where observations were confined to only ten and eight characters, respectively.

The complexity of the pigmentation pattern being expressed in different combinations in different genotypes might be attributed to the involvement of several major genes for pigmentation along with modifiers and inhibitors. Complicated nature of inheritance of pigmentation was reported by Jones (1921) and Ramiah (1945). Detailed study of the inheritance of the pigmentation pattern in crosses involving different sets of parents of Ahu rices is, therefore, essential.

Simple correlation coefficients were computed for pigmentation between plant parts studied (Table 3). Significant and positive correlation of BLS was observed with SP, CI, NS, L, SL, Ap and S. Sheath pulvinus colour (SP) was also significantly and positively correlated with CI, Ar, Ap, S and LPm. Culm internode colour (CI) exhibited positive and significant association with all the traits but C and P. Significant positive association was also observed between NS and L, SL, Ap; LB and L, SL, S; LC and SL, Ap, S; Ar and Ap, LPm; SL and Ap, S and between Ap and S. The higher frequency of positive correlation among these plant parts might be due to the linkage of genes governing anthocyanin pigmentation as also suggested by Ratho and Rao (1972), Hadgal (1980), Misro (1981) and Sinha *et al.* (1988). Lemma palea colour at anthesis (LPa) was correlated positively with only CI, while pericarp (P) colour exhibited positive and significant association with Ap and LPm. Collar (C) colour exhibited no significant association with other parts. From the above study it appears that significantly positively correlated pairs of characters were frequent in the parts other than lemma-palea and kernel. This might be due to the differences in linkage relationships of the genes governing pigmentation in these parts. Lemma-palea colour at maturity (LPm) did not exhibit correlation with LPa but was positively correlated with pericarp (P) colour.

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Table 3. Simple correlation coefficients for pigmentation among 14 plant parts in Ahu rices

Plant parts	BLS	SP	CI	NS	LB	C	L	A	SL	Ap	S	LPa	LPm
SP	0.32*												
CI	0.56**	0.26*											
NS	0.25**	0.13	0.17*										
LB	0.16	0.09	0.38**	0.14									
C	-0.03	0.13	-0.02	-0.01	-0.01								
L	0.52**	0.15	0.25**	0.20*	0.21*	-0.02							
A	0.05	0.24**	0.18*	0.01	0.16	-0.03	0.08**						
SL	0.40**	-0.02	0.31**	0.24**	0.36**	-0.03	0.23	0.05					
Ap	0.36**	0.32**	0.21*	0.22**	0.09	0.03	0.28**	0.17*	0.35**				
S	0.54**	0.18*	0.36**	0.08	0.30**	-0.03	0.18*	0.02	0.33**	0.25**			
LPa	0.16	0.09	0.18*	0.04	-0.02	-0.01	-0.03	-0.03	-0.03	-0.01	0.13		
LPm	0.05	0.27*	0.19*	0.15	0.14	0.12	0.14	0.20	0.03	0.23**	0.15	0.05	
P	0.03	0.20	0.09	0.02	0.09	0.07	-0.02	0.09	0.09	0.28**	0.13	-0.12	0.30**

* Significant at 5% level of probability

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

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Genetic Variability, Correlation and Path Coefficient Analysis for Seed Yield and its Component Traits in Berseem (*Trifolium alexandrinum* L.)

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Twenty seven promising genotypes of berseem were evaluated for seed yield and its component traits. The range of variation was from 3.60 to 5.97 for tillers/plant; 13.60 to 24.7 for number of heads/plant and 0.85 to 2.49 g for seed yield/plant. The estimates of GCV and PCV was maximum for seed yield and primary branches/plant, whereas, low estimates were observed for head length and head breadth. High estimates of heritability coupled with high genetic gain were observed for seed yield/plant and primary branches/plant. Tillers/plant, primary branches/plant, number of heads/plant and seeds/head showed significant and positive association with seed yield/plant. However, based on path coefficient analysis, number of seeds/head and tillers/plant were found to be the best characters for bringing desired improvement in seed yield/plant in berseem.

Key Words: Berseem, Correlation and Path Analysis, Seed Yield, *Trifolium alexandrinum*, Variability

Berseem or Egyptian clover (*Trifolium alexandrinum* L.) is very important fodder crop in India during winter season. It is entirely grown through seeds. Hence seed production in berseem is as important as the green fodder production. Substantial amount of research work on genetic variability, heritability, correlation and path coefficient analysis have been carried out for fodder yield and its components (Yadav *et al.*, 1974; Sidhu *et al.*, 1976; Jatasra *et al.*, 1980 and Jatasra, 1981) but studies on seed yield and its component traits are very meagre (Bakheit, 1988). Realizing this, present study was undertaken to estimate genetic variability, correlation and path coefficients for seed yield and its components in berseem.

Materials and Methods

Twenty seven promising strains of berseem grown for evaluation for fodder yield were also evaluated for seed yield and its contributing traits. The experimental material was sown by broadcast method in complete randomized block design with three replications. After the last harvest for green fodder taken during the last week of March, the crop was left for seed production. At maturity, the data on various traits such as number of tillers, number of primary branches, head length (cm), head breadth (cm), number of heads, number of seeds/head, 1000-seed weight (g) and seed yield/plant (g) were recorded on 5 randomly chosen competitive plants in each genotype replicated thrice. The mean value of each character for each genotype was subjected to analysis of variance as described by Panse and Sukhatme (1989). Genotypic and phenotypic coefficient of variation was estimated by the formula suggested by Burton (1952). Heritability in broad sense was calculated according to formula suggested by Hanson et al. (1956) and genetic gain as suggested by Johnson et al. (1955). Phenotypic and genotypic correlation coefficients were worked out by the method described by Al-Jibouri et al. (1958) and the direct and indirect effects of independent traits on seed yield/plant were estimated by the method of Dewey and Lu (1959).

Results and Discussion

The estimates of range in variation, average performance, genotypic and phenotypic coefficient of variation, heritability and genetic advance are presented in Table 1. The range in variation was from 3.60-5.97 for number of tillers/plant; 5.47-13.20 for number of primary branches/plant; 1.53-1.88 cm for head length; 2.87-3.80 cm for head breadth; 13.60-24.87 for number of heads/plant; 22.00-42.47 for number of seed/head; 1.78-3.07 g for 1000-seed weight and 0.85-2.49 g for seed yield/plant. An overall mean value averaged over 27 genotypes was 4.41 for tillers/plant; 8.17 for primary branches/plant; 1.68 cm for head length; 3.29 cm for head breadth; 17.29 for heads/plant; 31.70 for seeds/head; 2.51 g for 1000-seed weight and 1.36 g for seed yield/plant. Bakheit (1988) from Egypt reported that 1000-seed weight in berseem varied from 3.37-3.93 g with an average of 3.71g.

The maximum coefficient of variation was observed for seed yield/plant and primary branches/plant. Moderate coefficient of variability was observed for

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Table 1. Range, mean, coefficient of variability, heritability and genetic advance for eight characters in berseem

Components	No. of tillers/ plant	No. of primary branches/ plant	Head length (cm)	Head breadth (cm)	No. of heads/ plant	No. of seeds/ head	1000-seed weight (g)	Seed yield/ plant (g)
Range	3.60-5.97	5.47-13.20	1.53-1.88	2.87-3.80	13.60-24.87	22.00-42.47	1.78-3.07	0.85-2.49
Mean + S.E.	4.41+0.32	8.17+0.56	1.68+0.04	3.29+0.04	17.29+0.89	31.70+0.94	2.51+0.03	1.36+0.08
C.D. at (5%)	0.92	1.58	0.11	0.10	2.54	2.67	0.10	0.24
GCV (%)	14.49	23.69	5.90	7.17	14.43	16.89	14.80	24.27
PCV (%)	19.28	26.46	7.04	4.41	16.98	17.65	14.98	26.52
H2% (BS)	56.52	80.90	70.34	93.62	72.18	91.55	97.60	83.75
GA (% of mean)	22.45	43.70	10.20	14.28	25.25	33.28	30.11	45.36

seeds/head, 1000-seed weight, heads/plant and tillers/ plant. However, head length and head breadth showed low estimates of variation. Low amount of GCV and PCV has been reported for seed yield and 1000-seed weight by Bakheit (1988). The high estimates of heritability coupled with high genetic advance were observed for seed yield/plant, primary branches/plant, number of seeds/head and 1000-seed weight. So, these characters are amendable to improvement through simple selection. Moderate estimates of heritability and genetic advance for seed yield and moderate estimates of heritability and low genetic advance for 1000-seed weight has been reported by Bakheit (1988) in berseem.

Genotypic and phenotypic correlation coefficients among eight characters are presented in Table 2. Number of tillers/plant, number of primary branches/plant, number of heads/plant, number of seeds/head showed significant and positive association with seed yield per plant. Test weight however showed non-significant but positive association with primary branches/plant and number of heads/plant. Number of primary branches also showed positive and significant association with number of heads/ plant. Head length showed positive and significant association with head breadth, whereas head breadth showed negative and significant association with 1000-seed weight. Number of heads revealed negative and significant association with 1000-seed weight. Bakheit (1988) reported significant positive association between seed yield and 1000-seed weight in berseem.

Path coefficient studies revealed that 1000-seed weight had the maximum direct effect on seed yield/ plant followed by number of seeds/head, number of heads/ plant and tillers/plant. Of these all but 1000-seed weight had significant and positive association with seed yield/ plant. Primary branches/plant showed negative direct effects on seed yield/plant though it has significant positive association with seed yield/plant. Number of seeds/head though had high direct effect as well as positive significant association with the seed yield/plant but had maximum negative indirect effect through 1000-seed weight on seed yield/plant, likewise 1000-seed weight which had maximum direct effect but no positive significant association with seed yield/plant and also it showed high negative indirect effect through number

Table 2. Genotypic (in parentheses) and phenotypic correlation coefficients among eight characters in berseem

Characters	No. of primary branches/ plant	Head length	Head breadth	No. of heads/ plant	No. of seeds/ head	1000-seed weight	Seed yield/ plant
No. of tillers/plant	(0.668)	(0.238)	(0.027)	(0.776)	(0.087)	(-0.047)	(0.553)
	0.489**	0.103	0.029	0.504**	0.063	-0.009	0.412*
No. of primary branches/plant		(0.305)	(0.328)	(0.677)	(-0.056)	(0.155)	(0.486)
		0.184	0.273	0.614**	-0.064	0.146	0.456*
Head length			(0.532)	(0.055)	(0.354)	(-0.018)	(0.229)
			0.441*	0.014	0.257	-0.028	0.117
Head breadth				(0.212)	(0.364)	(-0.553)	(0.000)
				0.159	0.348	-0.519**	0.001
No. of heads/plant					(0.173)	(-0.014)	(0.771)
					0.153	-0.036	0.772**
No. of seeds/head						(-0.532)	0.443)
						-0.501**	0.455*
1000-seed weight							(0.276)
							0.250

*Significant at P = 0.05
**Significant at P = 0.01

Table 3. Path coefficient analysis of seed yield and its components in berseem

Characters	No. of tillers/plant	No. of primary branches/ plant	Head length	Head breadth	No. of heads/ plant	No. of seeds/ head	1000-seed weight	Genotypic correlation coefficient with seed yield/plant
No. of tillers/plant	**0.300**	-0.092	-0.052	0.007	0.364	0.067	-0.041	0.553
No. of primary branches/plant	0.200	**-0.137**	-0.067	0.082	0.317	-0.044	0.134	0.46
Head length	0.0713	-0.042	**-0.219**	0.134	0.026	0.274	-0.015	0.229
Head breadth	0.008	-0.045	-0.116	**0.251**	0.099	0.282	-0.479	0.000
No. of heads/plants	0.233	-0.093	-0.012	0.053	**0.169**	0.134	-0.012	0.771
No. of seeds/head	0.026	0.008	-0.077	0.091	0.081	**0.775**	-0.461	0.443
1000-seed weight	-0.014	-0.021	0.004	-0.139	-0.007	-0.413	**0.866**	0.276

Residual effect = 0.008

of seeds/head, hence neither number of seeds/head nor the 1000-seed weight fit into good selection criteria for increasing the seed yield/plant in berseem. Instead, number of heads/plant might be a good selection criteria for improving the seed yield/plant since it had highest positive significant association with seed yield/plant, high positive direct effect on seed yield/plant and also has high indirect effect on seed yield/plant through tillers/plant. In turn, tillers/plant showed high positive direct effect on yield as well as the strong positive association with seed yield/plant and also had high indirect effect through number of heads/ plant on seed yield/plant. So, selection for more number of heads/plant and more number of tillers/ plant might result in significant improvement in seed yield/plant in berseem.

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Jeypore Tract Revisited

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The southern region of Orissa is famous as a centre of genetic diversity of cultivated rice and also a probable centre of origin of this species. Studies indicated that southeast India, of which this forms a part, is probably the centre of origin of "seihr (southeast Indian hill rice)" ecogenetic group of *Oryza sativa*. In recent years documentation of ownership of landraces of rice has been done to protect the intellectual property right of the farmer-conservers.

Key Words: Genetic Diversity, Jeypore Tract

The southern part of Orissa, known as Jeypore tract has drawn the attention of rice biosystematics, geneticists and conservationists for the last half a century. In recent years, the area has gained again importance with regard to farmers' rights and on-farm conservation, which are new dimensions of genetic resources conservation. It is, therefore, desirable that the situation should not only be reviewed but also understood in proper perspective.

History

Place

The spatial aspect of the origin of the Asian cultivated rice has been much debated. Watt (1891) and Ramiah and Ghosh (1951) considered that Asian rice originated in peninsular India. Ting (1957) strongly believed that China is the center of origin of *Oryza sativa*. According to Hamada (1949) and Burkill (1953) Indo-China is the center of origin of cultivated rice. Gustchin (1938) proposed that rice might have originated on the slopes of Himalayas both on Indian as well as Chinese sides. Rochevich (1931) and Chatterjee (1951) considered that the whole region of south and Southeast Asia could have been the place where rice was domesticated. On the basis of ecotype inter-relationships, Morinaga (1968) proposed that the sub-Himalayan India could have been the center of origin of cultivated rice.

The relationships among the various ecogenetic groups within the cultivated species as well as their relationship with the progenitor species can, therefore, throw much light on the place of origin of cultivated rice. In this context, the Jeypore Tract of Orissa deserves special mention.

The so-called "Jaypore Tract" is now an obsolete term with no distinct geographical or political boundary. During the British rule, the areas around the Jeypore town (in South Orissa) were governed by the Zamindars (feudal lords) and supervised by a political agent. The area was known as Jeypore agency area. After independence, major part of this area was merged with the Orissa state and formed Koraput district of this state. Koraput used to be the southern most district of Orissa and is located between 20°08' and 17°50' and 81°27' and 84°01' E (Fig. 1). Around mid-nineties, this district has been split into further four districts, *i.e.*, Koraput, Nabarangpur, Malkangiri and Rayagada. However, all these four districts continue to be refereed to as "undivided" Koraput district.

Tribes

According to 2001 census the four districts have a population of 3.5 million out of which male population is 1.75 million. The population density, 131/km^2 is quite less comparing with other districts of Orissa. More than half (about 55%) of the State's Scheduled Tribe (ST) and 15.66% of the Scheduled Caste (SC) population reside in this region (in the sense that these tribes and castes are recognized and listed in the Indian constitution to receive special privileges). The Kandha, Langia Soura, Paroja, Bhatra, Gadaba, Amanatya, Halva, Bonda, Koya and Didayi tribes are the original inhabitants of the forests and hills of this area. The Kandha, Bonda, Paroja and Langia Soura tribes still practise shifting-cultivation along with settled cultivation. The Indian Government has rehabilitated Bangladesh refugees in the districts of Nabarangpur and Malkangiri. The refugees are different from the tribals of this region with regard to their culture, language and cultivation practices.

Hills

The district lies on a section of the Eastern Ghats and consists of five natural divisions having mean elevations of 154m, 30m , 615m, 769m and 923m above

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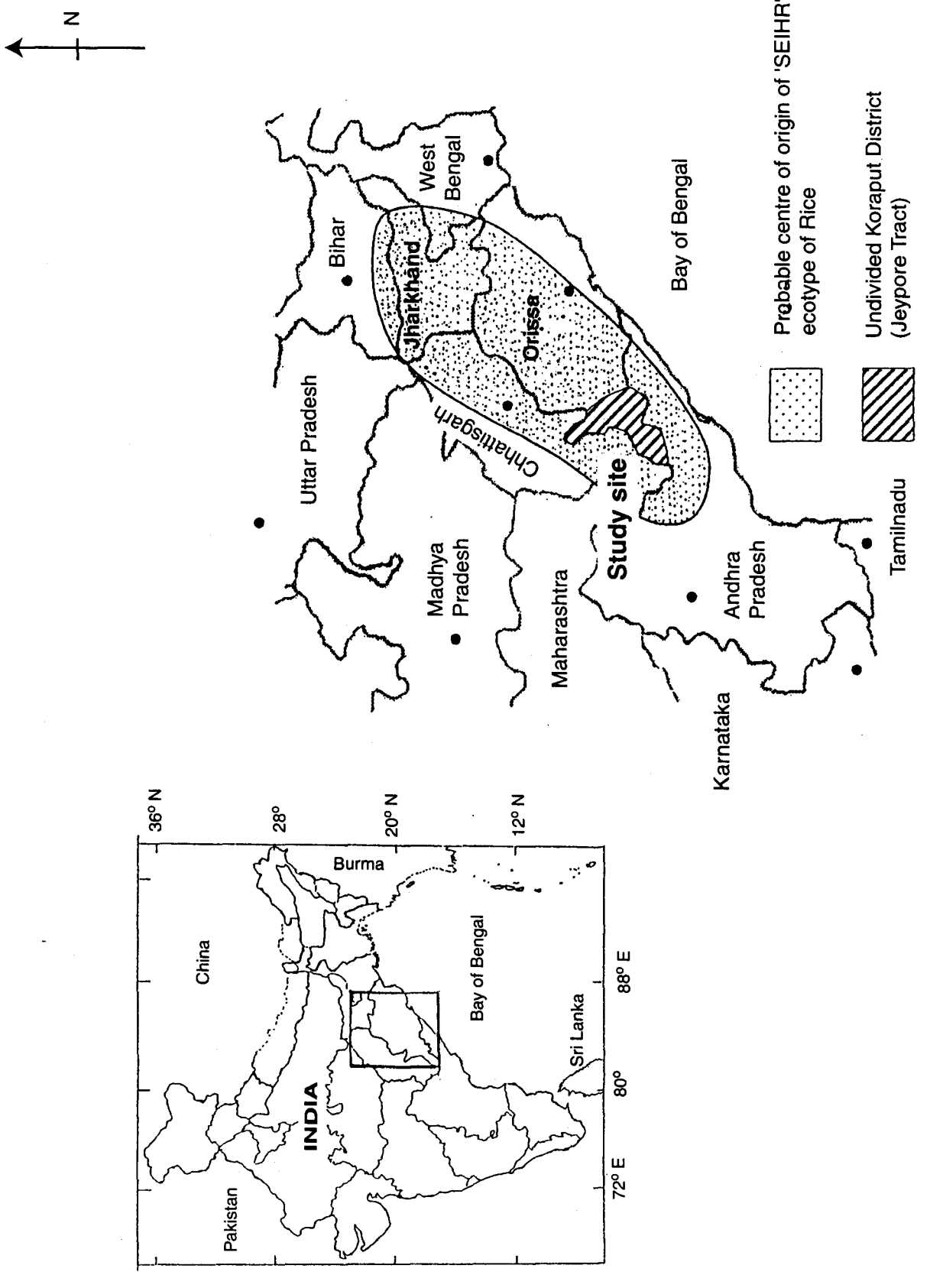

Fig. 1. Jeypore tract and the probable primary centre of origin of "Seihr" ecogenetic group of rice

mean sea level. A number of mountain ranges and isolated hills rise out of these tablelands.

Late Dr. K Ramiah (the renowned rice geneticist and breeder of India) visited the Jeypore agency area and was impressed with the morphological and ecological diversity of traditional rice cultivars. He remarked in his monograph (written before 1944 but published in 1953) on "Rice Breeding and Genetics" that this area might form another independent center of origin. Ramiah and Ghosh (1951) suggested that the Jeypore area might well be a "secondary center for origin of cultivated rice". Accordingly, he formulated a project on botanical survey of this tract for collection and study of these traditional rice varieties. This project was popularly known as Jeypore botanical survey and was executed by the Central Rice Research Institute (CRRI), Cuttack, Orissa during 1955-60. These collections (about 1750 altogether) are known as JBS collections in rice literature. The CRRI could study the morphological and agronomic characters only of these varieties and corroborated the views of Ramiah and Ghosh (1951) that this area could be a secondary center of origin of cultivated rice. The Japanese scientist H.I. Oka who studied the cultivated varieties and their wild relatives from this area proposed the view that the wild rice of this area have given rise to primitive landraces that have the capability to differentiate into *Japonica* and *Indica* ecotypes and hence he called the traditional rice varieties of this area as incipient *japonicas* and *indicas*.

Sharma and Shastry (1965) surveyed the whole of India including Jeypore Tract for the wild rice, collected samples of populations of wild rice far away from as well as near the cultivated rice fields, studied their progeny behaviour as well as morphological characters and came out with strong evidences about the existence of an annual wild species distinct and different from the perennial wild species (*O. rufipogon*) as well as from the natural hybrids (*spontanea*) and named it as *Oryza nivara* as this species lacked a valid name.

O. nivara is an annual wild species widely distributed in the Deccan Plateau of India particularly in its north-eastern part and in the central part of the Gangetic valley. It is also available in south and southeast China and in plateau regions of Southeast Asia.

The cultivated rice *O. sativa* and its close relatives, namely, the annual wild rice (*O. nivara*) and the perennial wild rice (*O. rufipogon,* syn. *O. perennis*) and the natural hybrids between the cultivated and these wild rice varieties form a complex, which has been rightly named as *Oryza sativa* complex by Tateoka (1962). All the elements of this complex have the same chromosome number (2n-24) and the same genome (AA) and the genetic barrier among them is incomplete so much so that the cultivated species hybridizes in nature with these wild species and forms hybrids which get back crossed to either parents to give rise to various types of interbreeds in nature. These intergrades known as *'spontaneas'* in rice literature can however be identified by their progeny behavior.

Prior to 1965, when *O. nivara* was not recognized as a different and distinct species, *O. rufipogon* (then popularly known as *O. perennis*) was considered to be the progenitor of the cultivated rice. But with the recognition of *O. nivara* as a different and distinct species, Sharma (1964) and Shastry and Sharma (1973) and Chang (1985) proposed that *O. nivara* could be the progenitor of *O. sativa.*

Any hypothesis regarding the origin of cultivated rice, however, must explain the origin of ecotype differentiation in this species. The cultivated rice (*O. sativa*) has two major ecotypes, namely, *japonica* and *indica* and their F_1 hybrids are often partly to highly sterile.

Biswal (1988), therefore, made collections of *O. nivara* from different parts of India, crossed the collections among themselves and studied their F_1 sterility. She observed that the wider the distance between two sites of collections of *O. nivara,* the greater the sterility of their F_1 hybrid. She, therefore, concluded that the sterility observed in the *japonica x indica* hybrids already existed in the progenitor species (*O. nivara*) and has merely been carried over to the progeny species (*O. sativa).*

Biswal (1988) also crossed the *nivara* collections with the landraces of Jeypore tract and with the seihr and *japonica* ecotypes and observed the same type of sterility as observed in *nivara x nivara* hybrids and concluded that *japonica* and *seihr* ecotypes have originated from two different populations of *O. nivara* one in southeast India and the other in south or southwest China.

The southeastern India *i.e.,* the northeastern Andhra Pradesh, eastern Madhya Pradesh, whole of Orissa (except coastal belt), southern Bihar, and the hilly tracts of southwestern. West Bengal form a contiguous geographical area having similar topography, climate, rainfall, etc. The Jeypore tract of Orissa, which has been considered to be a secondary center of origin of cultivated

rice by Ramiah and Ghosh (1951), Ramiah (1953) and Oka and Chang (1962) forms a part of this larger area. This area is inhabited by aborigines belonging to Proto-australoid ethnicity, practise primitive agriculture (including shifting cultivation) and still patronize the age-old landraces. These landraces show many primitive features and are most often photo-insensitive and early maturing.

Tripathy (1994) crossed these landraces with various other ecotypes of *O. sativa* and on the basis of pollen sterility of their F_1 hybrids as well as of F_1 hybrids of these landraces with their putative progenitors concluded that southeast India (that also includes Jeypore tract) could be the primary center of origin of 'seihr' ecotype. If so, the genetic diversity observed in the traditional rice varieties of southeast India becomes evolutionarily very significant and genetically very important as these cultivars might harbor many valuable genes that may prove useful in rice breeding.

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Indigenous Technical Knowledge of the Tribal Farmers of Visakhapatnam District of Andhra Pradesh

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A huge and unwritten wealth of knowledge on traditional crops, cultural practices, pest and disease management in agriculture, cropping systems and indigenous seed storage methods was found to exist with the farmers and some of it was documented. Practices like hanging maize cobs from kitchen roof for seed storage, use of ash to control pumpkin beetles and aphids, bird catching by using jackfruit latex and planting *Jatropa* around the fruit plants to protect them form external enemies, were of much interest and great practical value.

Key Words: Documentation, Exploration, High altitude tribal area zone, Indigenous technical knowledge

India is the treasure land of biological wealth, indigenous traditional knowledge and spiritual wisdom. The term 'Indigenous technical knowledge' (ITK) is used synonymously with 'traditional' and local technical knowledge to differentiate the knowledge developed over generations by a given community from the knowledge acquired from schools of learning. Further ITK is dynamic and not static, it covers the whole range of human experience. It has been tried and tested over centuries and against different agro-climatic conditions. The knowledge, which was found fit for the mankind has been used and passed on from generation to generation. According to Haverkort (1995) indigenous technical knowledge is the actual knowledge of a given population that reflects the experiences based on tradition and also includes more recent experiences with modern technologies.

However, many of our indigenous practices in agriculture and allied fields have been replaced by the so-called modern technologies and they have become obsolete, especially among the younger generations. Now these indigenous practices are dwindling and there is a possibility for them to become extinct particularly during this era of globalization, liberalization and commercialization.

High Altitude Tribal Area (HAT) Zone of Andhra Pradesh is rich in traditional knowledge. Such knowledge can be utilised effectively for the development of agriculture of this region. This would definitely help to evolve location specific technologies and would give boost to the sustainable agriculture

Material and Methods

Exploration trips were conducted from Regional Agricultural Research Station (RARS), Chintapalle under "Network Project on Tribal Area Crops of Madhya Pradesh, Andhra Pradesh and Orissa" to collect ITK. ITK was gathered by individual contact with the farmers of Anarbha, Bonangipalli, Boytili, Cherapalli, Gondipalli, G.M.Kotturu, Kappagondi, Karakaputtu, Katragadda K. Kodapalle, Kondrupalli, Korapalli Kottapakalu, Kottavalasa, Kottaveedhi, Minumuluru, Modapalle, Mondigedda, Nimmlapadu, Panasapalli, Pedakonda, Peddalanka, Pilligedda, P. Kotturu, Porlu, Singarbha, Rallagadda, Rohungaputtu, Thimulagunta, Thimulamamidi, Vanchela, Vartanapalli and villages of Paderu, G. Madugula and G.K. Veedhi, Chintapalle Mandals of Visakhapatnam District and a few villages viz., Chitrakonda, Maliguda, Dontuguda, Doraguda and Thimulamamidi of Andhra-Orissa State boarder. Around 20 exploration trips were conducted to collect germplasm as well as ITK. ITK was collected on various crops grown, their cultural practices, cropping systems followed, disease and pest control and seed storage methods.

Results and Discussion

Some of the ITKs on agriculture of this HAT zone is discussed below:

Cultural practices

Deep summer ploughing is done to control pests (especially paddy stem borer) and diseases like redgram wilt, to conserve soil moisture and to reduce soil erosion due to flow of rainwater. This finding is in agreement with Kasyapa (1998).

Pulse crops are generally affected by water logging conditions. Hence, pulses like red gram (*sirikandi*) black gram (*minimulu*), rice bean (*timmerlu*) and beans (*sriram chikkudu*) are generally grown by the tribal farmers along the mild hill slopes to avoid water logging due to heavy rains and to ensure the optimum moisture retention. Besides, it acts as vegetative cover in controlling soil erosion and helps in better management of sloppy and marginal soils.

Due to limited availability of plain and leveled land in the tribal areas, paddy (*budamalu, mettudhanyam*) cultivation is taken up in small and fragmented portions of land at the foothills by preparing the land into terraces along the slope with a mild gradient popularly called as bench terracing. This has been found to be highly effective in water management for paddy crop in the kharif season.

Importance of cow dung in tribal agriculture

In India the importance of cow dung to induce rooting was long known and it is a common practice of tribal people to place cow-dung mixture on the top of the cuttings in rose and *Manihot esculenta* for early and successful rooting.

One kg cow dung mixed with 100 ml cow urine (10:1) is applied during early vegetative stage by drenching the root zone of the chilli, tomato and brinjal plants at 15 days after transplanting. It acts against chilly fruit borer (*Spodoptera litura*) due to its ovicidal effect and induces tolerance due to the hormones and nitrogen present in the urine. The fresh cow dung emits an offensive odour and acts as an insect repellent. The adult insects find an unfavorable environment either to feed or perpetuate on the sprinkled crop and thus this practice is also eco-friendly. Similar practice is followed in Tripura to control bacterial blight in tomato (Chowdhuri, 1998).

Cow dung mixed with mud (4:1) is pasted in and around bamboo baskets (*Granary*) for grain storage. Cow dung is pasted on the floor and walls of huts. Cow dung and urine is used in ritual ceremonies called as *suddhi.*

Pest and disease management

Marigold is grown as an intercrop to control chilli nematode *Meloidogyne incognita* (*nulipurugu*). The disease is locally called as *pasuputeegelu.* The root exudates may act as antagonists to nematodes. Similar practice is followed by the farmers of Uttar Pradesh (Ambedkar, 1998).

Ash is dusted in the early morning to control pumpkin beetle and aphids in dolichos bean, rice bean and pumpkin. The abrasive nature of the ash is supposed to control these pests. The finer the ash, higher will be its effectiveness as the surface area of contact and abrasiveness of ash will increase with increase in fineness. It also blocks the trachea of the soft insects and causes asphyxiation, thus the aphid population can be kept under check by the combined action of both these factors. Similar practice is followed by farmers of Tamilnadu (Vivekananda, 2000).

Jatropa (*Adavinepalam*) plants are planted as a hedge around the field and vegetable crops. Jatropa twigs are also planted around jackfruit, mango and banana plants. Similar jatropa planting was reported to have been followed in Nigeria (Apantaku, 1998). The jatropa plant is repellent to goats and cattle. Therefore, it protects the trees from cattle browsing. It also acts as a binder in preventing soil erosion.

In field crops like paddy, small sparrows infest the crop at the time of maturity. To catch them or to drive them away, tribal farmers adopt a bird catching technique using the latex of jackfruit as an adhesive gum. *Artocarpus heterophyllus* latex and *Semicarpus anacardium* resin/ tannin extracts of seed are used for preparing adhesive gum. First the unripe seeds of *Semicarpus* are collected, resin/tannin is extracted with the help of locally made bamboo crusher. Sufficient quantity of *Artocarpus* latex is collected, a little amount of oil is added and the mixture is heated in an earthen pot with constant stirring until it attains setting stage (a thick jelly like gum).

Cropping systems

Some of the cropping systems followed in this region are as follows:

Coriander + Ginger + French bean mixed cropping: Ginger is grown at a distance of 50 cm by forming ridges and coriander is sown in between the ridges. Beans are planted in rows at every 4m distance. The beans are given support with bamboo stakes. Ginger takes more time for sprouting leading to weed growth. Coriander growing in the ginger field prevents the weed growth. Coriander is harvested early (one month) as leafy vegetable when ginger is in vegetative growth, thus coriander will not compete with ginger. Bean is a border crop and provides partial shade to ginger crop.

Maize + Lima bean mixed cropping: Maize is planted early in the season whereas lima bean is planted later

i.e., at its silking stage. Maize plants which are left in the field after the harvest of the cobs act as a live support to the lima bean.

Maize + Long pepper + Turmeric: In this system turmeric, a long duration crop is grown to get extra income, long pepper which is having spreading habit is grown to reduce weed problem. Long pepper and turmeric will not compete with each other for nutrients. Maize also helps in resting of birds to leaf eating caterpillar control.

Seed storage

Maize cobs are tied together (20-25 cobs approximately) with the help of a small rope and kept suspended from the roof of the kitchen. The same practice was reported from North Eastern hill region (Prakash *et al.,* 1999). Keeping cobs and seeds on kitchen roof will keep then in dry condition. The smoke of the kitchen drives away the insects as well as prolongs the storage period.

Seeds of pumpkin are stored by mixing them with ash. Similar practice in snake gourd was reported by Balajirao (1998).

Red soil and Ash (3:1) is mixed with pulse @ 5g/kg seeds and stored. This protects the seeds against stored grain beetles, especially bruchids. Similar practice was reported by Balajirao (1998).

Seeds of pulses/oilseeds crops are stored in a dried bottle gourd. The opening is plastered with mud. In case of ricebean, the mixing of the seed with ash and salt (10:1) is followed, however viability of seed is lost within a year.

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Variability, Correlation and Path Coefficient Analysis for Quality Seed Traits in Cowpea (*Vigna unguiculata* [L.] Walp.)

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Genetic variability, heritability, genetic advance, correlation and path coefficient analysis was studied for some quality seed traits in 50 diverse genotypes of cowpea. The range of variation was observed from 68.00 to 99.33 per cent for standard germination; from 10.73 to 20.07 cm for root length; from 21.33 to 35.73 cm for shoot length; from 696.76 to 2078.67 mg for fresh weight; from 12.67 to 270.67 mg for dry weight; from 0.25 to 2.60 dS/m for electrical conductivity and from 2478.13 to 4643.07 for vigour index in various genotypes. High estimates of GCV, PCV, heritability and genetic advance were observed for seedling dry weight and electrical conductivity. Path analysis studies revealed the maximum direct effect of seedling vigour, seedling dry weight and standard germination on seed yield. Hence, these quality seed traits should also be given due weightage along with other important contributing traits of seed yield.

Key Words: Cowpea, Genetic Advance, Heritability, Path Coefficient Analysis, Variability

Cowpea (*Vigna unguiculata* [L.] Walp.) is one of the important pulse crops which is used extensively in Indian vegetarian diet. Cowpea is a multipurpose crop and is grown as a grain legume mainly for dry beans, green vegetables, and also as forages, green manure and cover crop. Hampton and Tekrony (1995) stated that high seed vigour also leads to high grain yield potential. However, in cowpea, the studies on quality seed parameters are very scanty (Verma, 1978; Shridhar, 1994; Dahiya, *et al.*, 2001 a,b). Keeping in view the limited information available on these aspects, the present investigation was undertaken.

Materials and Methods

Three hundred seeds of each of the fifty genotypes were placed on sufficiently moistened rolled towel paper (BP) and kept in a germinator at 25±1°C. The final count of normal seedlings was made on 8th day (ISTA, 1999) and expressed in per cent. The root length and shoot length of 15 randomly selected normal seedlings taken from each genotype was measured in centimeters. The same seedlings were also used for weighing their fresh weight. After taking their fresh weight, the seedlings were kept for drying in hot-air oven at 80°C for 24 hrs to record their dry weight. For measuring electrical conductivity, one hundred fifty seeds of each genotype were soaked for 24 hrs in a 100 ml beaker containing 75 ml distilled water at 25°C. The electrical conductivity of the seeds leachate was measured with electrical conductivity meter and expressed as m mhos/cm or dS/m. The vigour index was calculated as: Vigour Index = Standard Germination (%) X Seedling Length (cm) where, Seedling Length (cm) = Root length (cm) + Shoot length (cm).

Results and Discussion

The analysis of variance revealed significant genotypic differences for all the traits studied (Table 1). The estimates of range and average performance for seven quality seed traits are presented in Table 2. The range of variation for standard germination was from 68.00-99.33 per cent. The lowest value of germination was recorded in GC-9714 and highest in GP-34, with an over all germination of 90.43 ± 1.63 per cent. Verma (1978) reported considerable amount of genetic variability for the area of first two leaves, initial 100-seed weight, seedling fresh and dry weight, normal seed germination and final 100-seed weight in cowpea. Dahiya *et al.* (2001a) reported that in cowpea the range for standard germination was from 33.33-94.00 per cent. The maximum root length was observed in CPD-15 (20.07 cm) and the minimum in HC 98-58 (10.73 cm). An average value for this trait was 13.73 ± 0.48 cm. Shoot length of seedlings varied from 21.33 cm to 35.73 cm with the maximum value observed in HC-98-24 and the minimum in TC-102. An average shoot length was 29.24 ± 0.67 cm. Dahiya *et al.* (2001a) reported a range of variation for root length (3.67-11.59 cm) and for shoot length (7.84-23.52 cm) in various genotypes of cowpea. Shridhar (1994) also reported significant amount of variability for root length. The range for fresh weight per seedling varied from 696.76 mg in HC 98-66 to 2078.67 mg

Table 1. Mean squares from analysis of variance

Source of Variation	d.f.	Standard germination (%)	Root length (cm)	Shoot length (cm)	Fresh weight/ seedling (mg)	Dry weight seedling (mg)	Electrical conductivity (dS/m)	Vigour index	Seed yield per plant (g)
Replications	2	47.02	2.06	0.66	2588.44	36.42	0.01	65608.51	1.34
Genotypes	49	224.89**	12.12**	24.24**	294808.25**	5002.34**	1.07**	784709.35**	60.60**
Error	98	8.00	0.69	1.34	1444.59	46.83	0.01	14685.27	3.31

Table 2. Range, mean, coefficient of variability, heritability and genetic advance for various quality seed traits in cowpea

Components	Standard germination (%)	Root length (cm)	Shoot length (cm)	Fresh weight/ seedling (mg)	Dry weight/ seedling (mg)	Electrical conductivity (dS/m)	Vigour index
Range	68.00-99.33	10.73-20.07	21.33-35.73	696.76-2078.67	12.67-270.67	0.25-2.60	2478.13-4643.07
Mean+SE	90.43±1.63	13.73±0.48	29.24±0.67	1344.50±21.94	58.27±3.95	1.07±0.04	3808.29±69.96
CD (5%)	4.59	1.35	1.88	61.68	11.11	0.12	196.66
G.C.V. (%)	11.73	14.21	10.24	23.49	69.75	55.73	13.30
P.C.V. (%)	12.36	15.45	10.98	23.66	70.74	56.19	13.68
H^2 (B.S) (%)	90.05	84.58	87.02	98.55	97.24	98.36	94.59
G.A. (% of Mean)	22.94	26.92	19.68	48.04	141.69	113.86	26.65

in DCP-1. An average value for this character was 1344.50 ±21.94 mg per seedling. The dry weight per seedling varied from 12.67 mg in HC 98-63 to 270.67 mg in DCP-1. The general mean value recorded for the trait was 58.27 ± 3.95 mg per seedling. Dahiya *et al.* (2001a) reported 25.06-27.30 mg variation for dry weight in cowpea. The electrical conductivity value varied from 0.25dS/m in GP-22 to 2.60dS/m in DCP-1. An over all mean value for this trait was 1.07±0.04dS/m. Dahiya *et al.* (2001b) reported that value for electrical conductivity in cowpea seed leachate varied from 12.13-42.00 mmhos cm^{-1} $seed^{-1}$. The range of variation for vigour index was from 2478.13 in TC-102 to 4643.07 in HC 98-30. The general mean value for vigour index was 3809.29 ± 69.96. Dahiya *et al.* (2001a) reported that vigour index varied from 4.06-27.49 among different cowpea varieties. Shridhar (1994) also reported varietal differences for this trait in cowpea.

The estimates of genotypic and phenotypic coefficients of variation (GCV, PCV), heritability (broad sense) and genetic advance (% of mean) for various quality seed traits are given in Table 2. High estimates of GCV and PCV were observed for dry weight per seedling and electrical conductivity; moderate for fresh weight per seedling and low estimates for shoot length, vigour index, root length and standard germination. All the quality seed traits showed high estimates of heritability, whereas estimates of genetic advance were high only for dry weight per seedling and electrical conductivity and moderate for fresh weight. The characters showing high estimates of both heritability and genetic gain can thus be improved through simple selection. Verma (1978) also reported high GCV and PCV for seedling fresh weight and dry weight and moderate to high heritability with high genetic advance for these traits in cowpea.

The genotypic and phenotypic correlation coefficients between eight characters are presented in Table 3. The standard germination per cent was found to be positively and significantly correlated with shoot length and vigour index. Seedling root length had positive and significant association with seedling dry weight while shoot length was positively and significantly associated with electrical conductivity. Dahiya *et al.* (2001a) also reported a significant and positive association of standard germination with seedling dry weight and vigour index. They also showed significant and positive association of root length with shoot length and vigour index and shoot length with vigour index. Verma (1978) reported a significant positive association of seedling fresh weight and dry weight with seed yield while Paul and Ramaswamy (1979) and Sinha *et al.* (1988) reported significant positive association between seedling dry matter production and seed weight.

The results of path analysis in the form of direct and indirect effects of seven seed quality traits on seed yield per plant are presented in Table 4. The standard germination per cent, vigour index and seedling dry weight although had non-significant positive association with seed yield per plant, yet vigour index had the maximum desirable direct effect on seed yield. Similarly, seedling dry weight and standard germination per cent also had desirable direct effects on seed yield. Vigour

Table 3. Genotypic (in parenthesis) and phenotypic correlation coefficients among seven quality seed traits in cowpea

Characters	Root length	Shoot length	Fresh weight per seedling	Dry weight per seedling	Electrical conductivity	Vigour index
Standard germination	(-0.204)	(0.318)	(0.017)	(-0.148)	(-0.055)	(0.803)
	-0.193	0.296*	0.015	-0.140	-0.059	0.767**
Root length		(-0.145)	(0.010)	(0.319)	(0.044)	(0.138)
		-0.140	0.008	0.280*	0.042	0.158
Shoot length			(0.021)	(-0.278)	(0.185)	(0.698)
			0.021	-0.254	0.164	0.687**
Fresh weight per seedling				(0.711)	(0.457)	(0.033)
				0.705**	0.450**	0.034
Dry weight per seedling					(0.444)	(-0.127)
					0.438**	-0.121
Electrical conductivity						(0.181)
						0.175

* Significant at P = 0.05
** Significant at P = 0.01

Table 4. Path coefficient analysis of seed yield and quality seed traits in cowpea

Characters	Standard germination	Root length	Shoot length	Fresh weight per seedling	Dry weight per seedling	Electrical conductivity	Vigour index	Genotypic correlation with seed yield per plant
Standard germination	**0.235**	0.109	-0.381	-0.192	-0.050	-0.008	0.714	0.230
Root length	-0.146	**-0.213**	0.118	-0.101	0.108	-0.066	0.237	0.101
Shoot length	0.136	0.141	**-0.110**	-0.002	-0.194	-0.026	0.307	-0.046
Fresh weight per seedling	0.018	-0.050	-0.054	**-0.101**	0.159	-0.064	0.080	0.092
Dry weight per seedling	-0.057	-0.311	0.320	-0.072	**0.336**	-0.062	-0.040	0.159
Electrical conductivity	0.058	-0.043	-0.279	-0.046	0.149	**-0.140**	0.118	0.123
Vigour index	0.247	-0.134	-1.054	-0.003	-0.043	-0.025	**0.946**	0.179

Residual effect = 0.1257

index and standard germination also had positive and desirable indirect effects on seed yield per plant *via* one another. In view of the present results, it is suggested that in addition to other morphological traits, these quality seed parameters should also be taken into account while breeding for high seed yield in cowpea.

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Leaf Morpho-Anatomical Variability in Mulberry (*Morus* spp.) Germplasm

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Leaf anatomical parameters in 330 diverse mulberry germplasm resources (indigenous-182, exotic-108 and polyploids-40) were studied to estimate the variability and to identify potential mulberry varieties for stress tolerance. Estimates of genetic parameters showed high coefficients of variation (GCV and PCV) coupled with high magnitude of heritability and genetic advance for idioblast length and frequency, and upper and lower cuticular thickness. The least coefficient of variation was recorded in respect of leaf thickness and number of chloroplast/stomata. The leaves of exotic accessions were more thick and succulent than indigenous accessions. Significant positive correlations were observed between stomatal size, idioblast length, palisade thickness, spongy thickness, leaf thickness and number of chloroplast/ stomata. Nine indigenous and 11 exotic accessions, which showed multiple drought tolerant characters were identified for stress condition.

Key Words: Leaf anatomy, Indigenous and exotic germplasm, Mulberry, Variability,

Mulberry, the principal food plant of silkworm (*Bombyx mori* L.) is cultivated for its leaf in different agroclimatic conditions for commercial production of silk. Major constraints to mulberry cultivation in India are the limited irrigation facilities, depleting ground water resources and prolonged dry spell with high temperature which reduces the crop yield to a greater extent. Thus, an assessment of variability of leaf anatomical parameters is of prime importance to identify the potential genotypes for stress tolerance.

Leaf anatomical features related to drought tolerance have been studied in crop plants (Dobrenz *et al.*, 1969; Oleinikowa and Kozhushoko, 1970; Miskin and Rasmussen, 1970; Ciha and Brun, 1975; Bhat and Andal, 1979 and Turner, 1979). Physiological and leaf anatomical parameters associated with drought tolerance was examined in mulberry by a few workers (Gupta *et al.*, 1988; Susheelamma and Jolly, 1986; Cappellozza *et al.*, 1996 and Dorcus and Vivekanandan, 1997). However, these studies in mulberry involved very few genotypes and were limited to a few parameters. Thus, an extensive study with a large number of mulberry varieties (330) was undertaken to estimate the nature and magnitude of variability of 12 leaf morpho-anatomical parameters related to stress tolerance.

Materials and Methods

In the present study, a total of 330 mulberry accessions (exotic-108, indigenous-182 and polyploid-40) were studied. The diploid exotics (2n=28) represent collections from 21 sericultural countries. The diploid indigenous accessions were collected from 13 Indian states including 47 locals besides 84 selections, 34 open pollinated hybrids, 2 cross pollinated hybrids, 5 mutants and 10 wild collections. The polyploid accessions (2n=42, 56 and 84) were collected from different sources. The plantations are maintained as tree with 2.4 x 2.4 m spacing and crown height of 1.5 m at the CSGRC, Hosur, Tamil Nadu situated at latitude 12.45° N, longitude 77.51° E and altitude 942 m. Four plants are maintained per accession, out of which three plants were used for leaf sampling and data recording. Fully expanded leaves (5th to 7th position from top) in descending order were collected at 9-10 am from 3 month old shoots and small rectangular pieces were taken out from the central portion of the leaf blade avoiding veins and veinlets (Metcalfe and Chalk, 1979) and preserved in FAA solution (formalin 5 ml, glacial acetic acid 5 ml and 70 % ethanol 90 ml). The stomatal and idioblast studies were conducted by taking a thin layer of Wimbley's quickfix impressions on the abaxial (lower) and adaxial (upper) surfaces of the leaf respectively which were observed under Leica Leitz, DMRB Wetzlar microscope. Stomata and idioblasts were counted per unit area and the frequency per sq. mm was calculated. For observing the cuticular, epidermal, palisade, spongy mesophyll, leaf thickness and idioblast length, thin hand sections were made and observed under microscope after staining with 1 % safranine and mounted in 50 % glycerine. Chloroplast number per stomata was counted using epidermal peelings of the freshly collected leaf samples and stained with 2 % potassium iodide-iodine solution and observed under microscope. In each case nine microscopic fields were observed for data recording. The statistical analyses were carried out using software package developed by INDOSTAT services Ltd, Hyderabad, India.

Results and Discussion

Estimates of genetic parameters (Table 1) show the wide spectrum of variability in the mulberry germplasm under study. Exotic accessions exhibited higher mean and range for palisade, spongy, cuticular, epidermal and leaf thickness and lower values for stomatal size, idioblast length and frequency than indigenous accessions and offer scope as potential genetic material for stress tolerance breeding programmes. Polyploids recorded higher mean values over diploid indigenous and exotic accessions in all the traits except palisade thickness, stomatal and idioblast frequency. The estimates of genotypic and phenotypic coefficients of variation varied very little for all the traits indicating the importance of additive gene effects in the expression of the characters. The indigenous accessions exhibited higher GCV and PCV values in respect of idioblast length and frequency, palisade, spongy, upper cuticle, lower cuticle and leaf thickness when compared to exotics. Exotic accessions recorded higher values for stomatal size, stomatal frequency, upper epidermal thickness than indigenous accessions. Polyploid accessions recorded higher GCV and PCV values in respect of stomatal size, idioblast length, upper and lower epidermal thickness and leaf thickness. The analysis of genetic parameters further showed that high GCV and PCV values coupled with high magnitude of heritability and genetic advance in respect of idioblast length and frequency followed by upper and lower cuticular thickness which indicates the scope for improvement through selection. The stomatal size and chloroplast number/stomata had less genotypic and phenotypic coefficient of variation with low heritability and genetic advance indicating low priority in selection programme.

Table 1. Estimates of variability and genetic parameters for leaf morpho-anatomical parameters in mulberry

Parameters	Acc.	Mean±SE	Range		GCV	PCV	h^2	GA
			Min.	Max.			(%)b.s	% of mean
Stomatal size	Ind	261.59 ± 4.52	142.85	468.40	21.48	26.66	64.92	35.65
(sq. μm)	Exo	250.55 ± 6.49	122.12	458.92	25.07	30.31	68.41	42.71
	Poly	316.07 ±14.63	173.43	542.79	27.39	32.72	70.08	47.24
Stomatal	Ind	673.35 ±12.40	338.70	1240.96	24.47	25.63	91.14	48.11
frequency/sq.mm	Exo	632.82 ±17.41	344.87	1333.39	28.40	28.95	96.23	57.39
	Poly	574.09 ±19.81	329.30	997.89	21.29	22.86	86.69	40.83
Idioblast length	Ind	10.73 ± 0.62	1.91	64.37	77.28	78.52	96.85	156.66
(μm)	Exo	10.67 ± 0.64	2.02	43.20	62.28	63.66	95.71	125.52
	Poly	14.97 ± 3.08	3.07	90.80	129.74	130.40	98.99	265.90
Idioblast	Ind	20.97± 0.68	6.66	81.28	43.19	43.95	96.57	87.43
frequency/sq.mm	Exo	17.60 ± 0.58	7.92	38.75	34.11	34.97	95.14	68.53
	Poly	17.45 ± 0.80	9.75	38.46	28.60	29.35	94.97	57.41
Palisade	Ind	52.29 ± 1.02	18.22	146.14	26.63	26.52	97.92	53.50
thickness (μm)	Exo	59.51 ± 1.34	33.33	107.66	24.13	24.32	98.47	49.34
	Poly	58.13 ± 2.14	39.46	102.68	23.32	23.52	98.27	47.62
Spongy	Ind	61.07 ± 1.07	27.00	104.46	23.63	23.89	97.77	48.12
thickness (μm)	Exo	62.14 ± 1.11	37.93	106.13	18.49	18.81	96.59	37.43
	Ploy	64.10 ± 2.13	36.79	103.45	20.96	21.13	98.33	42.81
Upper cuticle	Ind	5.03 ± 0.14	2.02	10.15	37.09	38.04	95.10	74.52
thickness (μm)	Exo	6.56 ± 0.21	2.02	11.81	33.38	34.27	94.88	66.97
	Poly	6.91 ± 0.31	3.55	10.73	28.14	29.37	93.94	56.19
Lower cuticle	Ind	2.51 ± 0.10	0.81	7.28	54.17	55.20	96.29	109.50
thickness (μm)	Exo	3.60 ± 0.14	1.01	7.28	40.56	42.81	89.78	79.18
	Poly	4.02 ± 0.24	1.68	10.15	37.92	39.36	92.79	75.24
Upper epidermal	Ind	22.36 ± 0.43	6.90	45.98	25.63	27.26	88.36	49.62
thickness (μm)	Exo	24.32± 0.64	10.23	43.20	27.07	27.88	94.24	54.13
	Poly	29.58 ± 1.41	11.11	49.81	30.06	30.63	96.26	60.75
Lower epidermal	Ind	8.14 ± 0.16	26.02	19.54	25.43	26.69	90.73	49.89
thickness (μm)	Exo	9.10± 0.23	3.45	18.77	25.42	26.46	92.30	50.31
	Poly	10.13 ± 0.67	5.17	24.71	41.49	42.07	97.27	84.30
Leaf	Ind	151.33 ± 1.71	84.03	239.96	15.15	15.36	97.31	30.79
thickness (μm)	Exo	165.23 ± 2.26	122.85	263.88	14.16	14.31	97.92	28.86
	Poly	172.86± 4.42	117.15	283.52	16.11	16.23	98.53	32.95
Chloroplast number/	Ind	10.18± 0.07	7.22	13.56	8.07	12.87	39.35	10.43
stomata	Exo	10.72 ± 0.13	8.89	13.89	10.71	14.60	53.79	16.18
	Poly	15.15 ± 0.28	14.00	22.00	10.32	13.85	55.56	15.85

Ind- Indigenous, Exo-Exotic, Poly-Polyploid

Correlation studies on leaf anatomical parameters in mulberry are very limited. Hence, in the present study character association was attempted. Genotypic and phenotypic coefficient of correlations (Table 2) was in the same direction and the genotypic correlations were higher than the phenotypic correlations both in indigenous and exotic accessions indicating the inherent association between the characters. Stomatal size and frequency are negatively correlated as reported in barley (Miskin and Rasmussen, 1970) and in mulberry (Yang and Yang, 1995). Stomatal size and idioblast length showed significant positive correlations with palisade, spongy, lower cuticular, epidermal and leaf thickness whereas stomatal and idioblast frequency showed non-significant and negative correlations with these characters. This indicated the role of stomatal size for water retention in the leaves. Similar results in mulberry were also obtained Susheelamma and Jolly (1986). Positive correlations were also found between palisade and spongy, leaf thickness and chloroplast number/stomata in both indigenous and exotic accessions.

The mulberry accessions are grouped into low, medium and high frequency groups based on observed range of variability for various leaf anatomical parameters (Table 3). The accessions from lower frequency group for stomatal size, stomatal frequency, and idioblast length and idioblast frequency are desirable for stress condition. Various stomatal characters like smaller size with lesser frequency which is responsible for low conductance have been suggested as desirable traits to improve drought resistance as they reduce water loss and lower the probability of dehydration (Dorcus and Vivekanandan, 1997). The mulberry genotypes which have leaves with small stomata and extensive deep root system reduce water loss and show better tolerate in stress condition (Susheelamma *et al.*, 1986).

Table 2. Genotypic (G) and phenotypic (P) coefficient of correlation in indigenous and exotic accessions

Parameters		1	2	3	4	5	6	7	8	9	10	11	12
1. Stomatal size	G		0.192**	0.204**	-0.121	0.222**	0.231**	-0.028	0.146*	0.286**	0.180*	0.373**	0.285**
(sq.μm)	P		-0.121	0.164*	-0.096	0.179*	0.189**	-0.019	0.017	0.214**	0.138*	0.299**	0.173**
2. Stomotal	G	-0.375**		0.142*	0.241**	0.071	-0.079	0.116	0.166*	-0.019	-0.097	-0.009	0.111
frequency/sq.mm	P	-0.307**		0.136	0.225**	0.067	-0.074	0.108	0.155*	-0.020	-0.086	-0.008	-0.069
3. Idioblast length	G	0.165	-0.061		0.035	0.179*	0.213**	-0.014	0.052	0.152*	0.287**	0.286**	0.102
(μm)	P	0.148	-0.061		0.033	0.175*	0.208**	-0.013	0.051	0.145*	0.267**	0.279**	0.068
4. Idioblast frequency/	G	0.356**	0.531**	-0.038		0.093	-0.217**	0.011	0.006	0.054	-0.091	-0.075	-0.060
sq.mm	P	0.289**	0.514**	-0.034		0.089	-0.210**	0.011	0.005	0.051	-0.083	-0.072	-0.030
5. Palisade thickness	G	0.464**	0.120	0.022	0.275**		0.109	0.041	0.034	-0.007	-0.017	0.661**	0.141*
(μm)	P	0.380**	0.116	0.020	0.267**		0.106	0.037	0.034	-0.005	-0.014	0.657**	0.098
6. Spong thickness	G	0.229*	-0.061	0.064	-0.144	0.181		0.045	0.037	0.087	0.233**	0.736**	0.228**
(μm)	P	0.187	-0.064	0.065	-0.138	0.175		0.045	0.035	0.080	0.219**	0.732**	0.154*
7. Upp. cuticle thickness	G	-0.191	-0.151	-0.043	0.314**	-0.018	0.138		0.604**	0.155*	0.087	0.207**	0.287**
(μm)	P	-0.143	-0.143	-0.048	-0.294**	-0.018	0.128		0.578**	0.147*	0.080	0.204**	0.188**
8. Lower cuticle thickness	G	0.063	0.068	0.188	-0.062	0.064	0.070	0.454**		0.231**	0.131	0.214**	0.268**
(μm)	P	0.074	0.064	0.176	-0.064	0.058	0.069	0.412**		0.213**	0.123	0.210**	0.165*
9. Upper epidermal	G	0.238*	0.007	0.165*	0.034	0.288**	0.093	0.020	0.291**		0.283**	0.355**	0.259**
thickness (μm)	P	0.178*	0.006	0.153	0.027	0.279**	0.093	0.019	0.266**		0.251**	0.359**	0.168*
10. Lower epidermal	G	0.109	-0.086	0.161	-0.135	0.007	-0.039	0.161	0.188	0.144		0.310**	0.097
thickness (μm)	P	0.064	-0.077	0.155	-0.132	0.007	-0.40	0.149	0.107	0.136		0.300**	0.053
11. Leaf thickness	G	0.461**	0.027	0.115	0.061	0.787**	0.642**	0.200*	0.272**	0.538**	0.147		0.344**
(μm)	P	0.374**	0.024	0.111	0.057	0.782**	0.641**	0.195*	0.260**	0.537**	0.147		0.230**
12. Chloroplast number/	G	0.307**	-0.010	-0.105	-0.058	0.144	-0.057	0.112	0.076	0.008	0.084	0.086	
stomata	P	0.160	-0.023	-0.075	-0.037	0.103	-0.036	0.081	0.036	0.015	0.068	0.067	

Above diagonal - Indigenous (diploid) and below diagonal - Exotic (diploid) **, * Significant at 1% and 5 % respectively.

Table 3. Frequency distribution of mulberry accessions in respect of leaf morpho anatomical-parameters

Parameters	Acc.	Frequency distribution					
		Low		Medium		High	
		Range	No. of acc.	Range	No. of acc.	Range	No. of acc.
Stomatal	Ind	< 200	17	200- 400	159	>400	6
size (sq.μm)	Exo		18		85		5
	Poly		4		26		10
Stomatal	Ind	<400	4	400- 800	144	>800	34
frequency/sq.mm	Exo		6		83		19
	Poly		2		36		2
Idioblast	Ind	< 5	28	5-15	120	>15	34
length (μm)	Exo		8		84		16
	Poly		7		23		10
Idioblast	Ind	< 15	42	15 - 30	123	>30	17
frequency/sq.mm	Exo		47		56		5
	Poly		15		24		1
Palisade	Ind	< 50	83	50 - 75	90	>75	9
thickness (μm)	Exo		24		71		13
	Poly		12		25		3
Spongy	Ind	< 50	44	50-75	104	>75	34
thickness (μm)	Exo		11		86		11
	Poly		3		28		9
Upper cuticle (μm)	Ind	< 4	52	4-8	119	> 8	11
thickness	Exo		13		66		29
	Poly		3		28		9
Lower cuticle	Ind	< 2	76	2-4	84	> 4	22
thickness (μm)	Exo		16		48		44
	Poly		1		25		14
Upper epidermal	Ind	< 20	64	20 - 40	115	>40	3
thickness (μm)	Exo		29		77		2
	Poly		5		31		4
Lower epidermal	Ind	< 5	7	5-10	144	>10	31
thickness (μm)	Exo		4		67		37
	Poly		0		24		16
Leaf	Ind	< 150	92	150-175	64	>175	26
thickness (μm)	Exo		31		47		30
	Poly		6		17		17
Chloroplast number/	Ind	< 14	182	14-16	0	>16	0
stomata	Exo		108		0		0
	Poly		0		34		6

Ind- Indigenous, Exo-Exotic indicates diploid accessions separately and Poly-Polyploid accessions both for indigenous and exotics

Idioblasts with long projecting spines in the leaves, which contain high quantity of tannins, affects the nutritional quality, palatability and digestibility of leaves by the silkworm (Cappellozza *et al.*, 1996). In the lower frequency group 28 indigenous, 8 exotic and 7 polyploid accessions (Table 3) have smaller idioblast length and 42 indigenous, 47 exotic and 15 polyploid accessions have fewer idioblasts per unit area.

The mesophyll tissue consisting of palisade and spongy parenchyma is the main photosynthetic zone. Thick, smooth, succulent and highly cutinized (glaucous) leaves, which can conserve water most efficiently, are desirable for dry sericultural zones. These two characters contribute most to leaf thickness and are highly heritable with moderate genetic advance. Hence, emphasis should be given for these traits during selection. The leaves of exotic accessions are comparatively thick and succulent which can be used in crossing with promising indigenous varieties.

Further, chloroplast number per stomatal guard cells among 330 accessions ranged between 8-14 for diploids (2n=28), 14-16 triploids (2n=42) and >16 for tetraploids (2n=56) indicating positive association of chloroplast number with ploidy status which was also reported by Yang and Yang (1995) and Tikader *et al.* (1999) in mulberry. Polyploids are characterised by increased vigour and hardiness and particularly triploids exhibit more drought tolerant characters (Singh and Handique, 1995).

A perusal of data on ten promising varieties (Table 4) revealed that the accessions MI-119, 77, 54, 141 among indigenous and ME- 51, 2, 2, 65 among exotics had lowest stomatal size, stomatal frequency, idioblast length and frequency, respectively. Similarly,

Table 4. Ten promising accessions for leaf morpho anatomical parameters

Parameters	Acc.	Range	Accessions
Stomatal size	Ind	142.85-180.50	MI-119,137,3,123,33,26,19,90,70,48
(sq.μm)	Exo	122.12-174.47	ME-51,20,116,115,49,98,113,114,108,99
	Poly	173.43-245.82	MI-205,184,201,200,ME-84,59,72,92,97,38
Stomatal frequency/sq.mm	Ind	338.70-455.72	MI-77,87,8,161,142,80,116,9,28,78
	Exo	344.87-422.90	ME-2,62,90,91,49,54,89,53,82,51
	Poly	329.30-514.18	MI-212,203,196,204,192,202,200,ME-81,126,72
Idioblast length	Ind	1.91-3.64	MI-54,98,123,58,85,102,177,57,92,94
(μm)	Exo	2.02-5.23	ME-2,65,116,57,62,128,22,47,87,25
	Poly	3.07-6.51	MI-195,199,183,181,173,205,189,187,192,ME-84
Idioblast frequency/sq.mm	Ind	6.66-11.37	MI-141,118,35,30,115,52,139,124,27,86
	Exo	7.92-12.07	ME-65,87,60,93,105,42,49,102,20,82
	Poly	9.75-13.83	MI-184,204,173 ME-84,92,59,38,126,56,97,
Palisade thickness	Ind	74.93-146.14	MI-67,76,12,53,99,31,168,30,153,10
(μm)	Exo	80.08-107.66	ME-110,65,76,9,32,136,43,60,80,90
	Poly	66.83-102.68	MI-191,185,164,212,ME-52,97,59,72,126,81
Spongy thickness	Ind	82.35-104.46	MI-109,78,141, 135, 22,52,85,66,60,116
(μm)	Exo	75.48-106.13	ME-48,64,9,32,110,36,39,66,94,80
	Poly	72.41-103.45	MI-205,200,172,185,180,191,164, ME-72,92,81
Upper cuticle thickness	Ind	8.05-10.15	MI-147,161,68,76,99,160,102,43,207,177
(μm)	Exo	9.86-11.81	ME-96,83,5,17,42,13,131,80,136,36
	Poly	7.86-10.73	MI-186,180,182,212,195,200,202,172,ME-97,72
Lower cuticle thickness	Ind	5.36-7.28	MI-150,175,117,127,210,171,121,166,207,168
(μm)	Exo	6.32-7.28	ME-95,107,64,130,96,42,88,4,23,77
	Poly	4.31-10.15	MI-178,188,182,191,172,203,ME-84,81,38,126
Upper epidermal thickness	Ind	32.57-45.98	MI-144,72,53,156,73,166,168,13,207,162
(μm)	Exo	34.10-43.70	ME-128,117,122,23,85,116,43,3,9,76
	Poly	36.01-49.81	MI-195,234,190,180,198,212,196,201,199,ME-81
Lower epidermal thickness	Ind	11.71-19.54	MI-52,66,77,83,86,207,159,124,81,162
(μm)	Exo	12.15-18.77	ME-11,35,43,60,53,28,20,48,105,131
	Poly	11.11-24.71	MI-212,195,184,234,182,191,204,ME-63,81
Leaf thickness	Ind	186.20-239.96	MI-22,135,166,99,162,116,76,168,207,67
(μm)	Exo	197.51-263.87	ME-77,66,110,85,32,76,9,43,90,80
	Poly	187.36-283.52	MI-172,185,199,180,164,212,191,ME-72,81
Chloroplast number/	Ind	12.00-13.56	MI-50,155,168,69,162,171,179,211,197,207
stomata	Exo	12..00-13.89	ME-14,64,91,102,77,108,78,85,67,68
	Poly	15.56-22.00	MI-181,201,212,195,203,164,185,234,ME-81,126

Ind- Indigenous, Exo- Exotic, Poly-Polyploid

the indigenous accessions MI-67, 116, 177, 168, 162, 162 and 67 and exotic accessions ME-90, 80, 36, 77, 76, 81, 131 and 80 which had highest palisade, spongy, upper and lower cuticular thickness, upper and lower epidermis and leaf thickness, respectively, are promising for further exploitation. However, the accessions like MI-212, 195, 197, 210, 116, 172, 234, 191, 162 and ME- 81, 80, 43, 9, 65, 90, 116, 49, 62, 63 and 84 which exhibited three or more drought tolerant traits may be useful for evolving drought tolerant genotypes through appropriate breeding programme. The promising triploids like MI-172, 173, 187, 188 and ME-52, 84, which had chloroplast number 14 to 16 are high yielders and possess all the desirable characters may also be used for direct exploitation. Thus, the results indicated that no single variety possesses all the desirable characters for drought tolerance hence, repeated intermating of the promising accessions followed by selection of the recombinants for pyramiding the drought tolerant traits are suggested.

Mulberry genotypes are heterozygous due to out crossing and hence selections can be practised for desirable variants among the progeny. The extent of variability in leaf anatomical parameters in the mulberry germplasm resources revealed in the present study gives better scope for breeders for selection. Stress tolerance in cross-pollinated crops is generally polygenic (Hurd, 1976). The promising genotypes identified through screening can be utilised to develop varieties through suitable breeding programmes.

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A Viable Approach for a Rapid *In Vitro* Multiplication of the Medicinal Plant *Aloe vera*

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Rapid shoot bud regeneration, directly from the rhizome portion of the medicinally important plant, *Aloe vera,* was obtained without formation of callus in MS medium supplemented with BAP at a high concentration (3.0-5.0 mg/l). At the initiation stage, a low concentration of NAA (0.1 mg/l) was also applied with BAP. In the subsequent subcultures, NAA was not required. Direct rooting of the shoot buds was achieved either by the application of charcoal (0.2%) or on transfer of the regenerants to sand: soil mixture (2:1) at high humidity. Since cytological study of the root tip of the regenerants upto 10th passage (one passage = 45 days) did not show any irregularity, it is assumed that this protocol would produce stable clones for *en masse* propagation of this important medicinal plant.

Key Words: *Aloe vera*, In vitro multiplication, Micropropagation

The *Aloe* plant (*A. vera* Tourn. ex Linn. Syn. *A. barbadensis* Mill) is an important medicinal plant (Anonymous, 1948; Kirtikar and Basu, 1973). The plant is often called a "Doctor in a pot" in USA and Mexico. It is xerophytic in nature with thick, fleshy, strongly cutinised, spiny margined leaves that are arranged in a rosette on a very short stem and its rhizome bears adventitious buds that sprout during rainy season. Use of the *Aloe* leaves in herbal cosmetics and medicines needs widespread cultivation of this plant.

Main practice of its propagation is by suckers. Owing to the widespread male-sterility (Keizer and Cresti, 1987), irregular pollen meiosis, high pollen sterility and failure in fruit set (Sapre, 1975), seed formation is very poor in this plant. Its vegetative propagation is slow and limited for a brief period of time in each season. Micropropagation could be an important tool for its mass scale propagation. Prior to this work, regeneration from callus tissue was reported (Roy and Sarkar, 1991). Present report is perhaps the first one for a direct *in vitro* regeneration of *Aloe* plant from rhizome explants and its successful transplantation and growth in the field.

Materials and Methods

Rhizomes of the *Aloe vera* were harvested from randomly selected plant materials grown in the experimental garden of the Department of Botany, University of Calcutta. The young rhizomes with vegetative buds (4-10 mm thick cubes) were washed thoroughly in running tap water and a 5% liquid detergent (Teepol, Reckitt & Colman, India Ltd.). These were then surface disinfested with 0.1% (w/v) mercuric chloride for five min, subsequently washed thoroughly thrice with sterile distilled water and placed in culture tubes (25mm x 150mm) with cotton plug containing 20ml freshly prepared media. Media consisted of salts medium Murashige and Skoog (1962), supplemented with 3% (w/v) sucrose, different concentrations of BAP (0.5, 1.0, 2.0, 3.0, 4.0, 5.0 mg/l) alone and in combination with NAA (0.1 and 0.2mg/l). The pH of the media was adjusted to 5.7 and solidified with 0.7% (w/v) agar (Hi-Media, India). The media after dispensing in culture tubes were sterilized at 1.05 Kg/cm^2 for 15 mins at 121°C.

Cultures were incubated at 25° ± 2°C with an illumination of 30 μmoles sec^{-1}m^{-2} from Phillips white fluorescent tubes for 16 hrs/day and at a relative humidity of 60%. Plants were subcultured at an intervel of 45 days. All the sets were repeated thrice and each set was replicated 10 times. For rooting, the regenerated shoots were transferred to MS, MS with activated charcoal (0.2%), and directly to the sand: soil (2:1) mixture at 75-80% humidity. Cytological analysis of the root tips of the regenerated plants was carried out following acetoorcein squash technique (Sharma and Sharma, 1980). Data on shoot proliferation, root initiation, survival rate in the field and chromosome study (up to 10th passage) were recorded. Each experiment was repeated twice; data are scored from ten replicates and the average values were reported.

Results and Discussion

Regeneration of Shoot Buds in the Medium

Shoot regeneration was obtained (Fig. 1) directly from the young rhizome bud explants in MS medium

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supplemented with low concentration (0.1 and 0.2 mg/l) of NAA and high concentration (1.0-5.0 mg/l) of BAP (Table-1). In the following subcultures, NAA was not required and BAP only was used (Table 2) for multiplication of shoot buds (Fig. 2). In higher concentrations of BAP (5.0 mg/1) shoot buds regenerated from the explants in high number but were difficult to separate. Superiority of BAP for shoot-induction was reported by many authors (Balachandran *et al.* 1999; Agretion *et al.* 1996). It is assumed that BAP is converted to other phytohormones in the tissues under cultural conditions (Sharma and Wakhlu, 2003; Zaerr and Mapes, 1982). However, effective concentration of BAP differs in different materials. For example, high BAP concentration reduced shoot bud number in *Acorus* (Harikrishnan *et al.*, 1999; Sabita Ram *et al.*, 2000) while a high BAP concentration was necessary in *Musa* (Krikorian

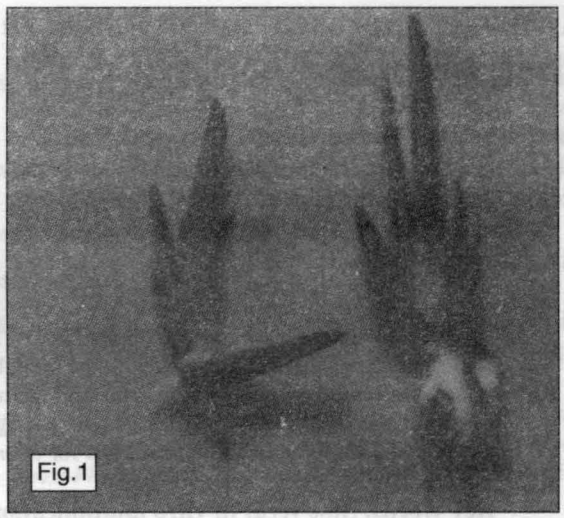

Fig. 1. Regeneration of shoot buds in MS+BAP (3.0 mg/1)+NAA (0.1mg/l)

Table 1. Direct regeneration of shoot buds in MS medium with BAP and NAA

BAP mg/1	NAA mg/1	Observation after 30 days of inoculation
1.0	-	Very few shoot buds (1-2/explant) in 20% cultures.
"	0.1	Very few shoot buds (1-2/explant) with callus formation at the cut ends
"	0.2	More callus formation, shoot buds very small and few
2.0	-	3-4 shoot buds/explants in 60% cultures
"	0.1	3-4 shoot buds/explants in 60% cultures & also callus formation
"	0.2	3-4 shoot buds/explants in 60% cultures, and rooting from the callus
3.0	-	7-8 shoot buds/explant in 90% cultures
"	0.1	6-7 shoot buds/explant and callus at the cut ends
"	0.2	Rooting from the explant, callus formation and 5-7 shoot buds/explant
4.0	-	Very small shoot buds, 8-9/explant in 90% cultures
"	0.1	6-7 shoot buds along with callus formation, leaves deformed
"	0.2	Deformed shoot buds and rooting from the explant in all the cultures
5.0	-	Very small 10-12 shoot buds, difficult to separate, along with callus
"	0.1	Deformed 8-10 shoot buds developed from the callus
"	0.2	Callus formation more pronounced and deformed & albino shoot buds

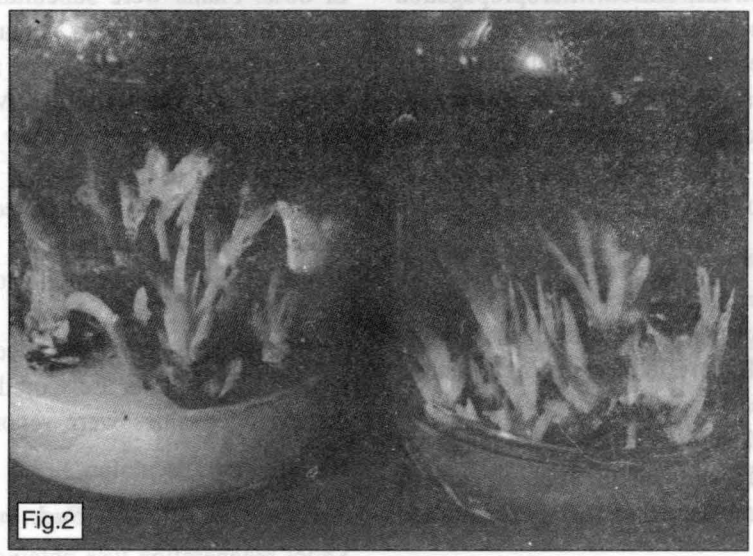

Fig. 2. Multiplication of shoot buds in MS containing BAP 3.0 mg/l at 3rd passage (one passage = 45 days)

and Cronauer, 1983) as well as in the present material. Occasionally, deformed leaves and albino shoots (2-3/ culture) at later stages were observed in MS medium containing high concentration (5.0 mg/1) of BAP. The deformed shoots when shifted to lower concentration of BAP (1.0 mg/1), immediately after detection, reverted to normal ones. However, if maintained there for more than seven days, they appeared to be permanently deformed. So for further studies, immediately after detection, these deformed shoots were discarded.

Rhizogenesis and Acclimatization

The regenerated shoot buds (2-3cm) were transferred to the basal MS medium, MS medium containing 0.2% activated charcoal or directly to sand: soil mixture (2:1) with high humidity (75-80%) at green house for induction of roots (Fig. 3). If the shoots after induction of roots were kept in the same medium (MS or MS + charcoal) for more than 7 days then the basal portion of the roots developed pigmentation (Fig. 3, arrow marked) due to accumulation of phenolics, which did not interfere in the survival of the regenerated plants in the field. Rooting and field survival was the best (100%), when the regenerated shoots were placed directly in the sand: soil mix (Table-3). The rooted plants are growing profusely in the field (Fig. 4). The plants rooted directly in the sand: soil showed better survival in the field, could skip one step in the process of acclimatization and so the process is cost effective. Therefore to make the process cost effective, direct rooting in the sand: soil mixtures were used regularly for mass scale rooting and transplantation to the field. Such *ex vitro* rooting has also been reported in *Agave* (Das, 1992).

Table 2. Effect of different concentrations of BAP on shoot bud multiplication

BAP Concentration (mg/1)	Percent of culture showing multiplication of shoot buds	Mean no. of shoots/culture ± SD (at 3rd passage)	Observation at 3rd passage
0.5	10	1.0+0.58	Poor growth of regenerated shoot buds, necrosis of lower leaves and no further outgrowth formation in the following passages.
1.0	30	3.0+0.33	Pale green leaves, poor growth, non increase in regeneration rate in the following passages.
2.0	60	7.0+0.58	Good growth of shoot buds and further regeneration of 7-10 buds/bud occurred in the later passages if separated form the clump at the end of the passage.
3.0	90	10.0+0.88	Healthy shoot buds develop forming a clump. Separation of each bud induces further regeneration of 8-10 shoot buds and rooting in the later passage.
4.0	90	20.0+0.88	Very small shoot buds, forming clump, difficult to separate, poor growth; shoot buds on transfer to low BAP (1.0mg/1) induced growth, without further regeneration of shoot buds.
5.0	90	25 + 1.20	Very small shoot buds, very poor growth, leaves deformed, callus formation at the base, no root formation on further subculture.

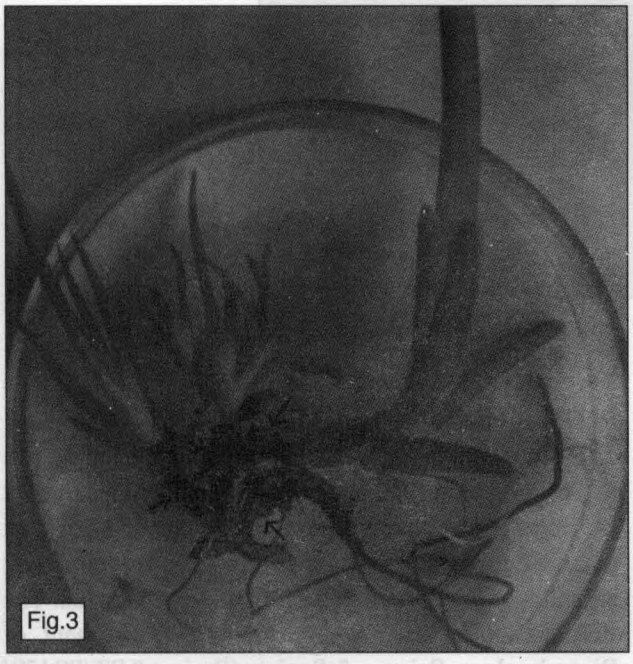

Fig. 3. Rooting in the MS + charcoal (0.1%)

Table 3. Rooting of the regenerated shoots, field trails and chromo some study

Treatment	Observation on rooting (%)	Field survival (%)	Chromosome study
MS	80%	70%	2n = 14
MS + activated Charcoal (0.2%)	100%	80%	2n =14
Sand: soil (2:1)	100%	100%	2n = 14

Fig. 4. Regenerated shoots after transplantation under field condition (plants are one year three months old)

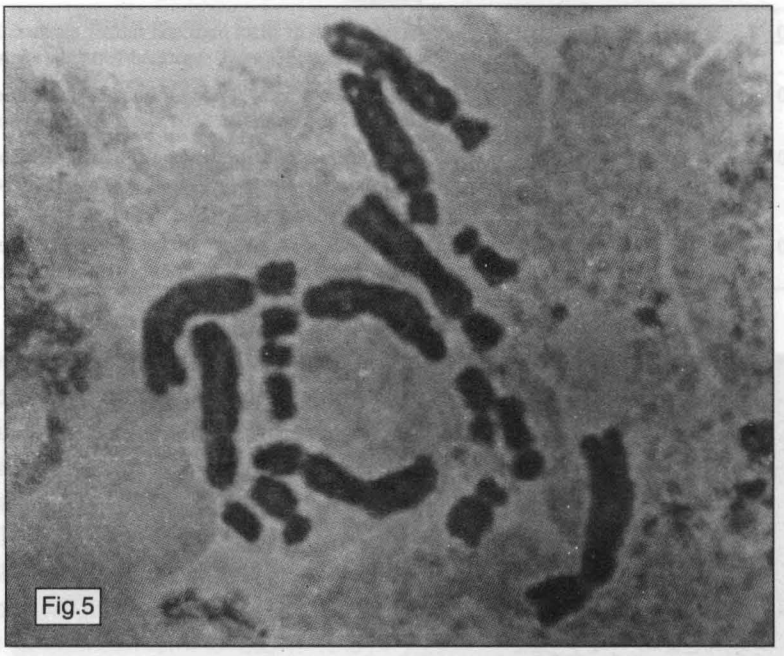

Fig. 5. Aceto-orcein squash of the root tip of the regenerated shoot showing normal chromosome complement (2n = 14)

Data of cytological analysis of the root tips (Fig. 5) of the regenerated shoots upto 10th passage under cultural conditions showed normal chromosome complement (2n=14), with no irregularity in number as well as apparent variation in chromosome morphology. Similar stable regenerants have also been reported earlier in *Asparagus* (Ghosh and Sen, 1992). Thus regenerated plants growing in the field were stable and free from any noticeable phenotypic variability.

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Genetic Divergence in Chickpea (*Cicer arietinum* L.)

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Genetic divergence as measured by D^2 technique was studied for seed yield and its components in 56 genotypes of chickpea. The genotypes were grouped into six clusters and the maximum intra-cluster distance was observed in cluster II comprising five genotypes. Clusters IV and V followed by I and IV, III and IV were identified as genetically divergent. Considering cluster mean and genetic distances hybridization involving genotypes BGD 116, BGD 115, KGDM 1181, BCP 17, BGM 524, BG 256, KGDB 1178 of cluster VI for seed yield plant^{-1}, hundred seed weight and plant height; H 95-25, H 95-37 and H95-30 of cluster IV for pods plant^{-1}; ICCV 97030, GCP 9610, ICCV 97039 of cluster II for early maturity; ICCV 97032, JSC 3 and ICCV 97034 of cluster I for primary branches plant^{-1} and early flowering; RSG 966, IPC 97-1, IPC 96-46, ICCV 97022 of cluster V for seed yield plant^{-1}, pods plant^{-1} and bold seed are expected to produce wider genetic variability and promising segregants for seed yield and other desirable traits.

Key words : Chickpea, *Cicer arietinum* L., Correlation, Genetic Divergence

Grain yield is a complex character and is attributed to several physiological and metric traits. Determination of the nature and magnitude of genetic diversity and variability for the character under improvement is a pre-requisite before launching any breeding programme. The present study on 46 chickpea accessions was aimed at (i) estimating the magnitude of genetic variability among selected genotypes for seed yield, (ii) determining the grouping pattern of genotypes in different clusters, (iiii) identify genetically diverse and agronomically desirable parents to be used in breeding programme for high seed yield.

Materials and Methods

Fifty-six genotypes of diverse origin were grown in randomized complete block design with three replications at Research Farm, Indira Gandhi Krishi Vishwavidyalaya, Raipur (IGAU), during *rabi* 2000-01 (Table 1). C 235 (small seeded), Vijay and JG 74 (medium seeded), BG 391 and BG 256 (bold seeded) recommended for Chhattisgarh state were included as standard varieties. Each plot consisted of 4 rows of 4 m length with 30 and 10 cm spacing between and within row, respectively. Recommended package of practices was adopted to raise a good crop. Basal dose of 20 kg N and 50 kg P_2O_5 was applied at the time of sowing. Two sprays of Monocrotophos 36 EC @ 750 ml/ha were applied to protect the crop from *Helicoverpa armigera*. Five competitive plants from each genotype were randomly selected for recording plant height (cm), primary branches/plant, pods/plant, seeds/pod, 100-seed weight (g) and seed yield/plant (g). Phenological observations were recorded on plot basis. The data were subjected to the Mahalanobis (1936) D^2 statistics to measure the genetic

Table 1. List of 56 genotypes of chickpea selected for analysis of genetic divergence of seed yield

Designation	No. of genotypes	Source
H 95-122, H 95-25, H 95-37, H 95-30	4	Haryana
PBG-78, C-235 (C), FG 559, FG 712, GL 96047, GL 96004,	6	Punjab
CSJD 901, GCP 9504, CSJD 869, RSG 964, GCP 9516,	9	Rajasthan
GNG 1275, RSG 966, GNG 469, GCP 9610		
Phule G 95007, Vijay (C), Phule G 93009, BCP 17	4	Maharashtra
ICCV 97017, ICCV 97001, ICCV 97031, ICCV 93118, ICCV 97033, ICCV 97038, ICCV 97016, ICCV 97024, ICCV 97039, ICCV 97030,	14	Andhra Pradesh
ICCV 97034, ICCV 97032, ICCV 95138, ICCV 97022	4	Madhya Pradesh
IG 338, JG 74(C), RG 938, JSC 3 (C),		
PG 97-6, IPC 96-27, IPC 97-1, I PC 96-46, KGDB 1178, KGDM 1181	6	Uttar Pradesh
BGD 112, BGD 109, BGD 72(C), BGD 115, BGD 116	5	Karnataka
BG 391(C), BGM 528, BGM 524, BG 256 (C)	4	New Delhi

divergence. The varieties were grouped into clusters by Tocher's method (Rao, 1952).

Results and Discussion

Analysis of variance revealed highly significant differences among the genotypes for all the characters under study (Table 2). High genotypic coefficient of variation (GCV) was found for seed yield/plant, pods/plant and 100-seed weight (Table 3). However, moderate values of GCV were recorded for seeds/pod, primary branches/plant, plant height and days to first flower. It indicated the scope for improvement of these traits in the material under the present study. Similar findings have also been reported in chickpea by earlier workers (Singh *et al.*, 1986; Bejiga *et al.*, 1991; Tripathi and Arora, 1991; Rao *et al.*, 1994). Genotypes exhibited a wide range of variation for most of the traits except seeds/pod and primary branches/plant (Table 3).

The 56 genotypes were grouped into six clusters, suggesting adequate scope for selecting superior and diverse parents to be exploited in a breeding programme (Table 4). Maximum number of genotypes (15) were accommodated in cluster III followed by 14 in cluster VI, 13 in cluster V, 6 in cluster I, 5 in cluster II and 3 genotypes in cluster IV. The maximum intra-cluster distance (D=1.988) was observed in cluster II followed by cluster I (D=1.880) and V (D=1.865), indicating existence of considerable genetic divergence among constituent genotypes (Table 4). Hence, parents within the cluster can be chosen for hybridization programme.

The relative distance (Table 5) of each cluster from other clusters (inter-cluster distances) indicated greater divergence between cluster IV and V (D=4.635) followed by I and IV (D=4.459), III and IV (D=4.344). Selection of genetically diverged parents from above clusters would produce a broad spectrum of variability, which may enable further selection for high seed yield and other desirable traits.

The cluster means of genotypes (Table 6) revealed that the average cluster mean was higher for seed yield in cluster VI followed by cluster IV; for size in cluster VI followed by cluster II, I and V; for pods plant^{-1} in cluster IV followed by VI and II; for primary branches plant^{-1} in cluster I followed by IV and VI; for early maturity in cluster II followed by III, IV and VI.

The genotype with high mean value in any cluster can either directly be used for adoption as pure line variety or can be used in hybridization for yield improvement. The genotypes ICCV 97032, JSC 3, ICCV 97034 of cluster I for primary branches/plant and early flowering; ICCV 97030, GCP 9610, ICCV 97039 of cluster II for early maturity; H 95-25, H 95-37, H 95-30 of cluster IV for pods/plant; BGD 116, BGD 115, KGDM 1181, BCP 17, BGM 524, BG 256, KGDB 1178 of cluster VI for seed yield/plant, 100-seed weight

Table 2. Analysis of variance for different characters

Source	d.f.	Mean Squares							
		Days to first flower	Days to maturity	Plant height	Primary branches/plant	Pods/plant	Seeds/ pod	100-seed weight	Seed yield/ plant
Replication	2	6.438	6.063	0.938	0.003	0.046	0.040	0.781	0.140
Treatment	55	85.861**	51.786**	70.478**	0.257**	420.043**	0.096**	73.119**	31.906**
Error	110	0.301	0.326	0.001	0.006	0.00009	0.0002	0.596	0.001

** = Significant at p<0.01

Table 3. Estimates of mean, range, genotypic coefficient of variation and genetic correlation for different characters

Characters	Mean	Range		GCV	r_g with seed yield
		Min.	Max.		
Days to first flower	58.88	44.00	70.00	9.07	0.556**
Days to maturity	104.21	96.00	118.00	3.97	-0.153
Plant height (cm)	49.67	39.40	59.40	9.76	0.210
Primary branches/plant	2.70	2.00	3.53	10.72	0.418**
Pods/plant	41.64	18.00	83.67	28.41	0.750**
Seeds/pod	1.39	1.77	1.03	12.82	-0.332**
100-seed weight (g)	20.36	13.24	31.50	24.15	0.577**
Seed yield/plant (g)	9.72	4.96	18.60	33.55	-

Table 4. Clustering pattern based on D^2 statistics in chickpea

Cluster	Number of genotypes	Name of genotypes
I	6	Vijay, ICCV 97038, ICCV 97016, ICCV 97034, JSC 3, ICCV 97032
II	5	JG 74, ICCV 97039, ICCV 97030, RG 938, GCP 9610
III	15	H 95-122, PBG 78, CSJD 901, GCP 9504, C 235, CSJD 869, FG 559, ICCV 97017, FG 712, IG 338, ICCV 97001, ICCV 97031, PG 97-6, RSG 964, GCP 9516
IV	3	H 95-25, H 95-37, H 95-30
V	13	Phule G 95007, ICCV 93118, BGD 112, ICCV 97033, BGD 109, GL 96047, Phule G 93009, ICCV 97024, RSG 966, IPC 97-1, ICCV 95138, IPC 96-46, ICCV 97022
VI	14	GL 96004, BG 391, GNG 1275, IPC 96-27, BGM 528, BGD 72, GNG 469, BGM 524, BG 256, BGD 115, BGD 116, KGDB 1178, KGDM 1181, BCP 17

Table 5. Mean intra-cluster (diagonal and bold) and inter-cluster distances among six clusters in chickpea

Cluster	I	II	III	IV	V	VI
I	**1.880**					
II	2.638	**1.988**				
III	3.281	3.244	**1.727**			
IV	4.459	4.052	4.344	**1.448**		
V	2.583	2.911	2.389	4.635	**1.865**	
VI	3.421	2.989	3.995	2.950	3.095	**1.692**

Table 6. Cluster means for seed yield and its components in chickpea

Cluster	Days to first flower	Days to maturity	Plant height (cm)	Primary branches/plant	Pods/plant	Seeds/pod	100-seed weight (g)	Seed yield/ plant
I	55.00	108.00	45.24	3.11	35.67	1.34	21.83	8.57
II	57.00	100.40	44.17	2.68	40.53	1.15	22.82	9.21
III	55.53	102.40	48.57	2.52	38.87	1.60	14.85	7.44
IV	68.67	102.67	45.73	2.89	69.56	1.41	17.15	13.10
V	58.46	107.31	52.50	2.54	32.15	1.38	21.02	7.67
VI	63.07	103.36	52.92	2.83	50.40	1.29	24.82	14.02

and plant height are expected to produce superior segregants in segregating generations as these genotypes were found to possess higher genotypic mean values for their respective traits and occupy different clusters. Beside these, four genotypes viz., RSG 966, IPC 97-1, IPC 96-46 and ICCV 97022 from cluster V can also be utilized in breeding programme for higher seed yield, pods/plant and bold seed size. Thus, these genotypes hold great promise as parents in hybridization programme for creating valuable genetic variability and obtaining promising segregants for higher seed yield in segregating generations.

In the present study seed yield/plant had significant and positive genotypic correlation with days to first flower, primary branches/plant, pods/plant and 100-seed weight, indicating that indirect selection for these traits can bring out improvement in seed yield (Table 3). Therefore, seed size, pods/plant, primary branches/plant and days to first flower should form the basis for selection of parents for hybridization from distantly placed clusters. It is clear that selection for bold seed size will also bring improvement in seed yield of chickpea. Similar results have also been reported by Bejiga *et al.* (1991), Shinde and Saraf (1991), Rao *et al.* (1994), Gumber *et al.* (2000) and Kulkarni (2001). Besides, bold seed size undoubtedly gets premium in the market. Hence, genotypes like BGD 116, BGD 115, KGDM 1181, BCP 17, BGM 524, BG 256, KGDB 1178 from cluster VI can be exploited in breeding programme for higher seed yield and bold seed size.

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Growth Pattern and Classification of Soybean Under Semi-sodic Soils

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Wide range of variation was observed in sixty genotypes of soybean evaluated under semi-sodic soil condition. Euclidian Non Hierarchical cluster analysis resulted in formation of four clusters. Cluster I exhibited the determinate habit, while cluster IV comprised indeterminate types. Cluster II and III both were found to be semi-determinate type. The semi-determinate growth habit recorded less biological yield in comparison to both determinate and indeterminate types but produced more seed yield and recorded the highest harvest index. The study demonstrated that selection of genotypes with semi-determinate growth habit would result in development of high yielding soybean lines under semi-sodic soils.

Key Words: Cluster analysis, Growth pattern, Semi-sodic soil, Soybean

Soybean [*Glycine maxI* (L.) Merr.] is one of the most important oilseed crop in India. Besides being a rich source of oil, it also constitutes an important part of human and animal feed.

There have been contradictory reports claiming superiority of determinate and indeterminate growth habit over one another (Ablett, 1988; Lampang *et al.*, 1988; Chinchilla *et al.*, 1988; Parvez *et al.*, 1989). The present investigation was undertaken study the effect of seed yield under semi sodic-soil condition.

Cluster analysis based on Principal Component Analysis (PCA) is a useful tool for categorizing a large number of germplasm accessions into morphologically similar groups. The present investigation was aimed at using this technique to study the pattern of variability in growth habit as well as other economic traits.

Materials and Methods

Sixty genotypes of soybean collected from various sources were evaluated in a Randomized Block Design with three replications in two successive seasons i.e. summer and *kharif* under semi-sodic soil condition at Banthra Research Station of National Botanical Research Institute (NBRI), Lucknow, Uttar Pradesh, situated between $80^0$45'–$80^0$53' longitude and 26° 40'–26^0 45' N latitude and at an altitude of 129m above the mean sea level. The area falls into a subtropical zone, characterized by hot, dry summers and cold winters. It receives an annual rainfall of 80-100 cm. Each genotype was grown in 5 rows of 2m length with row-in-row and plant-to-plant spacing of 50 and 20 cm, respectively. The observations were recorded on five randomly selected plants from each genotype for seven characters, namely, plant height at anthesis, plant height at harvest, plant height between flowering to harvest, degree of determination, plant biological yield, seed yield and harvest index. Degree of indetermination was calculated as per the formula given by AVRDC (1976).

The data were analyzed using Euclidian Non Hierarchical Cluster Analysis as described by Beale (1969) and elaborated by Spark (1973).

Results and Discussion

A wide range of variation was observed among the genotypes for the traits namely, growth in reproductive phase (H2-H1) and degree of indetermination (DDh), while the other attributes namely, plant height at anthesis (H1), plant height at harvest (H2), biological yield (BY), and harvest index (HI) exhibited medium range of variation. The lowest variation was recorded for seed yield (Table 1).

The Euclidian non hierarchical cluster analysis resulted in formation of four clusters based on the similarity among the constituent parameters. Cluster III was found to be biggest containing 28 morphological accessions

Table 1. Cluster mean, standard deviation and coefficient of variation (%) for seven characters in soybean

Characters	Mean	SD	CV (%)
Plant height (H1)	27.34	3.61	14.83
Plant height (H2)	31.14	3.85	12.36
Plant height (H2-H1)	3.73	1.86	49.86
Degree of indet. (DDh)	11.73	5.61	47.82
Biological yield (BY)	63.13	9.26	14.67
Seed yield (SY)	37.91	2.11	5.56
Harvest index (HI)	23.86	3.30	13.83

(Table 2). Cluster IV, which contained 13 accessions, was found to be comprising most promising accessions as demonstrated by high average degree of indetermination (16.08), biological yield (75.54) and harvest index (27.71). In cluster IV, highest variability among the genotypes was also recorded indicating further scope of selection within the said cluster (Table 3). Clusters I and II containing 12 and 7 accessions, respectively, differed mainly for average degree of indetermination, growth during reproductive phase and biological yield. Clusters II and III with semi-determinate growth pattern recorded the low biological yield in comparison to cluster I and IV, but produced high seed yield resulting in high harvest index. These results supported by studies of Ablett (1988) and Ablett *et al.* (1989) demonstrated that selection of genotypes with semi-determinate growth habit could result in development of high yielding soybean lines under semi-sodic soil conditions.

The average distance between cluster centroids represent the extent of diversity between the two clusters. In this study, clusters I and II were found to be most divergent (3.554) that could easily be traced to the difference in their average degree of indetermination. The other notable distances between cluster centroids were observed for clusters I and IV (3.526) and clusters II and III (3.467) which could readily by identified due to differences in average degree of indetermination and growth during reproductive phase, respectively (Table 4).

Average distance of cluster numbers from cluster centroid was recorded to be maximum in cluster II (2.168), indicating the within cluster diversity for future exploitation in selection programmes (Table 4). All the other clusters viz. I, III and IV exhibited the same degree of distance of cluster members from cluster centroids. Cluster II which comprised accessions having desired semi-determinate growth habit and maximum within cluster diversity, should be utilized in future breeding programme for developing high yielding soybean lines for semi-sodic soil conditions.

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Table 2. Clustering pattern based on Euclidian cluster analysis over growth pattern

Clusters	Growth habit	No. of genotypes	Populations
I	Determinate	12	UPSL254, 343ch, 425, 443, 555, 601,UPSM593, JS79-20 71-05, 87-59, L-1596, UPSE2048
II	Semi-determinate	7	UPSE2683, 2703, UPSL216, 326, 785, 796, UPSM651
III	Semi-determinate	28	UPSL29, 62, 92, 117B, 152, 272, 284, 298, 319, 365, 788, 858, UPSM20, 42, 68, 164, 657, 802, 853, 889, 1030A, 1034, UPSV 65A, 37, UPSM1090A, AGS99, UPSL181
IV	Indeterminate	13	UPSL1171, UPSM181, 858, 1099, 1115, PK308, 317, UPSL160, UPSM1705, 1094A, SL-3UGM-34, UPSL470

Table 3. Mean and standard deviation of four clusters for seven characters

Cluster No.	Plant height (HI) (cm)	Plant height (H2) (cm)	Plant height (H2-H1) (cm)	Degree of indetemination	Biological yield	Seed yield	Harvest index
I	30.30 (1.78)	31.52 (1.83)	1.22 (0.69)	3.85 (2.120)	65.88 (7.63)	37.21 (2.27)	24.43 (2.42)
II	32.85 (2.10)	38.19 (3.37)	5.33 (1.80)	13.78 (3.57)	6.147 (9.12)	39.23 (1.73)	24.15 (3.94)
III	25.16 (2.40)	28.93 (2.79)	3.77 (1.19)	12.56 (4.15)	56.53 (3.92)	38.44 (2.04)	21.76 (2.09)
IV	26.33 (2.72)	31.74 (2.37)	5.10 (1.40)	16.08 (4.38)	75.54 (3.78)	36.70 (1.64)	27.71 (1.99)

Table 4. Average distance of cluster members from cluster centroid and distances between cluster centroids

Clusters	I	II	III	IV
I	1.687			
II	3.554	2.168		
III	2.959	3.467	1.802	
IV	3.526	3.340	3.112	1.720

Diagonal values are average distances of cluster members from cluster centroids.

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Genetic Variability, Correleation and Path Analysis in the Selections Made from *Gossypium arboreum* Race *Cernuum* Collections of North-east India

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Genetic variability, character association and path analysis between yield and its contributing traits were studied in 29 single plant selection progeny of *Gossypium arboreum* race *cernuum* collections made from north-east region and two local checks RG-8 and LD-327. Highly significant differences between the selections were recorded for all the traits. High heritability coupled with high genetic advance for boll weight indicated predominance of additive gene effects controlling this trait and low heritability associated with low genetic advance for yield per plant and boll number per plant revealed high effect of environment on these traits. Correlation and path co-efficient analysis revealed that boll number per plant and boll weight were the most important characters for realizing improvement in seed cotton yield per plant.

Key Words: Character association, Cotton, North-east, Path analysis

North-eastern hill (NEH) in India is considered to be the important centre of *Gossypium* variability from where races *cernuum, sinense* and *bengalense* are supposed to have been derived from *Gossypium arboreum* race *burmanicum* (Paranjpe and Panigrahi, 1961). The *cernuum* cottons are suitable for upholstery, high absorbent cotton and mixing with wood and have a great export potential. These cottons have also been reported to be good donors for high boll weight, high ginning out-turn, high seed number per loculus and per boll and resistance to jassids and bollworms (Duhoon and Singh, 1980; Duhoon, 1981). Material of *Gossypium arboreum* race *cernuum*, collected from NEH region in 1992 were evaluated at CICR, Regional Station, Sirsa and single plant selections were made. For such types of collections, extent of association between yield and its components and relative importance of direct and indirect effect of yield contributing components is yet to be estimated. The present paper deals with the genetic constants and character association in 29 single plant selections made from collections in *Gossypium arboreum* race *cernuum.*

Material and Methods

Twenty nine genotypes (single plant selection progeny of *G. arboreum* race *cernuum* collections made in 1992 on the basis of difference in boll weight ginning out turn percent, mean fibre length and boll no./plant) from NEH regions, were grown with two local checks LD 327 and RG-8 in randomized block design with three replications at CICR Regional Station, Sirsa, Haryana during *kharif* 1997-98. These selections are denoted as CSA (Central Institute for Cotton Research, Sirsa *arboreum*). CSA11-1 and CSA11-2 are two single plant progenies different with respect to boll weight of collection No. 11 made from NEH region.

Each single plant progeny was evaluated in a plot of three rows of 5.4 m length. Observations were recorded on five random plants per selection in each replication for 6 quantitative characters namely, yield per plant (gm), boll weight, bolls per plant, ginning out turn percent (GOT), mean fibre length (mm) and seed index (g). Standard statistical procedures were followed for estimating phenotypic and genotypic coefficients 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 method of Dewey and Lu (1955).

Results and Discussion

The analysis of variance revealed highly significant differences between genotypes for all the characters studied. This indicated a considerable amount of variability in the selection made from *G. arboreum* race *cernuum* collections. The data on yield and its contributing traits, phenotypic (PCV) and genotypic (GCV) coefficient variation, heritability (H2) and genetic advance (GA) are presented in Tables 1 and 2. The variability estimates in general, revealed that the PCV was higher than the corresponding GCV for all the 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 seed cotton yield per plant. Moderate variability was observed for boll weight and boll no./plant. Relatively low PCV and GCV were recorded for GOT, mean fibre length and seed

index. The genotypic coefficient of variation ranged from a minimum of 7.63 per cent for seed index to a maximum of 20.06 per cent for seed cotton yield per plant. Seed cotton yield per plant showed the highest PCV value of 30.11 per cent in comparison to GCV of 20.06 suggesting more environmental influence on this character which was confirmed by its lowest heritability (44.41%). Similar was the case for boll no./plant. The difference between PCV and GCV was low for GOT followed by boll weight, mean fibre length and seed index. This observation draws support from very higher values of hertiability (>60%) recorded for these traits (Table 2).

Since broad sense hertiability includes both additive and epistatic effects, it will be reliable only when accompained by high genetic advance. Heritability estimates along with genetic advance are more useful than heritability alone in predicitingthe effectiveness of selection. High estimates of hertiability (>80%) and genetic advance (> 30%) were obtained for boll weight. Selection for this trait is likely to accumulate more additive genes leading to further improvement of their performance and hence may be used as selection criteria.

Table 1. Mean performance of *G. arboreum* race *cernuum* selections

S.No.	Selection	Seed cotton	Boll wt.	Boll no.	GOT	Halo length	Seed index
1	CSA 5-92	126.93	3.60	56.23	38.5	16.20	5.73
2	CSA592-1	108.13	2.80	43.20	39.83	17.00	5.23
3	CSA 592-2	89.60	2.93	39.33	42.00	18.40	5.23
4	CSA 593-3	61.23	3.30	43.00	40.0	16.87	5.90
5	CSA 493-1	78.43	3.57	49.10	46.83	15.17	5.03
6	CSA 893-1	88.80	3.03	41.10	43017	18.50	5.60
7	CSA 1213-1	112.13	3.70	42.10	38.33	17.13	5.97
8	CSA 1293-1	86.90	4.07	40.33	41.00	20.43	5.80
9	CSA 1393-1	93.27	3.93	41.23	43.67	17.70	5.97
10	CSA 1793-1	119.37	3.20	49.23	38.17	17.13	6.20
11	CSA 2393-1	63.10	3.70	36.23	40.83	18.60	6.07
12	CSA 5	82.43	3.27	53.43	35.83	22/23	6.43
13	CSA 17A	80.50	3.53	37.43	37.33	17.67	6.03
14	CSA 8	95.10	3.70	54.10	39.17	20.07	6.27
15	CSA 11-1	63.57	4.60	36.67	45.33	20.23	5.20
16	CSA 13-1	62.33	3.57	38.77	42.17	20.00	5.27
17	CSA 11-2	64.77	3.63	42.70	42.43	20.43	5.10
18	CSA 13-2	61.57	3.63	33.33	40.23	18.57	6.00
19	CSA 9-22	84.17	3.47	47.57	38.40	19.67	5.73
20	CSA 913	58.90	3.17	28.67	41.67	17.90	5.50
21	CSG 24	86.60	2.43	48.23	30.40	18.70	5.77
22	CSG 18	62.60	2.67	[illegible]	32.83	18.00	6.13
23	CSG 27	103.63	2.93	40.8	32.33	22.83	6.30
24	CSA 9-10	127.37	2.67	40.87	36.20	19.40	5.03
25	CSA-98	86.40	2.43	46.77	36.97	18.70	5.50
26	CSA 41	86.50	2.10	44.00	41.53	18.97	5.50
27	CSA 9-3	114.03	2.77	37.57	36.87	20.53	5.50
28	CSA 17	98.27	2.80	38.23	34.40	18.83	5.07
29	CSA 40	121.43	2.83	40.67	41.47	17.77	5.53
30	RG-8	100.30	2.73	41.00	36.67	16.00	6.00
31	LD 327	97.10	3.43	48.00	39.77	19.67	5.17

Table 2. Analysis of variance for seed cotton yield and its component traits in *G. arboreum* race *cernuum* selections

SOV	d.f.	Yield per plan	Boll wt	Boll no.	GOT	Halo length	Seed index
Replication	2	3838.79	0.14	227.42	3.07	0.66	0.31
Genotypes	30	1371.55*	0.90*	113.69*	41.54*	8.87*	0.67*
Error	60	403.85	0.05	47.50	0.98	0.80	0.10
H2(g)		44.41	83.92	31.72	93.25	77.19	65.76
G.A. (% of mean)		27.54	31.02	12.71	18.67	15.89	12.74
GCV (%)		20.06	16.44	10.96	9.39	8.78	7.63
PCV (%)		30.11	17.94	19.46	9.72	9.99	9.41

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

Simple selection procedures like mass selection and family selection would be effective for improvement of this trait. Low heritability with low genetic advance was found in respect of yield per plant and boll no./ plant indicating that this character is highly influenced by environmental effects and simple selection would be ineffective. Thus expression of these traits can be modified through hybridization followed by selection.The heritability of GOT, mean fibre length and seed index though high (65 to 93%) yet had low genetic advance (12.7% to 18.7). High heritability and low genetic gain for seed index was also reported by Mehla *et al.* (1988).

Yield of a crop is the result of interaction of a number of interrelated characters. Therefore selection should be based on the component characters after assessing correlation with yield. Character associations reveal 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. In the present study, seed cotton yield was found to be significantly and positively correlated with boll no. at genetic level. Therefore, this character should be kept in mind while making selection for seed cotton yield improvement in *G. arboreum* race *cernuum*. The association of seed cotton yield was negative with boll weight, GOT and mean fibre length at genotypic and phenotypic levels (Table 3). Boll no./ plant also showed positive and significant association with GOT both at genotypic and phenotypic levels. Tomar and Singh (1992) also reported positive association of seed cotton yield with boll no./plant and negative association with boll weight.

Seed cotton yield is the sum total of several component characters which directly or indirectly contribute to it. The information derived from the correlation studies indicates only mutual association among the characters.

Table 3. Correlation coefficient among yield components in *G. arboreum* selections

S.No.	Character	Yield per plant	Boll wt.	Boll no.	GOT	Halo length	Seed Index
1	G	1.00	- 0.3859*	0.5214**	- 0.3215	- 0.1426	0.0764
	P	1.00	- 0.2090	0.1661	- 0.1962	- 0.1054	- 0.082
	E	1.00	0.0888	0.0480	0.0548	- 0.0615	- 0.282
2	G		1.000	-0.1056	0.5493**	0.0739	0.0830
	P		1.000	-0.0848	0.5089**	0.0622	0.0723
	E		1.000	-0.0913	0.2201	0.0144	0.0452
3	G			1.000	-0.3202*	- 0.0519	0.1653
	P			1.000	-0.1594	- 0.0746	0.1669
	E			1.000	0.0686	- 0.1240	0.1891
4	G				1.000	- 0.2488	- 0.398
	P				1.000	- 0.2391	- 0.333
	E				1.000	- 0.2261	- 0.154
5	G					1.000	0.0345
	P					1.000	0.0674
	E					1.000	0.1532
6	G						1.000
	P						1.000
	E						1.000

** Significant at 1% level, * Significant at 5% level
G: Genotypic level
P: Phenotypic level

Table 4. Direct and indirect effects (Genotypic) keeping yield per plant as dependent variable and other characters as independent

Character	Boll Wt.	Boll No.	GOT	Halo Length	Seed Index	Genotypic Correlation with Yield/Plant
Boll wt.	(-0.332)	- 0.051	0.001	-0.006	0.002	- 0.39
Boll no.	0.035	(0.477)	- 0.001	0.005	0.005	0.52
GOT	- 0.182	- 0.153	(0.002)	0.023	- 0.011	- 0.32
Halo length	- 0.025	-0.024	- 0.001	(-0.093)	0.001	- 0.14
Seed index	- 0.027	0.079	- 0.001	-0.003	(0.03)	- 0.07

In parentheses are given values for direct effect
Residual effect = 0.608

Whereas, path-coefficient analysis gives the magnitude of direct and indirect contribution of each character, on the dependent character like seed cotton yield. The results of the present investigation on path coefficient analysis (Table 4) revealed that character boll no./plant had maximum positive direct effect on seed cotton yield while boll weight has maximum direct but negative effect. Dhoon (1989) and Samabamurthy (1995) also reported boll no./plant as primary component of yield. Low positive direct effect were estimated from characters GOT and seed index. Mean fibre length recorded low direct effect. On the other hand none of the characters indicated high positive or negative indirect effect on seed cotton yield via other characters.

In the light of the above findings it may be concluded that improvement in character like boll weight and boll number per plant both directly and indirectly will help in improving seed cotton yield. Therefore, these characters should be considered for yield improvement in *G. arboreum* race *cernuum* breeding programme.

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New Sources of Resistance to Yellow Rust (*Puccinia striiformis* f. sp. *hordei*) in Barely

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In order to identify new diverse sources of resistance to yellow rust (*Puccinia striiformis* f. sp. *hordei*) in barley germplasm a total of 607 accessions of indigenous and exotic origin were evaluated during four years (1999-2003) under artificial inoculation in the field with mix inocula of races 24, 57, G and M. The resistant accessions identified in the field screening for at least three years were further evaluated for seedling resistance test (SRT) with seven races (24, 57, G, G-1, M, Q and a new biotype). Based on the field screening, 47 accessions were found resistant for more than two years. Seventeen highly resistant accessions were used for SRT and ten were found resistant to all the seven pathotypes. Interestingly, all these seventeen resistant accessions are of exotic origin and expected to add to the diversity of resistance to the yellow rust in the national programme.

Key Words: Barley, Germplasm, *Puccinia striiformis* f. sp. *hordei*, Resistance, Yellow Rust

Barley is an important cereal crop grown in India and used for a variety of purposes including animal feed, human food and in industry for malting and brewing. It suffers from many diseases and amongst them the stripe rust and leaf blights (net blotch and leaf spot) are of major importance in the main barley growing area of the North-western plains in India, where better management is provided to the crop and the crop growth is luxuriant. The incidence of yellow rust (*Puccinia striiformis* f. sp. *hordei*) may create havoc in susceptible varieties and result in heavy yield losses (Suryanarayana, 1979). Several races of yellow rust have been reported on wheat and barley, however, race 24, 57, G and M are more prominent (Prasada *et al.*, 1967; Jain, 1978). Race 24 is only the one reported on barley in the Nilgiri Hills in South India but is also reported in Lahual and Spiti, Himachal Pradesh. Recently some more new biotypes, like M, G-1 Q etc. have been added to the list of barley pathotypes (Anonymous, 2002). The numbers of varieties under cultivation is very few and several of them have become susceptible to yellow rust because of either breakdown of resistance or by evolution of new virulent pathotypes. There are very few reports on sources of resistance to yellow rust in India (Gulati *et al.*, 1988; Upadhyay and Prakash, 1977; Mathur and Siradhana, 1990) and inheritance of the disease (Luthra, 1966; Luthra, 1988; Luthra and Chopra, 1990). Some of these identified genes have also been isolated in Fongtein barley background (Luthra, *et al.* 1991). But the numbers of diverse resistance genes are very few in present cultivars. Therefore, there is a need to screen barley germplasm from diverse sources against yellow rust under artificial epiphytotic condition for identifying new sources for utilization in the breeding programme.

Materials and Methods

A total of 607 barley genotypes consisting of indigenous and exotic germplasm accessions received from International Centre for Agricultural Research in Dryland Areas, Syria (ICARDA), and International Maize, Wheat and Barley Improvement Centre, Mexico (CIMMYT) were evaluated at DWR, Karnal, during 1999 to 2003 in four crop seasons for their resistance to yellow rust. The materials were grown in one row of 2.5 m length at 30 cm distance between rows. After every 20 lines one line of susceptible check (Bilara-2) was sown with the test materials. Also susceptible infector lines (mixture of susceptible cultivars) were sown bordering the test materials block from all sides. The susceptible infector rows were artificially inoculated repeatedly with mix inocula of four most common races (24, 57, G and M) of yellow rust in between 45-55 days after sowing. The inocula were mixed with water and syringe inoculated on alternate day in the evening and also sprayed over the infector line. At the later stages the test material was also directly sprayed with inocula collected from the injector rows. The crop was grown as per recommended agronomic practices. Data on yellow rust were recorded by combining severity (percent leaf area covered by rust) and response (infection type) according to the method developed by Loegering (1959). The categorization was made as F/R = Free/Resistant type, MR = Moderately Resistant, S = Susceptible HS = Highly Susceptible. The lines observed as resistant were repeated for screening in subsequent years, thereby having observation on such

lines for two to four years in continuation to eliminate any chance of escape and also to observe the stability of resistance.

Results and Discussion

Barley germplasm were subjected to artificial screening under heavy infection of yellow rust, with the advantage of suitable environment at Karnal, where lot of natural dew formation helps in rapid spread of yellow rust till the mid of March. Based on the four consecutive years' evaluation barley genotypes were classified into various categories (Table 1).

It was observed that 15 entries, BCU 424, BCU 455, BCU 492, BCU 519, BCU 532, BCU 543, BCU 544, BCU 546, BCU548, BCU 550, BCU 551, BCU 554, BCU 729, BCU 775, BCU 841 (Table 1) were consistently showing resistance for four years to yellow rust at audit plant stage under artificial epiphytotic condition and there were additional 13 lines, which were showing resistance to yellow rust for three years. Seventeen lines, which were giving immune and highly resistant type reaction out of these 28 lines (13+15) were screened for seedling resistant test (SRT) against seven races of yellow rust individually at DWR Regional Station, Flowerdale, Shimal under controlled inoculation conditions. The parentage and other details of these entries are given in Table 2.

Ten lines namely BCU 131, BCU 424, BCU 455, BCU 544, BCU546, BCU 550, BCU 551, BCU 554, BCU 729 and BCU 775 (Table 3) were showing complete resistance against all the races (24, 57, G, M, Q, G-1, and N.B.). Among the rest seven entries, five showed resistance against all the known races except against the new biotype and remaining two were susceptible

Table 1. Reaction of barley genotypes to yellow rust (*Puccinia striiformis* f. sp. *hordei*)

Reaction type	Years of evaluation	Total entries	Genotypes (BCU Nos.)*
Resistant	Four	15	424,455,492, 519, 532, 543, 544, 546, 548, 550, 551, 554, 729, 775, 841,
	Three	13	131, 134, 549, 571, 766, 1009, 1022, 1023, 1025, 1026, 1069, 1070, 1085
	Two	19	135, 387, 516, 530, 531, 575, 576, 628, 632, 641, 642, 644, 702, 730, 809, 812, 1065, 1088, 1091
	Total	47	
Moderately resistant		138	
Moderately susceptible	133		
Highly susceptible		289	
Total accession		607	

*BCU = Barley Coordinating Unit Number given to each barley accession maintained as active collection at DWR, Karnal.

Table 2. Parentage of accessions showing resistance at APR and SRT

Accession	Name/Parentage	Source	Origin	Botanical Name
BCU 131	HBL-113 (Selection from Zyphzee)	PALAMPUR, H.P., INDIA	Exotic	*H. distichon*
BCU 424	GLORIA "S"/COME "S"/LIGNE640/3/SUPER PRECOZ	CIMMYT EMBSN(91091)-19	Exotic	*H. distichon*
BCU 455	SUPER PRECOZ/5/HJA A33/ID601810/1102.2/STEUDELLT/3/EGYPT20/4/PYE "S"/6/ABN	CIMMYT EMBSN(91092)-50	Exotic	*H. vulgare*
BCU 492	GLORIA "S"/COME "S"//ORGEFICHEDRETT3270/ROW906.73	CIMMYT 19th IBON(91-92)-32	Exotic	*H. vulgare*
BCU 519	CAMPILLO LIBERNA/DAPHENE//SEN "S"	CIMMYT 19th IBON(91-92)-59	Exotic	*H. vulgare*
BCU 532	4259/CI5831/S.A1/3/, EMIET/4/GABRONE515/TEQ//G; PROA "S"	CIMMYT 19th IBON(91-92)-73	Exotic	*H. vulgare*
BCU 543	80.5056/NOHA "S"//GLORIA "S"/COME "S"	CIMMYT 19th IBON(91-92)-84	Exotic	*H. vulgare*
BCU 544	SUDAN/4/ASE/3/M/RO/3/SMAI/5/GLORIA "S"/IAR-H485	CIMMYT 19th IBON(91-92)-85	Exotic	*H. vulgare*
BCU 546	BARBEROUSSE/RUMOROSA/GLORIA "S"/COME "S"	CIMMYT 19th IBON(91-92)-87	Exotic	*H. vulgare*
BCU 548	BARBEROUSSE/P.STO "S"//GLORIA "S"/COPAL "S"	CIMMYT 19th IBON(91-92)-89	Exotic	*H. vulgare*
BCU 550	MJA "S"	CIMMYT 19th IBON(91-92)-91	Exotic	*H. vulgare*
BCU 551	GLORIA "S"/COME "S"	CIMMYT 19th IBON(91-92)-92	Exotic	*H. vulgare*
BCU 554	GLORIA "S"/COPAL "S"//TERAN/78/3/SHYRI	CIMMYT 19th IBON(91-92)-95	Exotic	*H. distichon*
BCU 571	M10080	CIMMYT 19th IBON(91-92)-89	Exotic	*H. vulgare*
BCU 729	LIGNEE 527/3/HARBING/AVT//ATHS	ICARDA IInd IWFBON-131	Exotic	*H. vulgare*
BCU 775	UC566/5/M64-76/BON/JO/YORK/3/MS/GALT//AS46/4/HJ34-80 ASTRIX	ICARDA BCH (91-92)-31	Exotic	*H. vulgare*
BCU 841	AS46/PRO/BAL. 16/API/4/11012/TERN//H252/3/ NOPAL "S"/5/ASSALA	ICARDABON-LRA(91-92)-42	Exotic	*H. vulgare*

to race G as well. The variation in adult plant reaction and seedling resistance test may be due to fact that new biotype was not used during field screening. The results indicated that there are several new exotic resistance sources in barley germplasm. Entries showing resistance against all races of yellow rust are selections from international trail/nurseries from ICARDA/CIMMYT except BCU 131 (HBL 113), which is a released variety in the NH Zone, but it is also a selection from exotic germplasm Zyphzee.

Out of the total 607 accessions tested, most of them fall into the categories of moderately susceptible (22%) to highly susceptible types (47%), making a total 69% in the susceptible category. Around 22.7% entries were observed as moderately resistant types. Only 47 accessions (8%) showed resistance against yellow rust a different years of screening.

Similar studies on identifying resistant sources for yellow rust in barley were undertaken by Upadhyay and Prakash (1977); Gulati *et al.* (1985, 1988); Luthra (1988); Luthra and Chopra (1990). However, most of them are either not available in national collection or have been utilized earlier.

Data were also recorded on a number of other characters (Table 4) which indicate that apart from resistance these lines are also having diversity for maturity duration, plant height and 1000-grain weight, three important traits of interest in barley breeding. All genotypes were of six row type except BCU 131, BCU 424 and BCU 554. This will provide the opportunity to choose the diverse material of choice from these resistant sources.

Table 4. Yield and related triats of resistance sources of barley germplasm

Genotypes	Row type (2/6R)	Heading days	Plant height (cm)	1000 grain weight (gm)
BCU 131	2	100	103	28.5
BCU 424	2	102	100	25.6
BCU 455	6	83	106	31.2
BCU 492	6	97	110	37.0
BCU 519	6	97	166	39.0
BCU 532	6	103	100	32.4
BCU 543	6	95	104	29.5
BCU 544	6	102	105	33.0
BCU 546	6	99	90	35.4
BCU 548	6	103	85	28.6
BCU 550	6	103	87	33.7
BCU 551	6	95	75	33.6
BCU 554	2	93	85	32.5
BCU 571	6	82	92	35.1
BCU 729	6	83	82	33.3
BCU 775	6	103	84	31.2
BCU 841	6	102	81	32.5

Since the national programme on barley has taken up the work on malt barley improvement for optimally managed condition of the NWP Zone the importance of resistance to the stripe rust has further increased in Punjab, Haryana, Western UP and Northern Rajasthan where weather conditions are congenial for the disease development and spread. The disease may affect the crop yield as well as grain quality, the two important aspect for malting.

These lines which showed resistance both at SRT and adult plant reaction (APR) may be utilized as donor parents in the hybridization programme for incorporation

Table 3. Seedling reaction (SRT) of new barley lines to individual races of yellow rust (Puccinia striiformis f. sp. hordei)

S.No.	Genotypes	Reaction* to yellow rust races**						
		24	57	G	M	Q	G-1	N.B.
1.	BCU 131	;	;	;	;	;	;	;
2.	BCU 424	0;	0;	0;	0;	0;	0;	0;
3.	BCU 455	0;	0;	0;	0;	0;	0;	0;
4.	BCU 492	0;	0;	2+	0;	0;	0;	2+,3
5.	BCU 519	0;	0;	3+	0;	0;	0;	2+,3
6.	BCU 532	0;	0;	0;	0;	0;	0;	2+,3
7.	BCU 543	0;	0;	0;	0;	0;	0;	2+,3
8.	BCU 544	0;	0;	0;	0;	0;	0;	0;
9.	BCU 546	0;	0;	0;	0;	0;	0;	0;
10.	BCU 548	0;	0;	0;	0;	0;	0;	3
11.	BCU 550	0;	0;	0;	0;	0;	0;	;
12.	BCU 551	0;	0;	0;	0;	0;	0;	2
13.	BCU 554	0;	;	0;	0;	0;	0;	;
14.	BCU 571	0;	;	0;	0;	;	0;	3+
15.	BCU 729	0;	0;	0;	0;	0;	0;	0;
16.	BCU 775	0;	0;	0;	;	;	0;	;
17.	BCU 841	0;	0;	3-	;	;	0;	;

of resistance to yellow rust in high yielding barley variety of the country.

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Short Communications

Evaluation of Chickpea Accessions Against Root-knot Nematode, *Meloidogyne incognita*

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Key Words: Chickpea, *Meldoidogyne incognita*, Resistance, Root-knot

Chickpea (*Cicer arietinum*) is an excellent source of high quality protein. During last three decades chickpea cultivation area has decreased progressively in the country, various pests and diseases including nematodes being some of the factors for reducing yield of this crop. About ten species of plant parasitic nematodes have been found associated with this crop. Among them, the root-knot nematode, *Meloidogyne incognita* is most predominant and causes 25-60% yield loss (Ali, 1997). Keeping this fact in view, a green house experiment was conducted to identify resistant genotypes, which could be exploited in breeding programme for development of resistant commercial cultivars.

Advanced breeder's seed material entries for multilocational testing under All India Co-ordinated Research Project on Improvement of Chickpea were included in this study as these entries are high yielding. Promising seeds were surface sterilized in 0.2% mercuric chloride solution and were sown separately in 15 cm diam. clay pots, containing 1 kg of steam sterilized soil. Three replications were maintained for each germplasm accessions. Thinning was done at 2-3 leaf stage, leaving one healthy seedling in each pot. Fifteen hundred freshly hatched (12 hr after hatching) second stage juveniles of *M. Incognita* were inoculated around each plant. After 45 days of inoculation, the plants were uprooted and roots were gently washed. Galls developed on the roots are indexed on 0-5 scale (Taylor and Sasser, 1978), where 1 = 0 or no galls (highly resistant), 2 = 1-10 galls (Resistant), 3 = 11-30 galls (moderately resistant), 4 = 31-100 galls (susceptible) and 5 = above 101 galls (highly susceptible).

It is evident from the Table 1 that out of 120 germplasm accessions of chickpea tested, RSG 902, RSG 974, BGD 109, RSG 931, BGM 532, BGM 534, BGD 72 were found to be highly resistant, RSG 895, CSJD 901, RSG 906, BGD 11, GPF 2, H 95-30, GNG 1331, GNG 1293 were resistant whereas, PG 95-27, Phule G 94601, BG 267, BG 1075, BG 1095, GNG 1340 were highly susceptible against this nematode. Four

Table 1. Host reaction of various chickpea accessions to *M. incognita* under green house condition

Accessions	No. of galls	Host reaction	Total
RSG 902, RSG 97, BGD 109, RSG 931, BGM 532, BGM 534, BGD 72	0	HR	7
RSG 895, CSJD 901, RSG 906, BGD 11, GPG 2, H 95-30, GNG 1331, GNG 1293	1-10	R	8
IPC 97-1, FG 664, RSG 888, RSG 865, RSG 965, BGD 98, RSG 959, FG 703, Phule G 95311, BGM 535, BGM 528, H 95-123, H 208, C 235, BG 1078, BG 256, BG 1063, BG 1065, BG 1096, BG 1079, BG 372, BG 1080, GNG 1296	11-31	MR	23
CSJG 869, CSJD 884, RSG 807, FG 559, FG 711, CSJD 916, RSG 823, BGD 110, GPF 133, RSG 945, GL 96004, PBG 1, GL 90236, PBG 127, PBG 68, PBG 34, L 550, Phule G 96126, Phule G 93009, Phule G 96022, Phule G 96108, VIJAYA, Phule G 5, Phule G 96104, BGM 531, BGM 519, BGM 524, BGM 536, HK 94-134, H 95-122, BG 362, BG 1097, BG 256, BG 391, BG 1o66, BG 1062, BG 256, BG 1003, BG 1089, BG 256, BG 372, BG 1084, BGD 108, BG 256, BG 1081, BG 1067, BG 256, BG 1003, BG 1088, BG 362, BG 1094, BG 267, BGD 112, GNG 1323, GNG 1308, GNG 1320, GNG 1174, GNG 469, GNG 1250, GNG 1345, GNG 1329, GNG 1237, GNG 1350, GNG 1275, GNG 1292, GNG 1192, GNG 1271, GNG 1178, GNG 1336, GNG 663, CSG 9391, CSG 9388, CSG 9428, CSG 9401, CSG 9505	31-100	S	76
PG 95-27, Phule G 96401, BG 267, BG 1075, BG 1095, GNG 1340	Above 101	HS	6

cultivars/lines namely BG 369, BGM 481, GL 88341 and GMS 815 have been reported to possess resistance against *M. javanica* (Ali, 1997). These sources of resistance could be utilized in breeding programme for developing commercial varieties possessing resistance against root-knot nematode.

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Genetic Divergence for Physico-Chemical Characteristics of Lemon Fruits Grown in Himachal Pradesh

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Key Words: Cluster Analysis, Germplasm Genetic Divergence, Lemon, Physico-Chemical Characteristics

Lemon (*Citrus limon* Burm.) is one of the important fruits of citrus family. In India, it is cultivated in Uttar Pradesh, Maharashtra, Tamil Nadu, Karnataka, Andhra Pradesh, Assam, West Bengal, Bihar, Rajathan, Orissa, Punjab and Himachal Pradesh (Singh, 1995; Mankand, 1994). Lemon trees are prolific bearers and have very high productivity as compared to other citrus fruits (Sharma *et al.*, 2001). One of the important characteristics of this fruit crop is that its fruits are available during December-February when the Kagzi lime is either not available or is rather scarce (Singh, 1995). Very little attention has been given to improve this fruit crop though it is almost at par with lime. A wide range of diversity in lemon germplasm exists in India which can form a basis for any crop improvement programme. Therefore, an attempt was made to evaluate the genetic diversity among 52 accessions collected from various lemon growing regions of Himachal Pradesh.

The experimental material consisted of 52 accessions of lemon collected from various lemon growing regions of HP such as Nurpur, Kangra, Una and Hamirpur. All the 52 accessions are planted in the experimental Orchard of Regional Horticultural Research Station, Jachh, (Nurpur) Distt. Kangra (HP) except one *i.e.* IL-1 (Italian lemon) which was procured from Kangra. All the accessions were evaluated for various physico-chemical characteristics of fruits harvested at their optimum maturity. The fruit length, diameter and flavedo thickness were measured using digital vernier calliper. Total soluble solids (TSS) were recorded by using hand refractometer and acidity of juice by the method detailed by Ranganna (1997). The juice was extracted through screw type juice extractor. The data on various physical and chemical fruit characteristics were analysed using Non-hierarchical Euclidean Cluster Analysis method (Beale, 1969; Spark, 1973).

Data presented in Table 1 show that the fruit weight of lemon ranged between 125-525 g with a mean weight of 332.71 g. The size parameters viz., fruit length varied between 9.00-13.50 cm (mean 11.27 cm) and fruit diameter varied between 5.27-9.68 cm (Mean 8.14 cm). The average flavedo thickness was observed to be 3.17 mm. The juice yield ranged between 16.0-51.2

Table 1. Mean, range, standard deviation and coefficient of variation for physico-chemical characteristics of lemon

Parameter	Mean	Range	Standard deviation	Coefficient of variation
Fruit weight (g)	332.71	125-525	88.10	26.48
Fruit length (cm)	11.27	9-13.5	1.36	12.07
Fruit dia (cm)	8.14	5.27-9.68	0.95	11.67
Total peel (%)	19.88	8.3.-42.8	6.91	34.76
Flavedo thickness (mm)	3.17	1.58-5.33	0.79	24.92
Juice (%)	31.29	16.0-51.2	7.64	24.42
Residue/Pomace(%)	48.95	25.0-64.9	9.51	19.43
No. of segments	9.92	8-12	1.22	12.30
No. of seeds	23.12	0-40	9.38	40.57
TSS of juices	8.10	7.1-9.5	0.65	8.02
Acidity of juice	5.43	4.9-5.9	0.33	6.08

* Total peel includes flavedo and albedo

cultivars/lines namely BG 369, BGM 481, GL 88341 and GMS 815 have been reported to possess resistance against *M. javanica* (Ali, 1997). These sources of resistance could be utilized in breeding programme for developing commercial varieties possessing resistance against root-knot nematode.

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Genetic Divergence for Physico-Chemical Characteristics of Lemon Fruits Grown in Himachal Pradesh

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Key Words: Cluster Analysis, Germplasm Genetic Divergence, Lemon, Physico-Chemical Characteristics

Lemon (*Citrus limon* Burm.) is one of the important fruits of citrus family. In India, it is cultivated in Uttar Pradesh, Maharashtra, Tamil Nadu, Karnataka, Andhra Pradesh, Assam, West Bengal, Bihar, Rajathan, Orissa, Punjab and Himachal Pradesh (Singh, 1995; Mankand, 1994). Lemon trees are prolific bearers and have very high productivity as compared to other citrus fruits (Sharma *et al.*, 2001). One of the important characteristics of this fruit crop is that its fruits are available during December-February when the Kagzi lime is either not available or is rather scarce (Singh, 1995). Very little attention has been given to improve this fruit crop though it is almost at par with lime. A wide range of diversity in lemon germplasm exists in India which can form a basis for any crop improvement programme. Therefore, an attempt was made to evaluate the genetic diversity among 52 accessions collected from various lemon growing regions of Himachal Pradesh.

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Table 2. Distribution of 52 accessions and average inter- and intra- cluster distance in lemon on the basis of physico-chemical characteristics of fruits

Cluster	Distribution of 52 accessions		Average inter and intra cluster distance									
Number	No. of trees	Tree numbers	I	II	III	IV	V	VI	VII	VIII	IX	X
I	3	J-6/2, J-3/2, IL-I	2.101									
II	2	J-16/6. J-8/6	4.625	1.392								
III	4	J-15/4, J-7/6, J-9/3, J 10/3	2.963	6.122	1.392							
IV	6	J-8/2, J-8/1, J-15/6, J-11/1, J-4/4, J-15/1	3.865	4.824	4.376	2.148						
V	6	J-7/5, J-9/6, J-18/3, J-9/5, J-4/12, J-5/3	3.649	4.281	4.265	5.048	1.960					
VI	3	J-19/5, J-5/8, J-16/5	5.895	5.034	6.497	3.924	4.693	1.341				
VII	10	J-19/6, J-10/5, J-19/2, J-21/2, J-10/2, J-10/1, J-17/6, J-10/6,8/5,9/7	3.697	5.322	3.254	3.279	2.805	3.724	1.746			
VIII	10	J-3/5, J-12/7, J-2/1, J-17/8, J-2/6, J-19/4, J-7/6, J-3/2, J-20/2, J-13/5	4.512	5.636	4.357	2.385	4.404	3.676	2.361	1.746		
IX	3	J-8/3, J-4/6, J-20/6	4.305	4.027	5.395	5.728	2.275	5.608	4.337	5.269	0.978	
X	5	J-19/1, J-10/1, J-20/4, J-20/1, J-10/4	4.868	3.543	5.888	3.591	3.544	2.583	3.453	3.563	3.664	1.579

* Diagonal elements represent intra-cluster distances

Table 3. Cluster mean, standard deviation and coefficient of variability of 10 clusters in different characters and per cent contribution of different fruit characteristics towards diversity in lemon

Characters		Cluster number										% contribution towards
		I	II	III	IV	V	VI	VII	VIII	IX	X	diversity in lemon
Fruit weight (g)	Mean	225.33	360.00	181.25	334.17	275.00	450.00	312.50	405.00	300.00	420.00	
	SD	65.58	14.14	51.54	57.92	54.77	66.14	39.53	53.75	43.30	44.72	31.66
	CV	29.10	3.93	28.44	17.33	19.92	14.70	12.65	13.23	14.43	10.65	
Fruit length (cm)	Mean	10.30	10.50	8.88	11.92	10.67	13.33	10.74	12.30	10.67	12.10	
	SD	0.26	1.41	1.11	0.92	0.8	0.76	0.97	0.75	0.58	0.89	28.07
	CV	2.52	13.43	12.50	7.72	8.25	5.70	9.03	6.10	5.44	7.35	
Fruit diameter (cm)	Mean	6.62	8.49	6.49	8.59	7.74	9.13	8.10	8.65	7.61	8.91	
	SD	1.13	0.81	0.87	0.83	0.81	0.07	0.41	0.51	0.24	0.24	13.45
	CV	17.07	9.54	13.40	9.66	10.46	0.77	5.06	5.89	3.15	2.69	
Total peel (%)*	Mean	24.47	38.30	20.73	27.18	16.35	22.50	15.70	17.33	13.60	20.18	
	SD	5.93	6.36	5.90	7.72	4.91	3.12	4.76	1.72	3.12	1.71	8.32
	CV	24.23	16.60	28.46	28.40	30.03	13.87	30.32	9.92	22.94	8.47	
Flavedo thickness (mm)	Mean	2.96	3.24	2.35	4.01	2.47	3.99	3.12	2.95	2.64	4.14	
	SD	0.49	0.23	0.60	0.73	0.40	0.26	0.67	0.52	0.26	0.69	5.70
	CV	16.55	7.10	25.53	18.23	16.19	6.52	21.47	18.63	9.85	16.67	
Juice (%)	Mean	33.77	40.50	25.08	24.52	39.09	30.20	29.21	25.33	46.83	36.08	
	SD	6.50	0.71	2.15	4.97	3.50	0.53	4.58	4.04	4.09	3.88	4.42
	CV	18.17	1.75	8.57	20.30	8.95	1.75	15.68	15.95	8.73	10.75	
Residence/pomace (%)	Mean	34.67	31.75	54.00	48.13	44.40	47.07	55.89	57.08	39.40	43.52	
	SD	9.24	9.55	5.30	7.51	6.51	3.72	7.31	4.41	1.82	4.35	3.70
	CV	26.65	30.08	9.81	15.60	14.66	7.90	13.08	7.72	4.62	9.99	
Number of segments	Mean	10.33	11.00	10.25	11.17	8.67	8.33	8.90	10.60	10.67	10.20	
	SD	0.58	1.41	0.96	0.75	0.52	1.53	0.88	0.84	0.58	0.45	2.44
	CV	5.61	12.82	9.36	6.71	5.99	18.37	9.88	7.92	5.43	4.41	
Number of seeds	Mean	13.33	26.00	20.00	23.67	18.83	39.67	22.90	22.90	20.00	27.60	
	SD	13.50	2.83	14.58	6.89	9.79	3.06	6.52	8.29	3.61	8.73	1.09
	CV	101.27	10.88	72.9	29.11	51.99	7.71	28.47	36.20	18.05	31.63	
TSS of juice (°Brix)	Mean	7.67	9.15	7.57	7.57	8.77	8.20	7.87	7.64	9.43	8.68	
	SD	0.51	0.07	0.17	0.20	0.43	0.20	0.23	0.25	0.12	0.34	0.67
	CV	6.65	0.76	2.25	2.64	4.90	2.44	2.92	3.27	1.57	3.92	
Acidity of juice (%)	Mean	5.20	5.85	5.17	5.05	5.83	5.57	5.40	5.18	5.87	5.78	
	SD	0.20	0.07	0.10	0.14	0.16	0.06	0.19	0.23	0.06	0.11	0.48
	CV	3.85	1.96	1.97	2.77	2.74	1.08	3.52	4.44	1.02	1.90	

* Total peel includes flavedo and albedo

per cent of fruit weight. Total peel (%) (flavedo + albedo) and residue/pomace (%) varied between 8.3-42.8 per cent and 25.0 to 64.9 per cent, respectively. The number of segments and seeds ranged between 8–12 and 0-40, respectively. However, the juice characteristics viz., total soluble solids and titratable acidity varied between 7.1-9.5 °Brix and 4.9 to 5.9 per cent, respectively in all the 52 accessions of lemon studied.

The 52 accessions were grouped into 10 clusters (Table 2). The cluster VII and VIII had maximum number of 10 accessions in each and cluster II had minimum of 2 accessions. The intra and inter-cluster variations among different accessions under study was of varying magnitude (Table 2). The maximum intra-cluster distance was observed in cluster IV (D = 2.148), followed by I (D = 2.101), V (D = 1.960), VII and VIII (D = 1.746). These clusters consisted of 6, 3, 6, 10 and 10 accessions, respectively. The above grouping indicates existence of wide genetic divergence among constituent accessions. The minimum intra-cluster value (D = 0.978) exhibited by cluster IX containing 3 accessions indicated limited genetic diversity among the constituents. The inter-cluster distance indicated greater cluster divergence between clusters II and VI, followed by clusters II and III, I and VI, III and X. Thus, a due emphasis in the breeding programme should be given to four accessions of cluster II, three accessions each of clusters I and IV, two accessions of cluster II and five accessions of cluster X. The selection of divergent genotypes from above clusters would produce a broad spectrum of variability for various physical and chemical characteristics of lemon fruits and its juice. The hybrids developed from the selected accessions within the limits of compatibility of these clusters may produce high magnitude of heterosis or desirable transgressive segregants which would be rewarding in varietal improvement programme. There was a wide range of variation in the cluster mean values for all the characters under study (Table 3). The contribution of different attributes towards genetic divergence revealed that fruit weight contributed maximum divergence, followed by fruit length, fruit diameter, peal (%), flavedo thickness, juice (%), residue/ pomace (%), number of segregants, number fo seeds, TSS of the juice and acid content. Data presented in Table 3 revealed that cluster VI recorded maximum fruit weight, fruit size and number of seeds, which consisted of 3 genotypes viz. J-19/15, J-5/8, J-16/5. Similarly the accessions present in cluster IX (J-8/3, J-4/6, J-20/6) showed highest yield, TSS and acidity of juice. The possible promising donors may be picked out of these clusters for further improvement in lemon.

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Inheritance of Pentafoliate Character in Groundnut (*Arachis hypogaea* L.)

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Hybridization between Spanish bunch and Virginia genotypes is the most common tool employed for creation of variability for various morphological and physiological attributes in groundnut. In this process, some morphological variants that are uncommon in Spanish or Virginia groups do appear in the segregating populations of such crosses. A pentafoliate single plant selection was made in segregating populations of an infraspecific cross, Tirupati 1/ICGV86398 in which both parents had tetrafoliate (paripinnate) leaves. Tirupati 1 is a high yielding variety suitable for kharif cultivation under rainfed conditions in drought prone areas of Andhra Pradesh. Its leaflets are narrow and moderately long with ashy coat on their surface. ICGV86398 is a Virginia bunch genotype obtained from ICRISAT. It is resistant to jassids and tolerant to *Spodoptera* (Vasanthi and Padmavathammas, 2000). The pentafoliate selection was assigned accession number, TCGS635. The pentafoliate (imparipinnate) character was reported earlier in groundnut (Patil, 1966; Ashri, 1970; Mouli and Kale, 1981). A variant with imparipinnate but with normal leaflet size was isolated from one of the F3 progenies of the cross TG16 X TG17 by Mouli and Kale (1981) in which both parents had paripinnate leaves and it bred true in succeeding generations. The variant, TCGS635 had 33 to 40% of the leaves that expressed pentafoliate character while the variant isolated by Mouli and Kale (3) had only 12% of the leaves that were pentafoliate. The radiation induced short mutant with small leaflets obtained by Patil (1966) showed 45% of the leaves that were imparipinnate. An attempt is made to understand the mode of inheritance of pentafoliate character, which could be of great value as a good morphological marker in groundnut breeding programme.

All the F1s had tetrafoliate leaves indicating the dominant nature of tetrafoliate leaf character. In F2, the segregation data in all the five crosses was a good fit to a phenotypic ratio of 15 tetrafoliate: 1 pentafoliate plants (Table 1). It shows that pentafoliate leaf character is expressed when the genes are in recessive condition and is governed by two duplicate genes present in different chromosomes which are independently inherited. Hammons (1973) in his review on qualitative inheritance in groundnut expressed that qualitatively inherited traits are probably controlled by at least duplicate genes due to alloploid nature of the crop which tends to confirm the theory of two genomes in *Arachis hypgaea.* Many of the earlier studies also showed involvement of two duplicated genes in inheritance of many qualitative traits in groundnut. Branch and Hammons (1981) reported digenic inheritance for flop trait in groundnut. Present study corroborates the involvement of at least two genes in expression of another character in groundnut.

In F3 generation, progenies from pentafoliate plants were all pentafoliate and they didn't segregate. It confirmed the recessive nature of pentafoliate leaf character in groundnut, which is a rare feature.

An understanding of the physiological/biochemical mechanisms which lead to the expression of pentafoliate character would be an interesting study. The pentafoliate leaf character helps in increasing the canopy density that increases photosynthetically active leaf area, which could be of value in kharif rainy season.

Table 1. F2 Segregation pattern for pentafoliate leaf character in groundnut (*Arachis hypogaea* L.)

Cross	F1 phenotype	F2 segregation		x^2 for 15:1 ratio	P value
		Plants with tetrafoliate	Plants with pentafoliate leaves		
Tirupati-3 X TCGS-635	Tetrafoliate	257	13	0.9491	0.50-0.20
TCGS-320 X TCGS-635	Tetrafoliate	363	27	0.3015	0.95-0.50
TCGS-245 X TCGS-635	Tetrafoliate	594	52	3.3471	0.10-0.05
TCGS-596 X TCGS-635	Tetrafoliate	368	27	0.2306	0.95-0.50
TCGS-645 X TCGS-635	tetrafoliate	630	41	0.2240	0.95-0.50
Pooled		2212	160	0.9934	0.50-0.20

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