Indian Journal of Plant Genetic Resources

ISSN 0971-8184

Towards Conservation and Sustainable Utilization of Plant Diversity

Published by

Indian Society of Plant Genetic Resources

NBPGR Campus, New Delhi 110012 (India)

Vol. 18 No. 3 2005

Morphological Diversity in Naked Barley Landraces from North-Western Himalayas of India

K Venkatesan[1], IS Bisht[1]*, KV Bhat[1], K Elayaraja[1] and KC Muneem[2]
[1]*National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012*
[2]*National Bureau of Plant Genetic Resources, Regional Station, Bhowali, Nainital-263 132*

The Himalayan barleys, particularly, naked forms, are important phylogenetically and require adequate research and marketing interventions because of their high feed value. In the present study, 84 naked barley landraces mainly from north-western Indian Himalayas comprising three main administrative regions, Jammu & Kashmir, Himachal Pradesh and Uttaranchal states were characterized for morphological traits. The range and pattern of variations were studied. Jammu & Kashmir accessions were more diverse than Himachal Pradesh and Uttaranchal accessions. Landraces from mid-elevational zones were relatively more diverse than landraces from lower and extreme high elevational zones in each administrative region. The multilocation evaluation of selected naked barley landraces revealed greater adaptability and potential of Himalayan naked barleys even to non-conventional plain zones for commercial cultivation. The importance of Himalayan naked barleys for agriculture and also their safe conservation *ex situ* and *in situ* (on-farm) was suggested.

Key words: Naked barley, *Hordeum vulgare* L., Genetic diversity, North-western Himalayas

Cultivated barley (*Hordeum vulgare* ssp. *vulgare*) can be classified into covered (hulled), those in which the lemma and palea (the chaff) are tightly fused to the pericarp of the caryopsis (grain) and naked (hull-less), those in which the chaff is easily separated from the grain. This character is not only unique to barley, but is also directly connected to its utilization. At present, most barley varieties are of the hulled form, and they are mainly used for brewing malt and animal feed. By contrast, naked barley is produced on a small scale and used mainly as human food because of the ease in processing and edibility. In recent years, naked barley is attracting attention as feed and as a healthy food because of the high feed value and abundance of dietary fibre, respectively (Liu *et al.*, 1996). According to a survey by Takahashi (1955), naked barley is distributed widely, but its frequency greatly differs among regions; naked barley accounts for more than 95% of the domesticated barley in the highlands of Nepal and Tibet, and almost 50% in China, Korea, and Japan, but the frequency decreases toward the west, becoming low in Europe. In fact, in the regions where naked barley is grown at high frequencies, it is an important staple food.

The Himalayan barleys particularly, naked forms, are of great potential utility, which require research and marketing interventions. The Himalayas, Ethiopia, and Morocco have all been considered as centers of barley domestication (Åberg, 1938; Bekele, 1983; Molina-Cano *et al.*, 1987). Harlan *et al.* (1976) refer to the Near East as the "centre of agricultural innovation" where barley was the first crop to be domesticated followed by wheat. The widespread distribution of naked barley makes the hulled or naked caryopsis character a key trait to follow the origin and domestication process of barley (Harlan, 1995; Salamini *et al.*, 2002). A recent study (Taketa *et al.*, 2004), however, indicates that naked barley has a monophyletic origin, probably in southwestern Iran, and all naked barleys are likely to share a common ancestor.

In many areas of north-western Himalayas, in proximity of Tibet, naked barley was widely cultivated till about 4 or 5 decades ago. Up to 1960s when free trade existed between India and Tibet, naked barley had specific uses. Being highly nutritious and rich in protein, it was eaten as 'sattu' during the long journeys on foot that the traders undertook crossing the mountain passes. This trade came to a standstill after 1962 when the borders between India and Tibet were sealed. The local farmers thereby lost the most important incentive of cultivating naked barleys and the result was that most of these landraces are on the verge of extinction now. Naked barley landraces have gradually been replaced by wheat in these areas as a cereal of direct human consumption. Much of the naked barley populations, however, are still grown in high plateaus

**Corresponding author: E-mail: bishtis@rediffmail.com; bishtis@nbpgr.ernet.in*

of China and Tibet for direct human consumption and eaten as 'tsamba'.

About 400 barley landraces including naked types have been collected recently from north-western Himalayas during 1999-2004 and are being maintained *ex situ* in National Genebank at the National Bureau of Plant Genetic Resources (NBPGR). These landraces are yet to be systematically characterized/evaluated. Limited information is, therefore, available on genetic diversity of existing naked barley landraces grown in north-western Himalayas. The extent of diversity between populations adapted to the high altitude region of north-western Himalayas would suggest need for their continuous collection and devising strategies for both *ex situ* and *in situ* (on-farm) conservation. It would also suggest possibility of using the useful genetic variation in these landraces for improved yield and a better utilization of these products in agriculture and industry.

Materials and Methods

Morphological Diversity of Naked Barley Landraces

The experimental material consisted of 84 naked barley landraces assembled from different parts of north-western Himalayas and represented all agro-ecological conditions of the region. The material also included 12 naked barley landraces from exotic sources including eight accessions from Ethiopia, two from Peru and one accession each from France and Nepal. Three cultivars from Udaipur (Rajasthan state of India) were also included in the study. The passport information on the origin of accessions are given in Table 1. The material was grown in randomized block design with two replications at NBPGR, New Delhi during rabi 2004-05. The accessions were grown in three 2m row plots, with a between-row spacing of 25cm, and a within-row spacing of 10cm. Five hulled (covered) commercial barley varieties (DL-36, DL-85, Jyoti, VLB-1 and VLB-60) were included as controls as no improved local controls for naked barley are available. Recommended agronomic practices were followed through various stages of crop growth. Data were recorded on 10 randomly chosen competitive plants per plot for 27 descriptors (18 quantitative and 9 qualitative, Table 2) following the IBPGR (1982) descriptor list and descriptors proposed by Murphy and Witcombe (1986). The data on quantitative traits were subjected to analysis of variance (ANOVA).

Table 1. Passport Information of Barley Landraces Studied

Origin	No. of accessions			Elevational
	Six-rowed	Two-rowed	Total	ranges (masl)
Jammu and Kashmir	38	–	38	1,700-4,200
Uttaranchal	15	1	16	1,500-4,500
Himachal Pradesh	13	2	15	1,500-4,200
Udaipur (Rajasthan)	3	–	3	400-500
Exotic	7	5	12	1,700-3,800

The frequency distribution and comparative summary statistics of barley accessions for quantitative and qualitative traits were computed for different administrative regions (States) in the north-western Himalaya, viz. Jammu & Kashmir, Uttaranchal and Himachal Pradesh, and a separate group of exotic accessions. The phenotypic frequencies of both quantitative and qualitative characters were also analysed by the Shannon-Weaver information index (H') in order to estimate the diversity of each character administrative region-wise and altitude-wise across administrative regions. The index was calculated as presented by Negassa (1985) and Engels (1991):

$$H' = -\sum_{i=1}^{n} p_i \log_e p_i$$

where p_i is the proportion of the accessions in the i^{th} class of an n-class character. In order to keep the values of H' in the range of 0-1 each value of H' was divided by its maximum value, $\log_e n$.

Classification (cluster analysis) and ordination (principal components analysis) analyses were also performed. Skewed data on quantitative traits were transformed before multivariate analysis. Ward's minimum variance clustering method was used to classify accessions in discrete clusters (Sneath and Sokal, 1973), whereas the Weighted Average Linkage technique using ISS similarity index was used for qualitative traits. The scores for various character states of different accessions were converted to a binary code before analysis using qualitative traits. Principal components analysis was performed using quantitative traits. The statistical analysis was carried out using INDOSTAT statistical package developed at the INDOSTAT Services, Hyderabad, India.

Multilocation Evaluation of Selected Naked Barley Landraces

A set of 30 selected naked landrace populations comprising 16 accessions from Uttaranchal, 5 from Jammu & Kashmir, 2 from Himachal Pradesh, 1 from Udaipur (cultivar) and 6 from exotic sources (4 accessions from Ethiopia and

1 each from Nepal and Peru) was also subjected to multilocation evaluation for quantitative traits at two NBPGR locations, Delhi (semi-arid, plain zone: latitude 28°35'N, longitude 78° 18' E, altitude 226 masl) and Bhowali (temperate, hilly area: latitude 29° 20' N, longitude 79° 04'E, altitude 1600 masl) during 2003-04 *rabi* season. The trials were conducted in order to assess the adaptability of Himalayan naked barleys for widespread cultivation. The material was grown in Randomized Block Design with two replications at both the locations. The material was grown in 4-row plots of 2m row length, and 25 x 10 cm row to row and plant to plant spacing, respectively. Data on all 18 quantitative traits (Table 2) at NBPGR, New Delhi and on 10 selected important traits at NBPGR, Regional Station, Bhowali were recorded. ANOVA was carried out separately for both locations. ANOVA for pooled analysis was also carried out. The multivariate analysis was also performed separately for data of both locations.

Table 2. List of Descriptors Used for Germplasm Characterization

S. No.	Descriptors/Characters	Frequency class*
Quantitative Descriptors		
1.	Days to flowering	1= <70; 2 = 70-85; 3 = 85-100; 4=>100
2.	Days to maturity	1= <100; 2 = 100-115; 3 = 115-130; 4=>130
3.	No. of tillers/plant	1= <10; 2= 10-15; 3= 15-20; 4 =>20
4.	No. of leaves	1= <100; 2= 100-125; 3=125-150; 4= >150
5.	Plant height (cm)	1= <80; 2= 80-100; 3= >100
6.	Height of top node (cm)	1= <50; 2= 50-70; 3= >70
7.	Length of top internode (cm)	1= <15, 2= 15-20; 3= >20
8.	Length of flag leaf sheath (cm)	1= <20, 2= 20-25; 3= >25
9.	Length of neck (cm)	1= <5; 2=5-10; 3=10-15; 4=>15
10.	Length of flag leaf (cm)	1=<10; 2=10-15; 3=>15
11	Breadth of flag leaf (cm)	1=<1; 2=1-2; 3=>2
12.	Length of penultimate leaf (cm)	1=<20; 2=20-30; 3=>30
13	Breadth of penultimate leaf (cm)	1= <2; 2=2-2.5; 3=>2.5
14.	No. of spikelet groups/spike	1=<15; 2=15-20; 3 = 20-25, 4=25-30; 5 =>30
15.	Length of main ear (cm)	1= <5; 2=5-7; 3= 7-9; 4=>9
16.	No. of grains/spike	1= <50; 2=50-65; 3=65-80; 4=>80
17.	Seed weight per plant	1=<15; 2= 15-20, 3=20-25; 4=>25
18.	100- seed weight	1=<2.5; 2=2.5-3; 3=3-3.5; 4=3.5-4;5= >4
Qualitative Descriptors		
19.	Row numbers/lateral florets	1= Six rowed; 2= Two rowed: lateral florets large and sterile; 3= Two rowed: lateral florets rudimentary
20.	Spike density	1= Lax (=4 mm); 2= Intermediate; 3= Dense (=2 mm)
21.	Hoodedness	1= Sessile hood; 2= Elevated hood; 3= Awnless or Awnletted (=2 mm) on all rows; 4= Awned (on central rows for 2 rowed and on all six rows for 6-rowed); 5= Awned on central rows only lateral rows awnless or awnletted
22.	Awn roughness	1= Smooth; 2= Rough
23.	Length of rachilla hair	1= Short; 2= Long
24.	Hairiness of leaf sheath	1= Hairless; 2= Hairy
25.	Pigmentation of leaf sheath	1= Green; 2= Purple
26.	Nature of collar	1= Closed; 2= Open; 3= 'V' shaped
27.	Grain colour	1= Pale; 2= Brown; 3= Blue; 4= Purple; 5= Black

*Codes used for diversity analysis

Results

Morphological Diversity of Naked Barley Landraces

Analysis of variance (ANOVA) of 89 barley landraces (including 5 hulled controls) for quantitative traits indicated highly significant differences for all quantitative variables. The range of variation for various quantitative traits is presented in Table 3. The Table 3 revealed maximum variation for length of neck, length and breadth of flag leaf, no. of tillers/plant, no. of leaves/plant, no. of grains/spike, seed weight per plant and no. of grains/spike. Many naked landraces were found to be superior to hulled controls (commercial varieties) used for comparison in the present study for agronomically desired traits like early flowering, high tillering capacity, no. of grains/spike, yield/plant and 100-seed weight.

The comparative descriptive statistics of barley landraces from different regions, Uttaranchal, Jammu & Kashmir, Himachal Pradesh and exotic sources is

presented in Table 4. It was revealed that the landraces from Jammu & Kashmir are relatively early in flowering/ maturity. The exotic accessions had the highest tillering capacity whereas the Uttaranchal accessions had the lowest no. of tillers/plant. The exotic accessions recorded the highest number of leaves/plant. Uttaranchal accessions were relatively taller than accessions from other areas. Uttaranchal accessions recorded highest no. of spikelet groups/plant but the Jammu & Kashmir accessions had relatively high seed weight/plant and 100-seed weight. Marked regional variations were also recorded for other characters viz. height of top node, length of top internode, length of neck, length and breadth of flag leaf, length of penultimate leaf, etc. (Table 4).

The frequency distribution for various quantitative characters revealed skewness, both positive and negative. Not much variation was, however, recorded for qualitative traits except spike density, nature of collar and grain colour.

The administrative region-wise diversity indices for both quantitative and qualitative characters are presented in Table 5. The diversity indices showed wide variations between characters administrative region-wise. The pooled diversity indices by characters (quantitative traits) indicate relatively high diversity for 100-seed weight, length of main ear and length of flag leaf whereas low diversity for no. of spikelet groups/spike and no. of grains/spike was recorded. For other quantitative traits, diversity was

Table 3. Range of Variation for Quantitative Traits in Barley Landraces

Descriptors	Lowest	Highest	Kurtosis	Skewness	Mean	CV
Days to flowering	56	112	-0.33	-0.51	86.57	14.61
Days to maturity	88	137	4.49***	-1.11	121.91	5.6
No. of tillers/plant	7	34	-0.39	0.28	18.66	28.21
No. of leaves	48	226	-0.48	0.29	132.62	28.93
Plant height(cm)	75	129	1.06**	0.29	101.98	8.66
Height of top node (cm)	19	92	2.46***	-0.43	66.12	14.58
Length of top internode (cm)	10.5	23.5	-0.45	0.3	16.81	16.46
Length of flag leaf sheath (cm)	15	27.5	0.08	0.13	21.22	10.66
Length of neck (cm)	2	20.7	1.16**	1.15***	7.36	55.52
Length of flag leaf (cm)	4.9	26.5	-0.22	0.38*	13.23	34.13
Breadth of flag leaf(cm)	0.4	5	12.36***	2.14***	1.41	36.37
Length of penultimate leaf (cm)	15.5	38	0.35	0.64***	23.98	18.74
Breadth of penultimate leaf (cm)	1.4	3	0.14	0.16	2.03	14.45
No.of spikelet groups/spike	16	38	-0.12	0.53**	23.99	18.06
Length of main ear(cm)	5.5	12	-0.4	0.13	8.17	15.37
No.of grains/spike	22	96	2.02***	-0.95	61.49	22.31
Seed weight/plant	5.34	37.7	-0.22	0.3	21.24	28.78
100-seed weight	1.98	5.54	-0.24	-0.28	3.67	19.48

Table 4. Comparative Summary Statistics of Barley Landraces from Different Regions of North-Western Himalayas for Quantitative Traits

S.No.	Characters	Uttaranchal	Jammu & Kashmir	Himachal Pradesh	Exotic
1	Days to flowering	92±7	79±11	94±11	94±10
2.	Days to maturity	120±4	120±6	126±5	124±12
3.	No. of tillers/plant	14±4	20±4	18±4	26±3
4.	No. of leaves	111±27	135±31	134±29	186±27
5.	Plant height	107±10	99±8	101±7	103±8
6.	Height of top node	72±10	63±9	68±9	66±5
7.	Length of top internode	17±2	18±3	15±2	16±2
8.	Length of flag leaf sheath	20±2	21±2	22±2	21±2
9.	Length of neck	7±3	7±3	4±2	9±6
10.	Length of flag leaf	9±3	14±4	13±4	14±4
11.	Breadth of flag leaf	1.2±0.7	1.4±0.4	1.7±0.6	1.5±0.3
12.	Length of penultimate leaf	20±2	25±4	23±3	26±5
13.	Breadth of penultimate leaf	2±0.2	2±0.3	2±0.2	2±0.3
14.	No. of spikelet groups/ spike	27±4	23±4	22±4	26±3
15.	Length of main ear	8±1	8±1	8±1	8±1
16.	No. of grains/spike	63±10	64±8	58±12	42±17
17.	Seed weight/plant	18±4	23±7	17±5	22±3
18.	100-seed weight	3±0.5	4±0.5	4±0.6	4±0.6

Table 5. Estimates of Diversity Indices (*H'*) for Quantitative Traits

S. No.	Characters	Administrative regions				
		J&K	UA	HP	Exotic	Average
Quantitative Traits						
1.	Days to flowering	0.72	0.76	0.45	0.52	0.61±0.2
2.	Days to maturity	0.59	0.81	0.36	0.52	0.57±0.2
3.	No. of tillers/plant	0.73	0.64	0.58	0.75	0.68±0.1
4.	No. of leaves	0.83	0.81	0.89	0.27	0.70±0.3
5.	Plant height	0.89	0.55	0.63	0.62	0.67±0.2
6.	Height of top node	0.72	0.76	0.63	0.59	0.68±0.1
7.	Length of top internode	0.91	0.64	0.63	0.82	0.75±0.1
8.	Length of flag leaf sheath	0.78	0.35	0.91	0.75	0.70±0.2
9.	Length of neck	0.77	0.51	0.59	0.92	0.70±0.2
10.	Length of flag leaf	0.78	0.64	0.91	0.84	0.79±0.1
11.	Breadth of flag leaf	0.71	0.44	0.88	0.27	0.58±0.3
12.	Length of penultimate leaf	0.73	0.61	0.22	0.75	0.58±0.3
13.	Breadth of penultimate leaf	0.81	0.63	0.67	0.84	0.74±0.1
14.	No. of spikelet groups/ spike	0.38	0.35	0.67	0.41	0.45±0.2
15.	Length of main ear	0.84	0.55	0.91	0.93	0.81±0.2
16.	No. of grains/spike	0.44	0.21	0.50	0.63	0.45±0.2
17.	Seed weight/plant	0.80	0.64	0.82	0.41	0.67±0.2
18.	100-seed weight	0.81	0.76	0.82	0.91	0.83±0.1
	Average	0.74	0.59	0.67	0.65	0.66+0.2
Qualitative Traits						
1.	Spike density	0.36	0.35	0.47	0.26	0.36±0.1
2.	Hoodedness	0	0.35	0.36	0	0.18±0.2
3.	Awn roughness	0	0	0.25	0.27	0.13±0.2
4.	Length of rachilla hairs	0	0.34	0.25	0.27	0.21±0.2
5.	Nature of collar	0.44	0.58	0.46	0.46	0.48±0.1
6.	Grain colour	0.44	0.43	0.41	0.14	0.35±0.1
	Average	0.25	0.41	0.44	0.28	0.34±0.1

J&K= Jammu & Kashmir; UA= Uttaranchal; HP=Himachal Pradesh

moderate. Based on administrative region-wise pooled diversity over all the characters, Jammu & Kashmir state was the most diverse followed by accessions from Himachal Pradesh, Exotic group and Uttaranchal State. Among qualitative traits, nature of collar, spike density and grain colour recorded relatively high diversity. Himachal Pradesh accessions were relatively more diverse for these qualitative traits followed by accessions from Uttaranchal, exotic group and Jammu & Kashmir. The pattern of diversity indices over characters within ecogeographic regions (altitude-wise) across region were relatively uniform. More diversity was recorded in relatively mid-elevational zones across all administrative regions (Table 6).

Cluster analysis using Ward's minimum variance technique classified the 84 barley accessions (controls excluded) into three major groups. Cluster III comprised 40 accessions followed by 22 accessions each in cluster I and II (Fig. 1).

A fair degree of association between geographical origin and genetic diversity was revealed. Cluster I mainly comprised landraces assembled from Uttaranchal state. Cluster II comprised accessions mainly from Jammu & Kashmir. Most of the exotic landraces were grouped in cluster III together with some accessions from parts of Jammu & Kashmir and Himachal Pradesh.

Table 6. Estimates of altitude-wise diversity indices (*H'*) for quantitative traits of barley landraces

S.No.	Characters	Altitude			
		Low (<2000 masl)	Medium (2000-3000 masl)	High (>3000 masl)	Average
1.	Days to flowering	0.43	0.91	0.68	0.67
2.	Days to maturity	0.43	0.72	0.60	0.58
3.	No. of tillers/plant	0.63	0.64	0.91	0.73
4.	No. of leaves	0.83	0.91	0.91	0.88
5.	Plant height	0.83	0.91	0.91	0.88
6.	Height of top node	0.63	0.58	0.83	0.68
7.	Length of top internode	0.63	0.92	0.91	0.82
8.	Length of flag leaf sheath	0.85	0.88	0.51	0.75
9.	Length of neck	0.63	0.78	0.68	0.70
10.	Length of flag leaf	0.70	0.91	0.91	0.84
11.	Breadth of flag leaf	0.91	0.54	0.94	0.80
12.	Length of penultimate leaf	0.79	0.80	0.76	0.78
13.	Breadth of penultimate leaf	0.85	0.66	0.60	0.70
14.	No. of spikelet groups/spike	0.86	0.91	0.91	0.89
15.	Length of main ear	0.91	0.94	0.83	0.89
16.	No. of grains/spike	0.70	0.70	0.28	0.56
17.	Seed weight/plant	0.84	0.87	0.91	0.87
18.	100-seed weight	0.91	0.91	0.91	0.91
	Average diversity	0.74	0.80	0.77	0.77

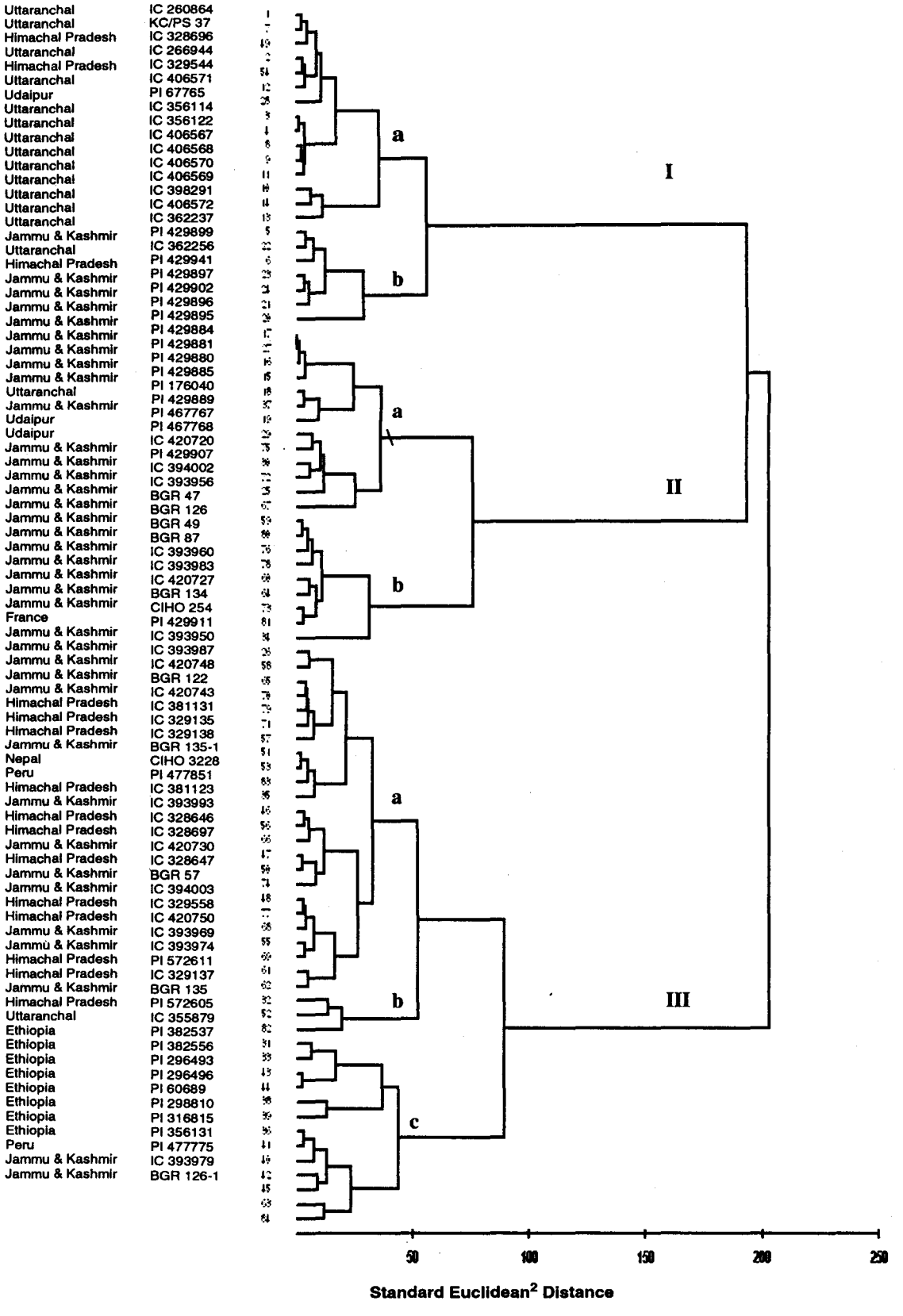


Fig. 1: Ward's minimum variance dendrogram of 84 barley landraces based on quantitative traits

Cluster I was characterized with accessions late in flowering, low tillering capacity, high number of grains/spike, low seed weight/plant and low 100-seed weight. Cluster II was characterised with accessions early in flowering/maturity, moderate numbers of tillers/ plant, high number of grains/spike, high seed weight/ plant and 100-seed weight. Cluster III comprised late flowering/maturing accessions with high tillering capacity, moderate seed weight/ plant and 100-seed weight. Cluster III was most diverse followed by cluster II and I.

Weighted average linkage clustering using qualitative traits classified the accessions into two major clusters (Fig. 2). Cluster I comprised only six accessions, two accessions each from Uttaranchal, Himachal Pradesh and Ethiopia with high degree of similarity at sub-cluster level. Cluster II comprised the remaining 78 accessions. At sub-cluster level association of geographical origin and genetic diversity was clearly evident.

Principal components analysis performed on quantitative traits revealed that the first three most informative components accounted for 51.15% variance. It also presented the characters with greater weightings in each of the three principal component axes. Important characters with greater weightings in principal component axis I included length of flag leaf, length of penultimate leaf, 100-seed weight and number of tillers/plant. Important characters with greater weightings in principal component axis II included days to flowering, length of top internode, days to maturity and length of neck. Important characters with greater weightings in principal component axis III included plant height, height of top node, number of leaves and number of grains/spike. The principal components analysis in general confirmed the groupings obtained through cluster analysis (the PCA scatterplot ordination not shown here).

Multilocation Evaluation of Selected Barley Landraces

The analysis of variance (ANOVA) performed on 30 selected barley landraces (in addition 5 check varieties for Delhi location and two check varieties for Bhowali location also included) and means of various quantitative traits indicate highly significant differences for important quantitative traits, such as, days to maturity, plant height (cm), length of flag leaf (cm), length of main ear, number of tillers/plant, number of grains/ spike, seed weight/ plant and 100-seed weight at both Delhi and Bhowali locations (Table 7).

Mean performance of selected barley landraces revealed that all the accessions flowered and matured early at Delhi location (Table 8) with high tillering capacity, greater plant height, high number of spikelet groups/spike and high seed weight/plant as compared to those at Bhowali location. There was high genotype x environment interaction and the populations behaved differently for quantitative traits at both the locations.

Based on F-test for homogeneity of error mean squares between locations, significant differences were observed between error mean squares of all the common characters recorded at both locations. Therefore, no pooled analysis was possible for these characters.

Cluster analysis using Ward's minimum variance technique classified the accession into four major groups at Delhi location and two major groups at Bhowali location. A fair degree of association of geographical diversity and genetic diversity was revealed. Principal components analysis performed on quantitative traits recorded at both the locations revealed that the first three most informative components accounted for 57.12% and 73.9% variation, respectively, for Delhi and Bhowali location. Important characters with greater weightings in principal component axis I from Delhi location

Table 7. ANOVA Summary for Important Quantitative Traits of Selected Barley Landraces

	DF	Days to maturity	Plant height (cm)	No. of spikelet groups/ spike	No. of grains/ spike	Seed weight/ plant	100-seed weight (g)
Delhi location							
Replicates	1	28.92*	17.20	3.21	0.01	10.63*	0.01
Treatment	34	60.72***	219.18***	29.54***	532.46***	39.38****	1.10***
Error	34	6.34	19.44	1.10	2.632	1.994	0.054
Total	69	33.46	117.84	15.15	263.671	20.546	0.571
Bhowali location							
Replicates	1	0.141	49.879	6.502	1.183	0.244	0.191
Treatment	31	45.74***	206.93***	1.84*	390.36***	12.38***	2.29***
Error	31	4.65	1.96	0.83	0.91	0.30	0.04
Total	63	24.80	103.58	1.42	192.55	6.24	1.15

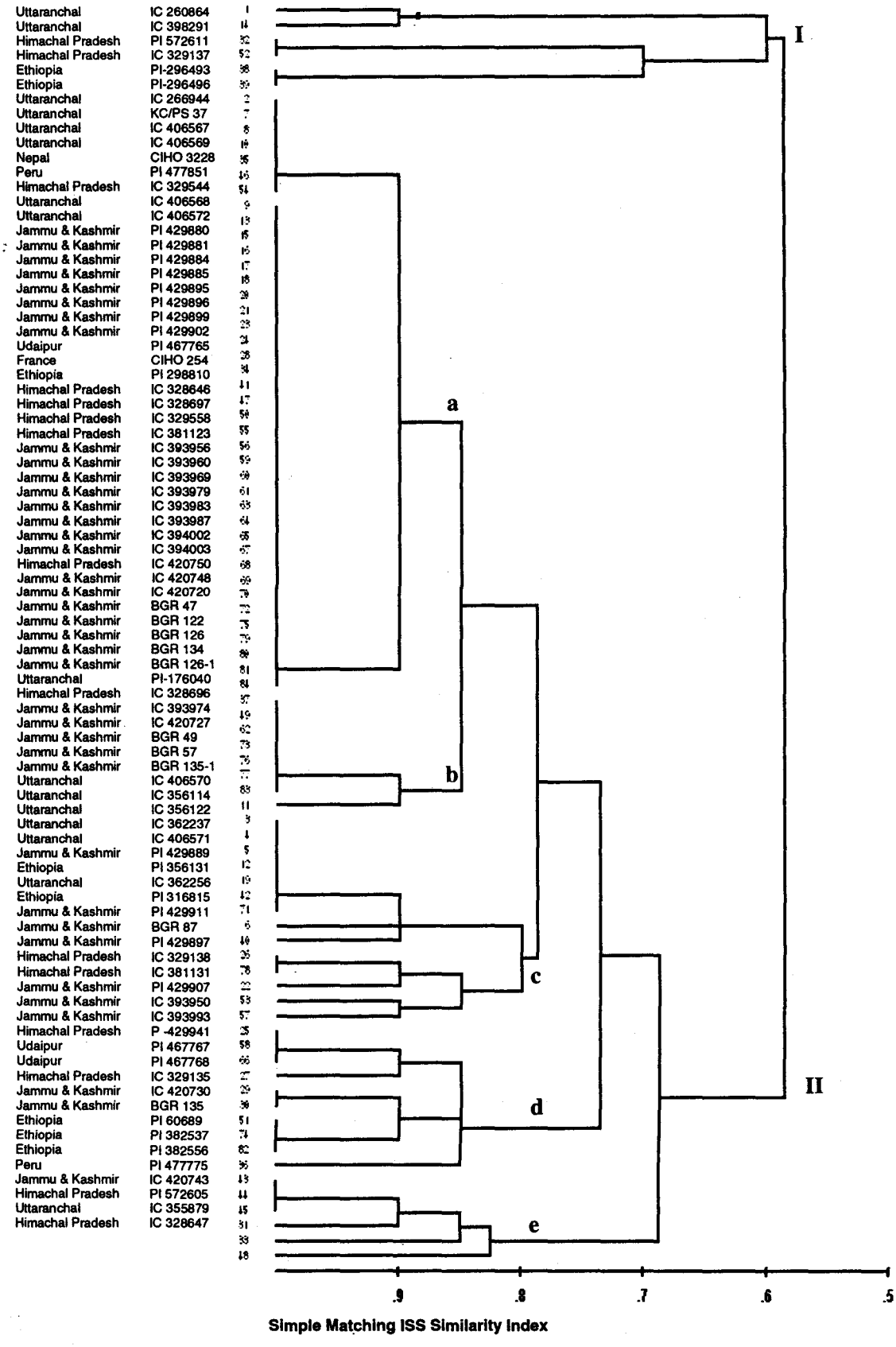


Fig. 2: Weighted average linkage dendrogram of 84 barley landraces based on qualitative traits

Table 8. Mean performance of selected barley landraces at Delhi and Bhowali locations for important quantitative traits

S. No.	Accession*	Days to maturity		Plant height (cm)		No. of spikelet groups/		No. of grains/ spike		Seed weight/ plant spike		100-seed weight (g)	
		D	B	D	B	D	B	D	B	D	B	D	B
1.	IC 260864	123.0	163.5	119.5	96.1	29.0	24.4	75.5	62.0	23.7	3.6	2.3	2.3
2.	IC 266944	126.5	161.5	115.5	93.5	30.0	23.4	69.0	38.0	18.1	4.9	2.2	4.7
3.	IC 355879	126.0	158.0	195.5	78.9	37.5	22.5	27.5	43.6	18.6	4.9	3.9	3.7
4.	IC 356114	118.5	158.0	101.5	78.7	27.0	23.2	66.0	43.1	15.3	4.9	2.5	4.0
5.	IC 356122	119.0	164.0	79.0	96.5	23.5	24.2	65.0	61.5	14.7	3.8	2.8	2.1
6.	IC 362237	117.5	162.0	104.0	95.0	22.5	24.6	60.5	61.0	22.2	4.1	3.0	2.1
7.	IC 362256	125.0	162.5	96.5	96.1	23.0	24.5	60.5	60.5	19.9	5.9	3.3	2.1
8.	IC 398291	120.0	162.5	95.5	96.1	29.5	25.1	65.5	60.5	26.5	3.6	3.5	2.3
9.	IC 406567	115.5	161.5	95.5	96.5	25.5	24.0	60.0	60.0	13.2	3.4	2.1	2.2
10.	IC 406568	113.0	161.5	97.0	95.5	25.5	23.5	65.5	61.5	14.0	3.6	2.0	2.3
11.	IC 406569	115.5	162.5	123.0	96.1	25.5	24.0	65.5	60.0	15.3	3.6	2.5	2.0
12.	IC 406570	118.0	162.5	91.5	94.5	20.5	24.5	66.5	61.5	16.9	3.6	2.4	2.0
13.	IC 406571	123.5	161.5	127.5	96.0	29.5	24.0	71.0	61.5	15.8	3.6	2.9	2.0
14.	IC 406572	116.5	160.0	116.0	72.6	23.5	23.1	60.5	27.7	18.2	6.7	2.9	4.1
15.	PI 467765	132.0	147.5	84.0	82.1	25.5	24.4	70.5	43.1	13.7	6.5	2.7	1.9
16.	PI 429907	119.5	154.5	91.5	80.8	21.5	23.2	72.0	45.1	20.9	8.9	3.9	3.6
17.	PI 429885	116.5	157.0	97.0	93.5	31.0	23.2	70.5	46.7	18.7	6.4	3.2	3.8
18.	PI 429895	136.5	148.0	159.5	78.7	26.5	23.2	74.0	35.1	5.7	3.9	2.9	2.9
19.	PI 429889	116.0	149.0	143.5	79.1	31.0	22.4	89.5	43.7	23.0	8.5	3.7	3.0
20.	PI 429896	117.0	157.5	124.5	80.4	30.0	23.0	67.5	23.3	23.6	6.4	3.3	2.9
21.	PI 429941	113.5	156.0	83.0	60.6	25.5	22.2	65.5	22.1	24.0	5.0	3.7	2.8
22.	CIHO 3228	127.0	163.0	152.5	94.0	26.0	23.4	65.5	37.5	15.9	4.9	3.3	4.9
23.	PI 176040	121.5	160.0	114.5	76.8	30.0	26.4	69.0	61.6	19.9	12.0	3.2	4.6
24.	PI 316815	125.0	158.5	177.0	87.4	27.0	24.1	54.0	43.8	21.5	5.4	3.0	2.7
25.	P 356131	124.5	160.0	181.0	76.4	29.0	24.4	43.5	43.6	23.6	4.9	3.2	4.0
26.	PI 382537	131.0	159.5	173.5	72.6	25.0	24.7	24.5	28.7	19.4	7.2	4.1	4.0
27.	PI 382556	131.0	159.5	130.0	66.0	25.0	25.5	24.0	26.7	19.2	6.2	4.9	5.1
28.	PI 477851	125.0	160.0	206.5	85.4	22.5	22.8	66.5	44.3	20.2	14.1	4.0	4.9
29.	KC/PS 37	123.5	162.0	95.5	94.5	29.5	24.6	65.5	61.5	17.6	3.6	2.8	2.3
30.	PI 572605	121.5	151.5	152.0	89.1	33.0	24.9	28.5	19.6	17.4	4.6	5.0	5.0
31.	DL-36 (Control)	120.0	–	102.0	–	24.0	–	85.0	–	24.2	–	3.7	–
32.	DL-85 (Control)	124.5	–	48.5	–	20.0	–	70.5	–	22.5	–	4.1	–
33.	Jyoti (Control)	119.5	–	95.5	–	23.0	–	95.5	–	23.2	–	3.8	–
34.	VLB 1 (Control)	126.0	163.0	65.5	78.8	30.5	22.8	68.0	48.2	15.3	8.5	3.5	4.1
35.	VLB 60 (Control)	122.0	168.5	70.5	77.5	23.0	24.6	72.5	63.1	27.7	7.2	4.2	3.2
Overall Mean		122.0	159.3	117.3	85.5	26.6	23.9	63.4	46.8	19.1	5.8	3.3	3.3
C.V. (%)		2.1	1.36	4.7	1.64	3.9	3.82	2.6	2.04	7.4	9.48	7.1	6.18
C.D. (5%)		5.1	4.40	11.3	2.86	2.1	1.86	3.3	1.95	2.9	1.12	0.5	0.41

D= Delhi; B=Bhowali; C.V.= Coefficient of Variation; C.D.= Critical Difference; * No local controls were available in naked barleys hence comparison was made with improved local covered controls

included number of tillers/ plant, number of leaves, days to maturity and 100-seed weight and from Bhowali location included flag leaf width, number of grains/ spike, plant height and 100- grain weight. Important characters with greater weightings in principal component axis II from Delhi location included days to flowering, length of flag leaf, length of main ear and length of flag leaf sheath and from Bhowali location included spike length, days to ear emergence, flag leaf length and days to maturity. Important characters with greater weightings in principal component axis III from Delhi location included plant height, height of top node, breadth of flag leaf and number of leaves, and from Bhowali location included number of tillers/ plant, leaf length, 100-grain weight and number of spikelet groups/ spike.

Discussion

Except two populations (intermediate types), all the landraces included in the present study were strictly spring type. The study revealed a wide range of variations among naked barley landraces for all the 18 quantitative traits studied (Table 3). Significant differences for most of the traits were recorded. In general, as per earlier observations (Manjunatha 2004), the naked barleys were poor yielder in comparison to hulled types but in the present investigation many of the naked barley landraces

were found to be superior to hulled controls (commercial varieties). Twelve accessions were very early in flowering (<75 days) than the earliest flowering hulled control Jyoti (75.5 days). The extra early flowering accessions include PI 429881 (58 days) and PI 429884 (58.5 days) assembled from Jammu & Kashmir and PI 429941 (56.5 days) from Himachal Pradesh. Accessions with high spikelet groups/spike include PI 572611 (37.5) from Himachal Pradesh, PI 429902 (33) from Jammu & Kashmir, PI 572605 (33) from Himachal Pradesh, PI 296493 (31.0) from Ethiopia, PI 429885 (31.0) from Jammu & Kashmir and PI 429889 (31.0) from Jammu & Kashmir as compared to the best hulled control VLB 60 (30.5). Similarly, for no. of grains/spike, several accessions viz. PI 429889 (89.5), IC 420720 (84.0) and BGR 47 (84.0) from Jammu & Kashmir, and IC 329544 (82.0) from Himachal Pradesh were comparable to the best hulled check VLB 1 (85.5). Likewise for 100-seed weight, several landraces viz. BGR 135 (5.38g) and IC 420730 (5.1g) from Jammu & Kashmir, and PI 572605 (5.0g) from Himachal Pradesh out performed the best hulled control DL 36 (4.2g). The above findings highlight the potential of naked barleys as important raw material for crop improvement for several of the desired traits.

The comparative statistics for different quantitative traits indicated that there were distinct regional variations for some important traits in barley landraces (Table 11). Landraces from Jammu & Kashmir Himalayas were relatively early flowering. These landraces, in general, also performed better for various yield related traits such as length of main ear, no. of grains/spike, seed weight/ plant and 100-seed weight. The exotic accessions, particularly from Ethiopia, had very high tillering capacity. No. of leaves/plant were also high in Ethiopian landraces.

For the qualitative characters, landraces differed considerably for spike density. Uttaranchal accessions, in general, had lax rachis, a primitive character of Himalayan naked barleys. Populations from Jammu & Kashmir and Himachal Pradesh had dense rachis whereas exotic accessions were intermediate types. Indian barleys were mostly 6-rowed, only three accessions, one from Uttaranchal and two from Himachal Pradesh were 2-rowed. Of the 12 exotic accessions, five were two-rowed, four from Ethiopia (PI 296493, PI 296496, PI 382537 and PI 382556) and one from Peru (PI 477775). Landraces varied little for seed colour. Majority of the landraces from Indian Himalayas had brown seed colour as against pale seed colour of exotic accessions. Two Ethiopian landraces (PI 60689 and PI 316815) had black seed colour (with high protein content). The blue seed colour, typical of Himalayan naked barleys described earlier (Takahashi *et al.*, 1968) was recorded in only 3 accessions, one from Uttaranchal (assembled from >4,000m elevation at Gunji in Pithoragarh), and two from Jammu & Kashmir (from Ladakh region). The pale and black seed coloured barleys with high protein content from exotic sources has great potential for exploitation in crop improvement. PI 382556, PI 382537, PI 356131 from Ethiopia and PI 572611 from Uttaranchal had more than 16% protein content (data on protein content not presented here).

The diversity indices were high for landraces assembled from Jammu & Kashmir followed by Himachal Pradesh, exotic group and Uttaranchal state. The higher diversity in landraces from Jammu & Kashmir may be because of relatively more number of samples in the study from this region. Further, there is high environmental heterogeneity in the state of Jammu & Kashmir and Himachal Pradesh. The higher Himalayan ranges in Jammu & Kashmir (Leh and Ladakh plateau) and Himachal Pradesh (Lahaul Spiti) where naked barley are still grown largely for direct human consumption are cold deserts. In these higher Himalayan ranges there might be greater natural selection in barley due to generally low rainfall. Greater natural selection for extreme cold and low rainfall also resulted in relatively low diversity in barley landraces from these higher Himalayan ranges (>3000 masl) as compared to middle Himalayan ranges (2000-3000 masl). The relatively low diversity in Uttaranchal state was attributed to low cultivation of naked barleys in this region. A few populations of naked barleys are, however, still grown mainly in higher elevations (>3000 masl). Covered barleys, however, are still popular in this region for brewing and animal feed. The naked barley grown in Uttaranchal state, however, seemed more primitive and unique as compared to landraces from Jammu & Kashmir and Himachal Pradesh. Study of population genetic parameters using STMS markers substantiated the presence of more locally common alleles in Uttaranchal populations (unpublished data). The exotic accessions, particularly the Ethiopian landraces were also diverse and unique indicating Ethiopian region as an important

centre of diversity for cultivated barley (Harlan, 1969; Engels, 1990, 1991).

Using quantitative traits, the cluster and principal components analysis (Fig 1,2,3) discriminated accessions in distinct groups based on their geographical origin. Though, at major cluster level the association between area of collection and genetic diversity was not that evident but close perusal of the within-cluster diversity pattern revealed a clear association between the cluster pattern and the topography/altitude of the place of collection. This highlights the regional/microclimatic adaptations of barley landraces from Indian Himalayas. The multivariate analysis therefore provides opportunity to select distinct and suitable types with desired traits for use in crop improvement.

The naked barleys are considered to be wholly oriental and that 80% of the covered forms are of the occidental types (Takahashi *et al.*, 1968). The naked barleys, in general, are far more variable than covered barley for morphological traits. These findings were also corroborated by Murphy and Witcombe (1986), Witcombe and Murphy (1986) demonstrating that covered and naked barleys from the Himalayas differed significantly from each other in a multivariate way. The variation within barley landraces in the Himalayas seems to be regionally distributed. Such regional variability could be due to geographic isolation, founder effects and microclimatic differences between regions.

The multilocation evaluation of selected landraces substantiated the potential of naked barley landraces in crop improvement. Relatively better performance of the landraces at Delhi location (Table 8) highlights the wider adaptability of Himalayan barleys for large scale cultivation even in non-conventional areas. The differences for various quantitative traits across locations, moreover, revealed high genotype x environment interaction. The multivariate analysis (cluster and PCA) performed separately for Delhi and Bhowali location trial data provides the opportunity to select suitable type of wider adaptability for use in crop improvement. The clustering pattern at Bhowali location (dendrogram not shown here) indicated high similarity among Uttaranchal accessions and their distinctiveness from accessions of other regions. This provides the opportunity of introducing desired landraces from other regions in the cropping systems of Uttaranchal state. Detailed population genetic study using molecular markers offers a very effective means of applying the knowledge gained to practical plant breeding (Venkatesan *et al.*, 2005).

The present study, therefore, highlights the importance of Himalayan naked barleys for research, marketing and conservation interventions. The use of quantitative characters which were scaled in an arbitrary way seems to be justifiable and useful as the barley accessions show considerable variation within and between administrative regions for these characters and they are in general of more interest to the plant breeder than the discrete qualitative characters (Engels, 1991). The fact that the naked barleys from the Indian Himalayas performed exceedingly at par with the commercial hulled cultivars (used as controls) at Delhi location, they are of potential utility as source of several desired traits including resistance/tolerance to various stresses and quality. Furthermore, the genetic differences between covered and naked barleys are potentially relevant to breeding programmes in that the variability created through hybridization of the contrasting forms could be exploited.

Acknowledgements

The authors are thankful to the Director, NBPGR for providing facilities for this study. We also thank the NBPGR scientists who helped in collecting the naked barley landraces from various administrative regions and exotic sources. The scholarship provided to the senior author (KV) by Indian Council of Agricultural Research for Master's degree is gratefully acknowledged.

References

Aberg E (1938) *Hordeum agriocrithon* nova sp., a wild six-rowed barley. *Ann. R. Agric. Col. Swed.* **6:** 159-216.

Bekele E (1983) A differential rate of regional distribution of barley flavanoid patterns in Ethiopia, and a view on the centre of origin of barley. *Hereditas* **98:** 269-280

Engels JMM (1990) The genetic diversity in Ethiopian barley in relation to altitude. In: Iyama S and Takeda G (eds), proceedings, 6th International Congress of the Society for the Advancement of Breeding Research in Asia and Oceania, pp. 107-110. SABRAO, Tsukuba, Japan.

Engels JMM (1991) A diversity study in Ethiopian barley. In: Engels JMM, Hawkes JG and Worede Melaku (eds) Plant Genetic Resources of Ethiopia. Cambridge University Press, p. 131-139.

Harlan JR (1969) Ethiopia: a centre of diversity. *Economic Botany* **23:** 309-14.

Harlan JR (1995) Barley. In: Simmonds NW (ed) Evolution of crop plants. 2nd edn. Academic Press, London, p 140-417.

Harlan JR, de Wet JMJ and Stemler ABL (1976) Plant domestication and indigenous African agriculture. In: Harlan JR, de Wet JMJ and Stemler ABL (eds) Origin of African plant domestication. Mouton, The Hague, Netherlands.

IBPGR (1982) Barley descriptors. International Board for Plant Genetic Resources, Rome.

Liu ZW, Biyashev RM and Saghai-Maroof MA (1996) Development of simple sequence repeat DNA markers and their integration into a barley linkage map. *Theor. Appl. Genet.* **93:** 869-876.

Manjunatha T (2004) Assessment of genetic diversity in barley (*Hordeum vulgare* L.) landraces from high altitude areas of western Himalaya using morphological and molecular characterization data. M.Sc. Thesis, Indian Agricultural Research Institute, New Delhi, 104p.

Maxted N, Hawkes JG, Ford-Lloyd BV and Williams JT (1997) A practical model for *in situ* genetic conservation. In: Maxted N, Ford-Lloyd BV, Hawkes JG (eds), *Plant Genetic Conservation: The In Situ Approach.* Chapmen & Hall, London, p. 339-367.

Molina-Cano JL, FraMon P, Salcedo G, Aragoncilo C, Roca De Togores F and Garcia- Olmedo F (1987) Morocco as a possible domestication centre for barley: biochemical and agro-morphological evidences. *Theor. Appl.Genet.* **73:** 531-536

Murphy PJ and Witcombe JR (1986) Covered and Naked barleys from the Himalayas. 1. Evidence of multivariate differences between two types. *Theor. Appl. Genet.* **71:** 730-735.

Negassa M (1985) Patterns of phenotypic diversity in an Ethiopian barley collection, and the Arussi-Bale Highland as a centre of origin of barley. *Hereditas* **102:** 139-50

Salamini, F., Ozkan, H., Brandolini, A., Schafer-Pregi, R. and Martin, W. 2002. Genetics and geography of wild cereal domestication in the near East. *Nat. Rev. Genet.* **3:** 429-441.

Sneath PHA and Sokal RR (1973) Numerical Taxonomy. Freeman, Sanfrancisco, CA

Takahashi R (1955) The origin and evolution of cultivated barley. *Adv Genet.* **7:** 227-266.

Takahashi RJ, Hayashi T, Hiura U and Yasuda S (1968) A study of cultivated barley from Nepal, Himalayas and North India with special reference to their phylogenetic differentiation. *Ber. Ohara Inst. Landwirtsch. Biol. Okayama Univ.* **14:** 85-122.

Taketa S, Kikuchi S, Awayama T, Yamamoto S, Ichii M and Kawasaki S (2004) Monophyletic origin of naked barley inferred from molecular analysis of a marker closely linked to naked caryopsis gene (nud). *Theor. Appl. Genet.*, **108:** 1236-1242.

Venkatesan K, Bisht IS and Bhat KV (2006) Diversity in Himalayan hull-less barley (*Hordeum vulgare* L.) landraces using AFLP and STMS markers. *Indian J Plant Genet Resourc* (In press).

Witcombe JR and Murphy PJ (1986) Covered and Naked barleys from the Himalayas. 2. Why do they differ from each other so extensively? *Theor. Appl. Genet.* **71:** 736-741.

Collection of Diversity in Castor (*Ricinus communis* L.) Germplasm from Parts of Andhra Pradesh

N Sunil, A Ashok Kumar*, P Ashokavardhan Reddy and KS Varaprasad**
National Bureau of Plant Genetic Resources, Regional Station, Hyderabad
**Regional Agricultural Research Station, Palem, ANGRAU, Mahaboobnagar dist., Andhra Pradesh*
*** Directorate of Oilseeds Research, Rajendranagar, Hyderabad*

A crop specific exploration was conducted to collect diversity in castor *(Ricinus communis* L.) from different parts of Andhra Pradesh having a tradition of growing castor as sole crop, trap/shade crop and as backyard plant. A total of 122 accessions including landraces and primitive cultivars were collected. Variability was observed for different characters viz., bloom (waxy coating on aerial parts of plant), stem coluration, plant height and node numbers, nature and size of raceme, spike shape and compactness and type, size and dehiscence nature of capsules. Probable sources for resistance/tolerance to wilt, botrytis, sucking pests besides early maturing types, have been identified based on phenotypic characters. The collected germplasm with the wide diversity needs to be further characterized and evaluated for utilization in improvement programmes.

Key words: Castor, Diversity, Andhra Pradesh, Germplasm

Castor (*Ricinus communis* L.) is believed to be a native of Tropical Africa. India is considered as a secondary centre of diversity/origin of castor. It is an important oilseed crop of India. India is the largest producer (7.7 lakh tonnes.) and has a monopolis in the international castor oil trade (Hegde, 2002). The castor oil export brings a sizable amount of foreign exchange into the country for utility in paints, soaps, lubricants, detergents, printing inks, pharmaceuticals and cosmetic industries. It is mainly cultivated for seeds, which yield fast drying; non-yellowing oil upon dehydration used mainly in industry and medicines. Castor seeds contain 35-55 per cent of oil having 85-95 per cent ricinoleic acid.

The centre of origin of castor and Indo-Gangetic plains are the centres of variability (Kulkarni and Ramamurthy, 1977; Anjani *et al.*, 1999 and Duhoon *et al.*, 1996). The species is common throughout the country in all climates ranging from tropical, sub-tropical to temperate regions with high concentration of diversity in drier parts of the tropical climates.

To effectively tap the varied uses of castor, availability of diverse germplasm that harbours good traits *viz.*, production potential, tolerance/resistance to biotic and abiotic stresses is essential. Evaluation of castor germplasm in the hot-spot areas has resulted in identification of number of resistant/moderately resistant accessions to fusarium wilt. However, explorations in new areas to collect the diverse germplasm sources harbouring resistance to botrytis gray rot and fusarium wilt, the two major biotic challenges in castor cultivation at present (Padmaraju and Ashok Kumar, 2002) are necessary. Efforts were made to collect, conserve and study the variability from the entire country (Anjani *et al.*, 1999, Duhoon *et al.*, 1996). An exploration was undertaken to augment germplasm from this unexplored area and to find out sources of resistance to botrytis gray rot and wilt, was undertaken in parts of telangana region and coastal districts of Andhra Pradesh under NATP-Plant biodiversity project during December 2001. The material has been deposited in the National Gene Bank (NGB) NBPGR, New Delhi for conservation.

Materials and Methods

The survey was undertaken in four districts of Andhra Pradesh *viz.*, Warangal, Khammam, West Godavari and Guntur, with varied agro-ecological system and having a tradition of growing castor as a shade crop in ginger and turmeric fields. The districts Warangal and Khammam form part of northern Telangana zone, and receive an annual average rainfall of 900-1150 mm from the south west monsoon with the maximum and minimum temperatures of 32°C - 37°C and 21°C - 25°C respectively. The region is predominated by red soils. The districts West Godavari and Guntur (under Krishna–Godavari Zone) receive an average rainfall of 800-1100 mm with maximum and minimum temperatures of 32°C-36°C and 23°C-24°C with predominantly alluvial, red and black soils. Keeping in view the collection gaps in the representative diversity of castor a survey team of breeders and botanists focused on collection of diversity in castor after procurement of the mandal wise information

on area under castor cultivation from Directorate of Statistics and Economics. The research stations of Acharya NG Ranga Agricultural University (ANGRAU) at Warangal, Malyal and Maruteru were consulted for identifying potential areas for castor germplasm collection during the survey. The altitude of the area surveyed (30-460 m) and route map of the survey were depicted in (Fig). Mature capsules/heads/seeds as per the availability were collected following random (Hawkes, 1976) and biased (Harlan, 1975) sampling methods to collect specific genotypes (Sinha, 1981).

Results and Discussion

A total of 122 castor germplasm accessions comprising

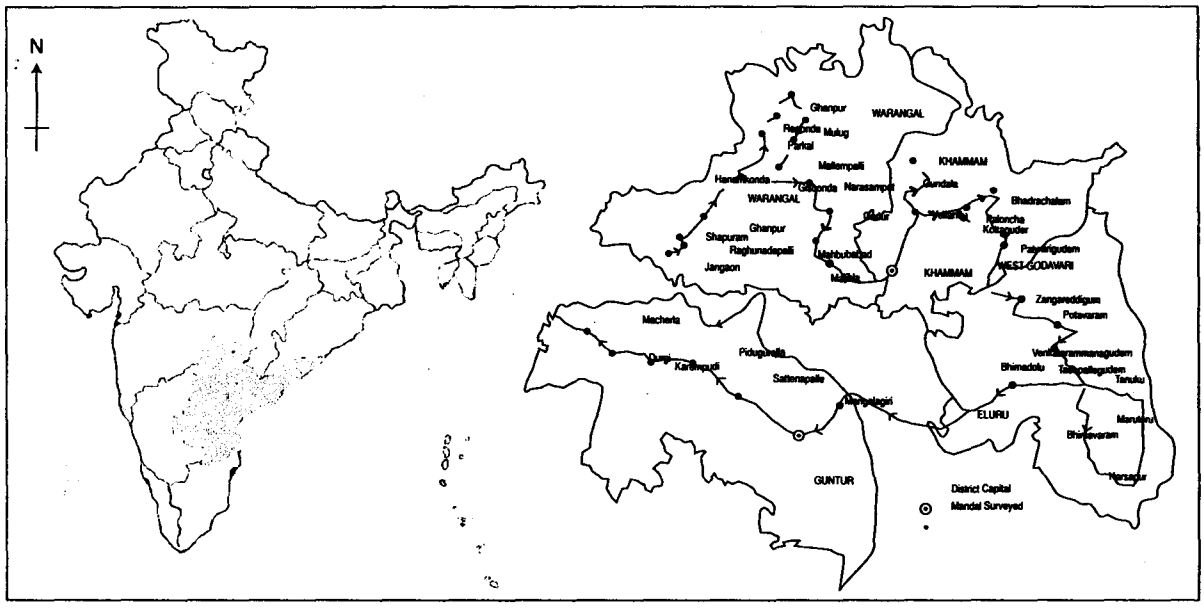


Fig: Route map of the survery undertaken for collection of castor germplasm in Warangal, Khamman, West Godavari and Guntur districts of Andhra Pradesh

of 63 from the cultivated fields being grown as a trap and shade crop in cotton and ginger fields as a trap and 59 from wild and semi wild areas along roadsides and wastelands were collected from 66 villages in four districts of Andhra Pradesh. The castor collections exhibited variations in stem colour (green, red and pink),bloom (zero, single, double and triple bloom), node number (low and high), plant height (dwarf,medium and tall), nature of raceme (partially female, female raceme and male raceme), spike size (small, medium and large) and shape of spike (cylindrical and triangular), compactness of spike (compact and loose), nature of capsule (spiny and non-spiny) and dehiscence of capsule (dehiscent and non-dehiscent).

Three distinct plant types *viz*., tall and woody (68%), medium tall (26%) and dwarf types (6%) were observed among the collections. Tall and woody types grown as a border crop on crop bunds were found free from wilt and these may harbor sources of resistance/ tolerance to wilt (Table 1). Medium and dwarf types of castor were grown mainly as an inter crop in cotton and as a shade crop in turmeric and ginger. Colour of the stem varied as red (64%), green (30%) and pink (6%) among collective germplasm. Green stem character is highly heritable and is used as distinguishable morphological feature in varietal identification (Anonymous, 2004).

The presence of bloom, is an important character towards resistance to sucking pests, of the collected accessions. 20% had zero bloom (no waxy coating on aerial parts), 19% single bloom (waxy coating on stem and peduncles only), 53% double bloom (waxy coating on stem, peduncles and lower portion of of the leaf) and 16% had triple bloom (waxy coating on stem, peduncles, lower and upper portions of the leaf). In castor, jassid infestation is the lowest in accessions with triple bloom nature while that of white fly and thrips is lowest in accessions with zero bloom (Table 2). There is excellent variability available in the present collections for bloom nature.

The accessions collected varied in node number, wherein 17% of the accessions had a very high node

Table 1. Tall and Woody Accessions–Probable Sources for Wilt Tolerance

Traits	Accessions
Tall and woody	IC-329684,IC-329687,IC-329692, IC-329693 IC-329695,IC-329696,IC-329697,IC-329700, IC-329701,IC-329710,IC-329713,IC-329720, IC-329721,IC-329722,IC-329731,IC-329738, IC-329740,IC-329749, IC-329750,IC-329751, IC-329753,IC-329755,IC-329756,IC-329758, IC-329759,IC-329766,IC-329768,IC-329777, IC-329778, IC-329782,IC-329787

Table 2. Germplasm lines with zero and triple bloom-probable sources for white fly and Jassids tolerance receptively

Trait	Accessions
Zero bloom	IC-329668,IC-329684,IC-329704,IC-329714, IC-329733,IC-329740,IC-329741,IC-329742, IC-329758,IC-329760,IC-329761,IC-329762, IC-329763,IC-329767,IC-329770,IC-329773, IC-329776,IC-329776,IC-329781,IC-329782 IC-329783,IC-329784,IC-329785,IC-329788, IC-329790
Triple bloom	IC-329676,IC-329679,IC-329680,IC-329685, IC-329687, IC-329694,IC-329707,IC-329718, IC-329737,IC-329744,IC-329747,IC-329748, IC-329750,IC-329789,IC-329791,IC-329793, IC-329797, IC-329800, IC-329801

number, while 10% of accessions had low node number (Table 3). The germplasm accessions with low node number were of dwarf types with early maturing nature. Early maturity is highly desirable in castor to fit in to various cropping systems. In low rainfall conditions unequal distribution and early cessation, early maturing genotypes are desirable. Moreover early maturing genotypes escape the heavy incidence of botrytis grey rot which generally appears late in the season.

The size and nature of the spike, *viz.*, very long (90-100 cm) with 90 per cent female flowers showed direct positive relation with yield (Raghuram Reddy *et al.*, 2000) in castor. In the collections, 10% showed long spike nature, which is highly desirable.

The loose spikes prevent free movement of capsule borer and spread of *botrytis grey rot,* is an important character preferred by plant breeders. 65 per cent of the accessions exhibited loose spike nature. In most of the long duration varieties of castor the presence of a non-dehiscent capsule is beneficial, 80% of the accessions had non-dehiscent capsules. In the castor

Table 3. Accessions having low node number-Probable early maturing types

Trait	Accessions
Low node	IC-329681,IC-329683,IC-329685,IC-329699 IC-329719,IC-329748,IC329769, IC329773, IC-329774, IC-329797

Table 4. Non-spiny and loose spikes-probable sources for grey rot tolerance

Traits	Accessions
Non - spiny and loose spikes	IC-329669,IC-329694,IC-329711, IC-329717,IC-329792,IC-329796, IC-329798,IC-329799,IC-329800, IC-329801

germplasm accessions collected 90% of the capsules were spiny and 10% non-spiny. Non-spiny entries generally showed low incidence of botrytis gray rot, e.g. 48-1, Kiran. Presence of high humidity is very congenial for infection and spread of Botrytis fungus. In non-spiny entries as spines on capsules are absent the water drops are not retained on capsule thus the microclimate is not suitable for the growth and spread of fungus. Accessions having loose sipke and non spiny capsules are given in table 4. Accession having pink coloured capsules (IC-329696) were identified as genetic marker in varietal identification programmes.

All the above desirable characters observed in the collected castor germplasm accessions will be of immense value in castor improvement programmes. However, the entries have to be screened further in wilt sick plots (for wilt) and culture room conditions (for botrytis gray rot) to identify promising sources of resistances/tolerance.

Acknowledgements

The authors are thankful to Dr BS Dhillon, Farmer Director, National Bureau of Plant Genetic Resources, New Delhi, Dr. SK Pareek, Principal Investigator, NATP (PB) and Dr Ravi Khetarpal, Head, Division of Plant Quarantine, NBPGR New Delhi for their help and encouragement.

References

Anjani K, WS Yadav and SS Duhoon (1999) Collecting castor (*Ricinus communis* L.) germplasm in north western India. *Plant Genetic Resources Newsletter*, **120:** 48-51.

Annual Progress Report. 2000-2001 Castor. Directorate of Oilseeds Research, Hyderabad. 15p.

Anonymous (2004) Morphological, chemical and Electrophoretic descriptors for Castor (*Ricinus communis L.*) NSP (crops) IARI New Delhi. Technical bulletin no.25 Pp.2.

Bennett E (1970) Tactics of Plant Exploration. In *Genetic Resources in Plants*. OH Frankel and E Bennett (Eds.) Blackwell, Oxford, pp 157-179.

Duhoon S, K Anjani and MN Kooper (1996) Collecting castor (*Ricinus communis* L) and *Jatropha* germplasm in Indo-Gangetic plains. *Indian J Plant Genet Resourc* **9(1):** 171-174.

Harlan JR (1975) Population Structure and the effects of Breeding System. In *Crop Genetic Resources for Today and Tomorrow*. OH Frankel and JG Hawkes (Eds.) Cambridge University Press, London, p 111-115.

Hawkes JG (1976) Sampling Gene Pools. Proc. NATO Conf. Conservation of Threatened Plants Ser. 1 Ecology, Plenum, London.

Hegde DM (2002) Castor research and development in India. Paper presented at National workshop on "*Castor production technology for drylands*", February 25-26, 2002. PP. B1-11.

Kulkarni LG and GV Ramanamurthy (1977) *Castor. Indian Council of Agricultural Research*, New Delhi, India.

Padmaraju A and Ashok Kumar A (2002) Research thrusts for Castor in Andhra Pradesh. Paper presented at National Workshop on "*Castor production technology for Drylands*" February 25-26, 2002. PP A1-2.

Popova GM (1930) Castor Oil Plant. Lenin Academy Agricultural Science Institute. *Applied Botany and New Culture*, Leningard

Raghurama Reddy P, GR Maruti Sankar, M Vanaja, C Hanumantha Rao, S Venkateswarlu and JD Eastin (2000) Studies on genetic parameters in castor (*Ricinus Communis* L.) under irrigated and rainfed conditions in an alfisols. *Indian Journal of Dry Land Agricultural Research and Development* **15(1):** 73-77.

Sinha GC (1981) Gene pool sampling in tree crops In: *Plant Exploration and Collection*. KL Mehra, RK Arora and SR Wadhi (Eds) National Bureau of Plant Genetic Resources, New Delhi.

Indigenous Knowledge and Ethnobotany Associated with Saffron (*Crocus sativus* L.) in Kashmir

AK Singh, Vandana Tyagi and Deep Chand
Germplasm Exchange Division, National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012

India is amongst the richest ethnobotanical treasure in the world, which must be fully documented, utilized and conserved. Dried stigma of Saffron (*Crocus sativus* L) flower is used for different purposes. It has got more than 85 species, distributed from Mediterranean region to Indian subcontinent. During an exploration in the Kashmir valley, information on indigenous knowledge and ethnobotany associated with saffron were gathered along with diversity collection. Data were also collected on socioeconomic status of the growers. Information gathered revealed that it is used as a spice, food additive, cosmetic, coloring agent and medicine in different systems (Ayurveda, Unani, Tibestian and Chinese system) and in religious functions. Indigenous uses of saffron are briefly discussed as described. Being the most expensive spices, quality and adulteration aspects are also addressed in this paper.

Key words: Indigenous Technical Knowledge, Ethnobotany, Saffron (*Crocus sativus*), Exploration, Landraces

Introduction

Saffron (*Crocus sativus* L.) is probably the most precious and most expensive plant species in the world. Its filaments or threads are actually the dried stigmas of the saffron flower. The quality of saffron is dependent on its colouring power (crocin concentration), odour (safranal) and taste (picrocrocin). The best quality saffron has a high safranal content. Essential oils are responsible for its therapeutic properties (Sujata *et al.*, 1992). The name saffron comes from Arabic word, where the spices are known as Zafran. Eastern Greece is said to be the origin and today it is cultivated from the Western Mediterranean (Spain) to India (Kashmir). Saffron is known by various names in different Indian language like Keshar in Hindi, Kunkumam in Sanskrit, Kunkumppu in Tamil Kunkumakesari in Kannad, Kunkumappuvu in Malayalam and Kunkumapuvvu in Telugu. Saffron is one of the ancient plant species in the world. *Crocus sativus*, known as a wild plant, is considered to be a mutant that has derived from *Crocus cartwrightianus*. The cultivated clone was probably selected for its triploid vigour and extra long stigmas and has been maintained in cultivation for over 3000 years. Saffron (*Crocus sativus* L.), a member of large family Iridaceae, comprising some 85 species is well adapted to cold winter with autumn–winter–spring precipitation and warm summer with very little rainfall. The plant being in active growth from autumn to late spring and survives the summer drought, below ground by means of compact corm. Above ground growth commence with the onset of autumn and flowers almost immediately producing their leaves and flowers. Saffron is a bulbous, autumn-flowering, perennial of the iris family (Dhar *et al.*, 1988). The flowers have three bright, orange-red stigmas, which are the true saffron. The three stigmas are handpicked from each flower, spread on trays, and dried over charcoal fires for use as a food flavouring and coloring. About 1,65,000 to 1,75,000 flowers are needed for producing one kg of saffron. Saffron contains 0.5 to 1.0 per cent essential oil, the principal component of which is picrocrocin. The colouring matter of saffron is crocin only. In India, its commercial cultivation is mainly confined to Kashmir valley, about twelve kilometer from Srinagar, near Pampore on the banks of the Vitasta (Jhelum) behind the small mountains. In addition to Pampore, saffron is also grown in sizeable area in Kishtwar valley of Doda district, Jammu division (Nauriyal and George,1977). Though the area under saffron cultivation dramatically fluctuates in India i.e. in the state of Jammu and Kashmir and varies from 240 ha to 2440 ha. However, the saffron trade takes place in India from Pampore, Srinagar and New Delhi. This study was undertaken with an objective to gather the Indigenous knowledge, ethnobotany and indigenous technical knowledge (ITK) associated with saffron crop.

Materials and Methods

Plant exploration is the quickest instrument to provide genetic diversity for crop improvement programmes. To collect *Crocus* germplasm available in the Kashmir valley, an exploration was conducted from August 16 to 19, 2001. In this area local varieties of saffron are under cultivation and their names are based on the name

of a village, person, mountain, river etc. This exploration was a part of National Agricultural Technology Project on Plant Biodiversity, conducted by National Bureau of Plant Genetic Resources, Regional Station, Srinagar, Jammu and Kashmir. Area surveyed and explored included Srinagar (Sanatnagar and Rangreth) (34N 06 74E 48), Charar-e-Sharif (74E 46 33N 52) and Ananatnag (33N 44 75 E 09). During the exploration and collection of saffron germplasm, we also collected information on indigenous knowledge, ethnobotany and indigenous technical knowledge associated with saffron crop along with socioeconomic status of saffron growers of Kashmir valley. For the purpose of acquiring information as mentioned above, we prepared a questioner for all possible information regarding their knowledge on saffron uses, cultivation practices, major problems faced by growers, their holding etc. In the process of gathering information, we interacted with more than 100 farmers, which were actively engaged in saffron cultivation or trade in one or other ways.

Results and Discussion

The area surveyed is famous for saffron growing. The details of Saffron germplasm collected during the exploration and indigenous technical knowledge (ITK) collated from growers are presented below.

i) Diversity in Saffron Germplasm

A total of 28 accessions were collected comprising 11 accessions from Pampore, 5 accessions from Charreshareef, 6 accessions from Khannabal and 6 accessions from Rangreth. Maximum corm weight was 28 g and minimum 12 g, both the accessions belonged to Pampore. Location wise Pampore has got maximum diversity in relation to corm weight. However, we found variation in size (diameter) and shape of the corm ranging from near round to oval /oblong. Colour of pericarp (skin) also exhibited diversity that ranged from light brown to light red.

ii) Socioeconomic Status of Saffron Growers

Although the terrain of Jammu and Kashmir is highly diversified, only a small portion of its total area of approximately 85,000 square miles (220,000 square km) is well suited to human settlement. Of particular note is the fertile Valleye of Kashmir, a valley roughly 80 miles long and up to 35 miles wide (130 × 55 km) astride the upper Jhelum River. This densely settled and surpassingly beautiful area lies at an average elevation of approximately 5,500 feet (1,675 m). In normal times, it supports an economy based on tourism, handicraft industries and intensive agriculture. The area, which is not under cultivation, support rich stands of mainly coniferous forest. According to the 2001 census, the population of Indian Kashmir is 10, 069,917 with a density of 256 persons per square mile.

iii) Saffron Soils and Major Constraints

Saffron is grown on marginal and poor soil by small and marginal farmers. As per information received from farmers, lack of improved varieties is single major constraint resulting in poor production and productivity and fluctuating area under this crop. Lack of mechanization is another problem associated with this crop, as majority of operation is done manually.

iv) Indigenous Technical Knowledge (ITK) Gathered from Farmers

The fact is that Indians in general are crazy about this exotic spice. In India, to serve dishes laced with saffron is regarded as mark of honour to the guest and have become the norm rather than an exception. Indigenous uses of saffron in different parts of world are mentioned here first by people of Kashmir then other parts of India and in the last brief account of some other countries, which also consume saffron since long time (Sharma 1999). Some useful Indigenous Technical Knowledge (ITK) collected during the exploration is presented here. The use of saffron is grouped into two category i.e. local medicine, other uses and in the preparation of different dishes, which are made on special occasion. A few of them are listed here.

a) Indigenous Uses

Use of Saffron in Kashmiri Local Medicine and Other Uses

- As a facial cream for decolouring of skin
- To cure skin disease, fever
- Colouring agent
- Used in rituals and religious functions
- To prepare stimulant and tonic
- Useful in bronchitis, cold and cough
- Carminative and diaphoretic
- Saffron is sprinkled on the various occasions
- Above ground vegetative part is used as fodder

Use of Saffron in Different Indian Dishes

This spice is also widely used in sweet recipes like kheer, rasmalai, Indian yoghurt drink (lassi), butter lassi

(makhaniya lassi) milky rice or vermicelli puddings and sweet custard-like desserts from India. It is an essential commodity in high quality milk/ cream based confectioneries and Mughlai dishes in India wherein it imparts a rich colour and distinct flavour. It flavors baked goods and is one of the ingredients in the liqueur, Chartreuse. It is used in sedatives, as an antispasmodic and for flatulence. It is also used in perfumes and dyes. (Mehta *et al.*, 2002). In Kashmir it is widely used for preparation of ***Kehawa:*** A drink prepared for stimulant, in which saffron is one of the major constituents;***Tea:*** Saffron is also a chief ingredient of tea of high esteems; ***Wajwan:*** A group of non-vegetarian dish prepared to serve during the marriage party in Kashmir, in which saffron is one of the major spices; ***Sewai:*** A sweet preparation in which saffron is also used prepared during 'Id' festival; ***Biryani:*** A non-vegetarian dish in which saffron is principal constituent of spices.

b) Ethnobotanical Uses

Due to the large number of experienced users in India and the frequency of use also being very high, the consumer in India is very discerning. Saffron finds a variety of uses in India and abroad. In India, it is used as herb in Ayurvedic Medicines, which heal a variety of diseases ranging from Arthritis to Impotence and Infertility. Here is the list of a few uses where saffron is put to medicine as a cure and as a preventive. The list is just to give an idea of the usefulness of this exotic herb (Maheswari 1996; Sharma 1999).

c) Saffron in Indian Indigenous Medicine System

Saffron in Ayurveda

- Curing Asthma and Cough
- Useful in Colds
- To treat Alcoholism
- To treat Acne and Skin Diseases
- To prepare Chyawanprash

Saffron in Unani Medicine

- Used in medicines that reduce inflamation
- For treatment of enlarged liver and infection of urinary bladder and kidneys
- As an ingredient in recipes useful in menstrual disorders
- For strengthening the heart and as nervine tonic
- As a diuretic if soaked overnight in water and administered with honey
- Pounded with clarified butter (ghee) it is used for treating diabetic patients.

v) Documented Properties and Actions

There is a long history of the use of saffron in the Indigenous medicines of many cultures. As a result of a variety of recent scientific investigations, there is now convincing evidence for the biological activity of saffron and its constituents. One of the activities of saffron, which has the greatest potential in medical applicability, is its ability to inhibit carcinogenesis. A number of recent studies have shown that saffron extract possesses antitumor activity against transplanted tumors and anticarcinogenic activity against chemically induced carcinogenesis *in vivo*, and cytotoxic effects on tumor-derived cells *in vitro*. These findings have raised the possibility that natural saffron and/or some of its constituents might be used as alternative antitumor or anticarcinogenic agents, either alone or in combination with synthetic substances having anticancer activity (Nair *et al.*, 1996 and Nair *et al.*, 1992). The recent scientific findings on the biological activities of saffron, for its therapeutic activity against a number of diseases, provide strong indications that saffron and/or its components may be useful agents in modern medicine.

Saffron Properties Documented in Indian Ancient Literature:

A brief account on saffron properties and their uses in Indian medicine system and other occasional uses documented in different Indian ancient literature are cited here.

Kunkumam ghusrnam raktam kashmiram piakam varam

Sankocham pisunam dhiram vahnikam sonitabhidham ***(Bhavaprakasam)***

Kunkumam katukam tiktam usnam slesmasamirjit

Varndrishtishirorogavisahrt kayakantikrt ***(Dahnvantarinighantu)***

Snigdhosnam vatasamanam varnakrddehagandhakrt

Kunkumam rasatastiktam kasayam krminasanam ***(Madanadinighantu)***

vi) World Wide Indigenous Uses of Saffron

It is known to have aphrodisiac properties and is widely used in Asia and the Middle East as such. Chinese and Tibetan system of Medicine also find many uses of this exotic herb. Ancient Greeks demonstrated the infinite wealth of the gods by describing *Zeus* having a bed of saffron. Knossos on Crete had frescoes of

a man gathering saffron. The Egyptians cultivated vast fields of it to mix with honey, and Romans sought saffron as a curative and aphrodisiac. Wealthy Romans sprinkled their marriage beds with saffron. In the Middle Ages, saffron traveled across North Africa, along with Islam, into Spain. Medieval Spain quickly became the center of saffron production. Not only was saffron used as a medieval flavoring, but scholars as notable as Roger Bacon claimed that saffron would defray the effects of aging and add to the joy in one's life. A native of the Mediterranean, saffron is now imported primarily from Spain, where Moslems had introduced it in the 8th century along with rice and sugar (Maguelonne, 1992).

vii) Saffron in Western Medicine

In the western world it is used primarily as a spice. But it is also discovering its uses as a health tonic that naturally does not have side effects. About 50 mg of Saffron dissolved in a glass of 200 ml milk and a spoonful of sugar makes a very tasty drink that is also a health tonic. A regular intake of this every day for a period of time enables the body to build resistance against a lot of common diseases such as Asthma, and Common colds as claimed by Ayurvedic Practitioners (Abdullaev 1993 and Basker and Negbi, 1983). It is essential to have a regular intake for it to be effective.

viii) Saffron Varieties in Indian Ancient Literature

Saffron is cultivated by means of corm and as such no commercial variety has been released by any agency /research organization. Bhavaprakasham has mentioned three varieties of Indian saffron (kunkumam) viz., Kashmir, Baluchistan and Persian, which are based on geographical region. Of which the Kashmir variety is reported to be superior one (Sala 1994).

ix) Saffron Varieties in Modern Trade

As such no variety has been released for cultivation. It is propagated by vegetative means. But in world trade there are some varieties. These varieties are totally based on geographical boundaries. A few of them, which have wide impact in saffron trade, are discussed briefly (Negbie1999).

Kashmiri Mogra Cream Saffron: Saffron of Indian (ie. Kashmir) origin is acknowledged to be the finest in the world. The dark red color and long perfect strands are as beautiful as they are colorful and flavourful. It is very rarely available outside India because of its high cost and the fact that Indians hardly leave any to be exported, consuming nearly the entire produce. India is the largest consumer of Saffron having knowledge of its benefits since ages. Thus, the high standard of its quality is not very well known outside the Indian sub-continent. Kashmir Mogra Cream Saffron is truly wonderful.

Spanish Coupé: Saffron is the top grade of the Spanish Saffron crop. Extra hand labour is used to remove every bit of the yellow saffron style material, leaving 100% beautiful pure red saffron threads -hence the name: coupé means, "to cut", as in cutting off all the yellow bits. Spanish Coupé Saffron is a truly excellent crop, especially nice for the Indigenous Spanish dishes.

Spanish Superior: It is the most widely available saffron and is a very good crop. Spanish Superior Saffron has a bit of the yellow style material left attached to some of the saffron stigmas, so it is not quite as strong as Spanish Coupé or Kashmir Indian Saffron.

Iranian Saffron: In Iran the style is still attached to the stigmas, they are almost always in a loose tangle. The main difference being in the yield of stigmas which is about 75%.

Mancha Saffron: Common brand name for Spanish saffron grown in the five provinces of the La Mancha region of southeastern Spain. This name should not be taken as a direct reference to the quality of the saffron as coloring strength is the only way to measure saffron quality scientifically.

American/ Mexican Saffron: Refers to the thistles of the flower heads of the safflower plant, which grows wild all over the US, and Mexico. The red-orange thistles, produce a slight yellow dye but no saffron flavor or aroma in cooking or baking. Those unfamiliar with saffron's real qualities sometimes mistake these thistles, sold very inexpensively in packages sometimes labeled "saffron" for saffron stigmas.

x) Commercial Saffron

No one can dare to ignore saffron easily without amazed by its uniqueness in the spice world. Saffron has an aroma and flavour which cannot be duplicated, and a chemical make-up which, when understood, helps the chef or home cook to know how to best release that flavour and aroma in cooking and baking. Saffron is sold in two forms, powder and threads. Commercial saffron comes from the dried (cured), bright red stigmas of the saffron (*Crocus sativus*). Each red stigma is like

a little capsule that encloses the complex chemicals that make up saffron's aroma, flavor, and yellow dye. In order to release these chemicals, one must steep the threads. Powdered saffron is more efficient because it does not need to be steeped provided that if not adulterated.

xi) Saffron Qualities and Adulteration

Saffron is grown commercially in India, Spain and Iran. Though it is also grown in a few other European Nations, the production there is negligible. Of these the Spanish variety always has a portion of yellow (style) attached to the red thread (the stigma). In Iran the stigma is very thin and small in size and the saffron is of two basic varieties. One contains only the stigma (red) part without the yellow style and the other is a bunch wherein the full style is attached to the stigma and tied in a bunch of several hundred stigmas with their styles. The effective yield of Saffron in this quality is only about 50% of red stigmas. The male parts of the saffron flower, the stamens, are half the size of the stigmas, and are deep yellow and have no culinary value. Unfortunately, they are sometimes added to the red stigmas to increase the weight of commercial saffron. Ground yellow stamens is sold as powdered saffron. Legitimate powdered saffron is red-orange and is made by grinding saffron stigmas. Under no circumstances pure powdered saffron would have any shade of yellow. (Narasimhan *et al.*, 1992: Sujata *et al.*, 1992)

Acknowledgements

The authors are grateful to Dr. BS Dhillon, Director NBPGR and Mission Leader of National Agricultural Technology Project on Plant Biodiversity and Dr. SS Malik, Head, Plant Exploration Division for facilities provided. We sincerely thank Dr. Arjun Lal, Principal Scientist, Plant Quarantine Division for technical help in manuscript preparation.

References

Abdullaev FI (1993) Biological effects of saffron. *BioFactor* **4**: 83-86.

Basker D and Negbi M (1983) The uses of saffron. *Economic Botany* **37**: 228-236.

Dhar AK, Sapru R and Rekha K (1988) Studies on saffron in Kashmir I. Variation in natural population and its cytological behaviour. *Crop Improvement* **15**: 48-52.

Maguelonne Toussaint-Samat (1992) *A History of Food.* Cambridge MA, USA: Blackwell, p. 518-519.

Maheswari JK (1996) *Ethnobotany in South Asia.* Scientific Publisher Jodhpur p 459.

Mehta BM, Borkhatriya VN and Boghra VR (2002) Saffron the colouring and flavouring agent in dairy and food industry. *Journal of Medicinal and Aromatic Plant Sciences* **24**: 1038-1049.

Nair SC, Salomi MJ, Varghese CD, Panikkar B and Panikkar KR (1992) Effect of saffron on thymocyte proliferation, intracellular glutathione levels and its antitumor activity. *Bio Factors* **4**: 51-54.

Nair SC, Kurumboor SK and Hasegawa, JH (1996) Saffron chemoprevention in biology and medicine: A review. *Cancer Biotherapy* **10**: 257-264.

Narasimhan H, Chand H and Rajalakshmi D (1992) Saffron: quality evaluation by sensory profile and gas chromatography. *Journal of Food Quality* **15**: 303-314.

Nauriyal R and George CK (1977) Saffron in India. *Arecanut and Spice Bulletin* **8**: 59-72.

Negbie M (1999) Saffron: *Crocus sativus* L. Medicinal and aromatic plants – industrial profiles. Amsterdam, Harwood Academic Publishers.Mc Gimpsey, 154 p.

Sala AV (1994) *Indian Medicinal Plant.* vol.2. p 212-217. Orient longman Limited, Chennai.

Sharma SK (1999) *Plants of Bhava Prakash,* National Academy of Ayurveda Vidyapeeth, New Delhi, p-176-323.

Sujata V, Ravishankar GA Venkataraman LV (1992) Methods for the analysis of the saffron metabolites crocin, crocetins, picrocrocin and safranal for the determination of the quality of the spice using thin-layer chromatography, high-performance liquid chromatography and gas chromatography. *Journal of Chromatography* **24**: 497-502.

Studies on Carpological Traits in Ber (*Ziziphus mauritiana* Lamk.) Genotypes

PL Saran, AK Godara, SK Sehrawat and IS Yadav
Department of Horticulture, CCS Haryana Agricultural University, Hisar, Haryana.

Thirty five ber genotypes were studied for their fruit and stone characters. Different types of fruit shapes were observed such as oblong , oval , ovate, round and obovate. The shape of fruit apex and base were found from round , broad and beaked. The skin colour of unripe and ripe fruit also showed considerable variation, as light green (Kaithli), green (Dandan), dark green (Desi Alwar and ZG-3), green with pinkish purple colour (Kathpal) in unripe, while in ripe fruit greenish yellow (Kaithli), pinkish yellow (Katha Rajasthan), chocolate smooth brown (Chhuhara), and yellowish with red brown blush (Kathaphal) were observed. Fruit surface in majority of genotypes was smooth (Gola, Dandan etc.) and warty (Illachi, Mirchia, Banarsi Karaka and Chonchal). In most of the genotypes oblong stone shape was observed but some were oval to ovate. The carpological traits can be used for improvement programme of ber.

Key words: Ber Genotypes, Carpological traits, Diversity, Fruit and Stone characters, *Ziziphus mauritiana*

Ber (*Ziziphus mauritiana* Lamk.) is one of the most common fruit indigenous to India which belongs to family *Rhamnaceae*. It is growing throughout the tropical, subtropical and arid region and is quite popular due to its low cost of cultivation, wide adaptability, ability to withstand drought and good economic returns. A large number of genotypes are available in India but many of them are still unidentified due to lack of systematic information with respect to morphological traits. The identification of genotypes through carpological traits is useful to the horticulturists, breeders and fruit growers. A wide variation is available for fruit and stone characters in ber and helpful in identification of best combiners for use in breeding programmes as well as for getting rid of cultivar synonymity. The description of fruit and stone character will help in distinguishing ber genotypes at different stages of development and will aid in selection and popularization of good varieties for wider commercial cultivation.

Material and Methods

The present investigations were made on 35 genotypes grafted on *Ziziphus rotundifolia* rootstock at the Experimental Orchard of CCS Haryana Agricultural University, Hisar, Haryana, India. The selected genotypes constituted plants of twenty five years age, planted at 8 x 8m spacing having uniform training and pruning. The identification of ber genotypes was made using fruit and stone characters as described in Table 1. The fruit description by Zielinski (1955) served as a guide. For recording various observations on fruit characters a random sample of twenty fruits were collected from three trees of each genotype.

Table 1. Fruit and stone characters and their states

Character	Character state
Fruit shape	Ovate, oblong, oval, round, obovate, beaked
Colour of unripe fruit	Light green, green, dark green, green with purple blush
Skin colour of ripe fruit	Light green, green, yellow, yellowish green, golden yellow, yellow with purple blush, pinkish yellow, chocolate brown
Fruit surface	Smooth, smooth with glossiness, ridged warty, slightly coarse
Fruit apex	Broad, round, round with ridge, shallow, shoulder with slight ridge, flate with depression
Fruit base	Broad, round, flat, flat with ridges, depressed, pointed, beaked
Flesh colour	Creamy white, white, light yellow
Cavity at stem end	Presence, absence
Cavity at styler end	Presence, absence
Stone surface	Smooth, rough
Stone shape	Oval, oblong, obovate
Stone apex	Acute, pointed, round, obtuse
Stone base	Acute round, oblong, obtuse.

Results and Discussion

The characters like fruit shape, fruit colour, fruit base, apex, cavity at both end, fruit surface and flesh colour (see Fig 1 to 5) were taken into account for characterization of germplasm. The observation recorded in the present investigation suggested that the different germplasm varied markedly with respect to fruit shape and colour etc., obviously due to their differential genetical behaviour (Table 2). Oblong, oval, ovate, round and obovate type fruit shape was observed in different genotypes. The results obtained in the present investigation were different

Table 2. Fruit characters of ber germplasm

Name of Germplasm	Fruit shape	Skin colour (unripe fruit)	Skin colour (ripe fruit)	Fruit surface	Fruit apex at stylar end	Fruit base	Flesh colour	Cavity at stem end	Cavity at stylar end
Kaithli	Oblong	Light green	Greenish yellow	Smooth	Round	Distinctly pointed	Creamy white	Present	Absent
Umran	Oval	Green	Golden yellow	Ridged	Round with clear ridges	Round with slight depression	White	Present	Absent
Safeda Rohtak	Oval	Green	Light yellow	Smooth	Round	Round	White	Present	Absent
Katha Bombay	Oval	Green	Yellowish green	Ridged	Round with ridges	Round with depression	White	Present	Very small
Seo	Round	Green	Greenish yellow	Depression present	Round (slight ridges)	Round	White	Present	Absent
Chonchal	Oblong	Green	Light yellow	Smooth with stricked	Round	Beaked	White	Present	Absent
Noki	Oblong	Green	Yellowish	Rough and warty	Shoulder rising	Clear beaked	White	Present	Absent
Katha Rajasthan	Oval to oblong	Light green	Pinkish yellow colour	Smooth	Round with slight depression	Round	White	Present	Very small
Laddu	Round	Green	Golden yellow with light brown blush	Smooth with glossyness	Round with slight depression	Round	Light creamy colour	Present	Absent
Chhuhara	Ovate	Green	Chocolate smooth brown	Smooth	Round with slight ridges	Distinct beaked	White	Present	Absent
Sandura Narnual	Ovate	Green	Yellowish green	Warty Slightly coarse	Showed prominent	Slight beaked	White	Present	Absent
Illaichi	Ovate	Green	Golden yellow	Ridged	Flattened ridged	Flat with ridge	Creamy white	Present	Present (very small)
Dandan	Oblong	Green	Golden yellow	Smooth	Round (slight ridged)	Round	White	Present	Absent
ZG-3	Obovate	Dark Green	Greenish yellow	Smooth (ridge on stem end)	Round (ridged)	Round	White	Present	Absent
Kathaphal	Obovate	Green with Pinkish purple colour	Yellowish green with red brown blush	Smooth	Shallow	Round	White	Present	Present (very small)
Akhrota	Oblong	Green	Yellowish	Smooth and glossy	Round	Round	White	Absent	Absent
Bhadurgarhia	Oblong	Green	Yellowish	Smooth	Shoulder with slight ridge	Slight beaked	Creamy white	Present	Absent
Govindgarh Selection	Oblong	Green	Yellowish	Smooth with warty	Round with ridge	Beaked	White	Present	Absent
Thornless	Oblong	Green	Yellow green	Smooth	Round	Round	White	Present	Absent
Gola Gurgaon No. 3	Round	Green	Yellow	Smooth	Flat with depression	Round	Creamy white	Present	Present
Gola Gurgaon No. 2	Round	Green	Yellow	Smooth	Round	Round	Creamy white	Present	Present
Desi Alwar	Oblong	Dark Green	Yellowish green	Smooth	Distinctly ridged (necked)	Clear beaked	Creamy white	Present	Absent
Sanori No. 5	Oval	Green with slight purple colour	Golden yellow with purple colour	Slightly coarse	Round (slight ridged)	Clear beaked	Creamy white	Present	Absent
Sanori No. 1	Beaked (oval)	Green with slight pinkish colour	Golden yellow with purple colour	Slightly coarse	Round (slight ridged)	Clear beaked	Creamy white	Present	Absent
Seo Bhadurgarh	Round	Green	Greenish yellow	Depression present	Round with depression	Round	White	Present	Absent

Contd.

Table 2. Contd.

Name of Germplasm	Fruit shape	Skin colour (unripe fruit)	Skin colour (ripe fruit)	Fruit surface	Fruit apex at stylar end	Fruit base	Flesh colour	Cavity at stem end	Cavity at stylar end
Sua	Ovate	Green	Yellow green	Smooth	Round with more depression	Round	White	Present	Absent
Kishmish	Oblong	Green	Reddish yellow	Smooth	Roundish	Slight beaked	White	Present	Absent
Popular Gola	Round	Green	Yellowish	Smooth	Round with depression	Round	White	Present	Absent
Mirchia	Beaked (oblong)	Green	Golden yellow	Warty	Bluntly tapering	Clear beaked	Cream white	Present	Absent
Jogia	Oblong	Reddish pigmentation in green colour	Light brown	Coarse with ridge	Round ridged	Round	White	Present	Absent
Mundia Murhara	Oblong	Green red spot	Yellow with some	Smooth with smooth with depression	Tapering shallow notch	Roundish	White	Present	Absent
Ponda	Round	Dark green yellow	Greenish	Smooth depression	Flat with	Round white	Creamy	Present	Absent
BS-2	Oblong	Green	Yellow	Smooth with glossyness	Round with slight ridges	Round	White	Present	Absent
Gola	Round	Green	Bright yellow	Smooth with glossyness	Round	Round	White	Present	Present
Banarsi Karaka	Oval to oblong (slight beaked)	Green	Light yellow	Smooth glossy and warty	Round smooth with slight ridge	Slight beaked	Creamy white	Present	Absent

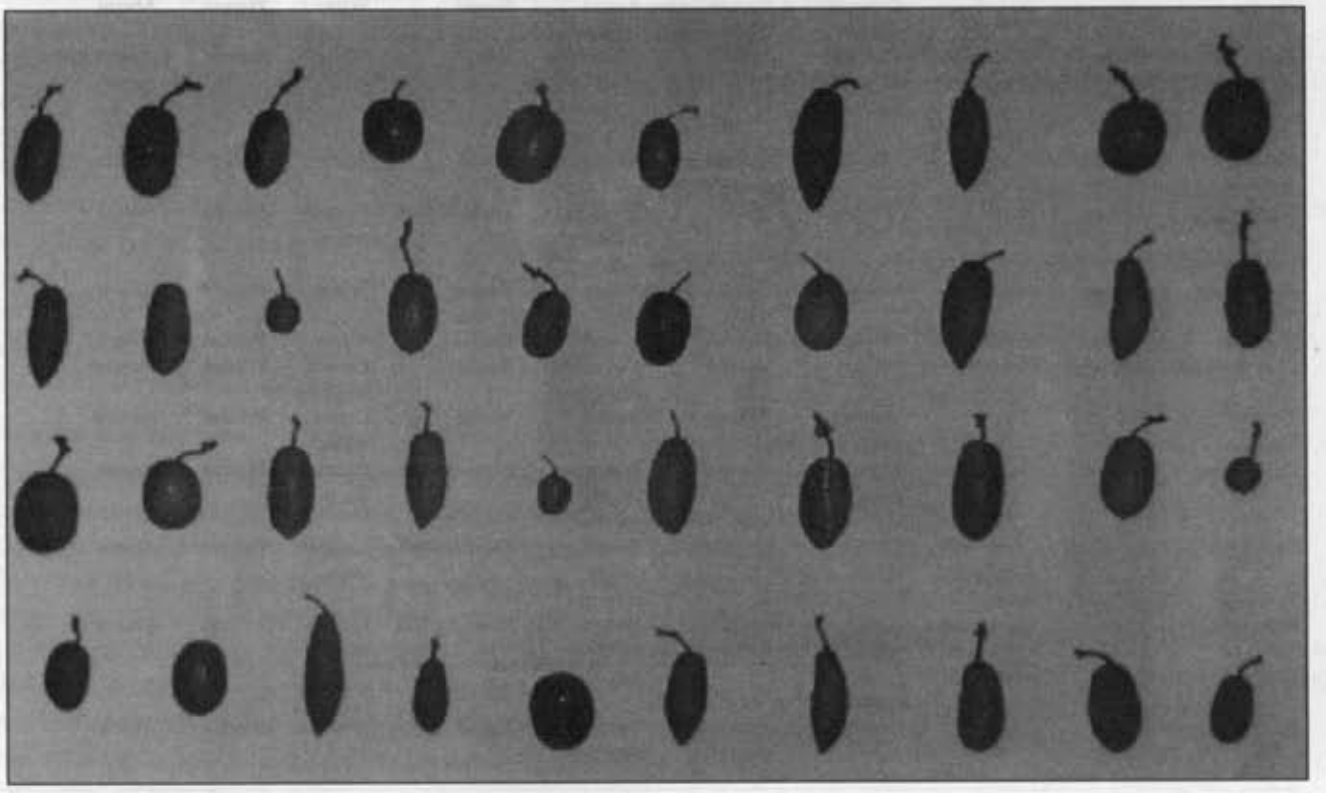


Fig. 1: Ber showing variability for shape, surface and size of fruits

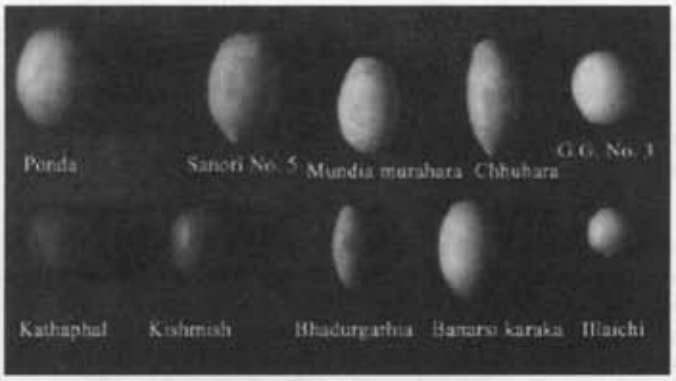


Fig. 2: Morphological variability of fruits

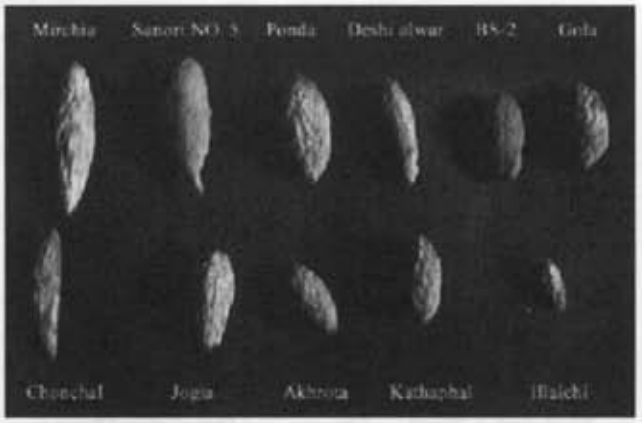


Fig. 3: Morphological variability of stones

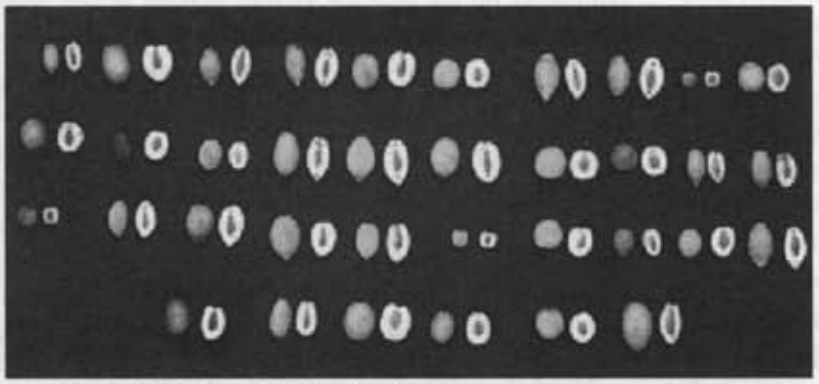


Fig. 4: Morphological variability of fruits

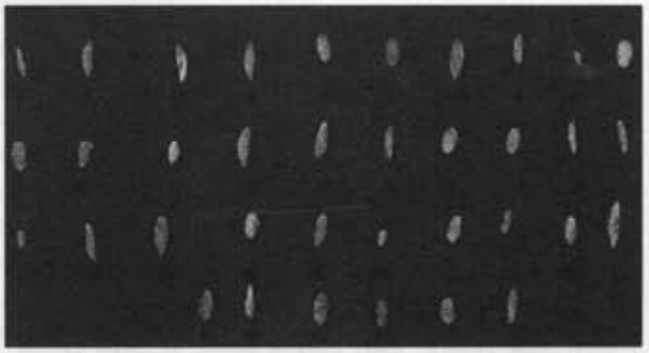


Fig. 5: Morphological variability of stones

Table 3. Stone characters of ber germplasm

Name of germplasm	Stone surface	Stone shape	Stone apex	Stone base
Kaithli	Rough	Oblong	Obtuse	Obtuse
Umran	Rough	Oblong	Obtuse	Obtuse
Safeda Rohtak	Rough	Oblong	Obtuse	Obtuse
Katha Bombay	Rough	Oblong	Obtuse	Obtuse
Seo	Rough	Oval	Obtuse	Obtuse
Chonchal	Rough	Oblong	Acute	Acute
Noki	Rough	Oval	Acute	Acute
Katha Rajasthan	Rough	Oblong	Obtuse	Obtuse
Laddu	Rough	Oval	Obtuse	Obtuse
Chhuhara	Rough	Oblong	Obtuse (pointed)	Acute
Sandura Narnual	Rough	Ovate	Obtuse	Obtuse
Illaichi	Rough	Obovate	Obtuse	Obtuse
Dandan	Rough	Oval	Obtuse	Obtuse
ZG-3	Rough	Oblong	Round	Round
Kathaphal	Rough	Oblong	Round	Obtuse
Akhrota	Rough	Obovate	Obtuse	Obtuse
Bhadurgarhia	Rough	Oblong	Acute	Acute
Govindgarh Selection	Rough	Oval	Acute	Acute
Thornless	Rough	Oval	Oblong	Oblong
Gola Gurgaon No. 3	Rough	Oblong	Obtuse	Obtuse
Gola Gurgaon No. 2	Rough	Oblong	Obtuse	Obtuse
Desi Alwar	Rough	Oblong	Oblong	Obtuse
Sanori No. 5	Rough	Ovate	Obtuse	Acute
Sanori No. 1	Rough	Ovate	Obtuse	Obtuse
Seo Bhadurgarh	Rough	Oblong	Obtuse	Obtuse to Acute
Sua	Rough	Oblong	Oblong	Obtuse
Kishmish	Rough	Oval	Obtuse	Obtuse
Popular Gola	Rough	Oblong	Obtuse	Acute
Mirchia	Rough	Oblong	Obtuse	Obtuse
Jogia	Rough	Oval	Obtuse	Round
Mundia Murhara	Rough	Ovate	Obtuse	Round
Ponda	Rough	Oval	Obtuse	Round
BS-2	Rough	Ovate	Obtuse	Round
Gola	Rough	Oval	Obtuse	Round
Banarsi Karaka	Rough	Ovate	Obtuse	Round

from those of earlier workers. However, some results are in conformity with the findings of Singh *et al.*, 1971; Kundi *et al.*, 1989; Bal 1992; Sobha *et al.*, 2001 at different places. The difference in the findings may be due to environmental factors, location, age of trees and cultural practices adopted in ber cultivars and wild forms. Shape of fruit apex and base was observed from round, broad, ridged and beaked in different genotypes. The variation were also reported by Gupta (2001) in four varieties of ber. Skin colour of unripe fruit showed considerable variation as, green, light green and green with purple blush, green yellow, bright yellow, greenish yellow and yellow with purple blush in skin colour of ripe fruit. Fruit surface of majority of genotypes was smooth (with or without glossiness) while few genotypes had warty with ridged surface.

Presence of cavity at stem end was observed in all the genotypes except Akhrota. Presence of cavity at stylar end was observed in Katha Bombay, Katha Rajasthan, Illaichi and Kathaphal while in rest of the genotypes it was absent. The variation for this character were also recorded by Raja (2004) in 12 genotypes of ber.

Flesh colour showed variation which was observed from creamy to light yellow. Similar results with respect to this character was recorded by Gupta, 2001 and Raja, 2004.

It is evident from the Table 3 the genotypes possessed grooved stone surface. In majority of genotypes, oblong stone shape was observed but some genotypes had oval to ovate stone shape. The stone apex was observed to be round in ZG-3 and Kathaphal. The genotypes like Bahadurgarhia and Govindgarh Selection had acute type stone apex. Obtuse type stone apex was observed in remaining genotypes. The stone base also showed pronounced variability like round, acute, pointed and obtuse. Although variation in stone morphology is a varietal character but upto a certain limit it can be influenced by the climatic factors as well as size and growth of the fruit. Similar observations were also noticed by Gupta (2001) in four cultivars and two species of ber.

Reference

Bal JS (1992) Identification of ber (*Ziziphus mauritiana* Lamk.) cultivars through vegetative and fruit characters. *Acta Hort.* No. **317**: 245-253.

Gupta RB (2001) Cytomorphological studies in wild and cultivated species of ber. M.Sc.Thesis, CCSHAU, Hisar, Haryana, India.

Kundi AHK, Wazir FK, Abdul Ghafoor and Wazir ZDK (1989) Morphological characteristics, yield and yield components of different cultivars of ber (*Ziziphus jujuba* Mill). *Sarhad J. Agril.* **5(1)**: 53-57.

Raja S (2004) Morphological and molecular characterization of ber germplasm. M.Sc. Thesis, CCSHAU, Hisar. Haryana, India.

Singh P, Bakhshi JC and Singh R (1971) Identification of some ber (*Ziziphus mauritiana* Lamk.) cultivars through vegetative characters. *Punjab Hort. J.* **11**: 176-187.

Sobha D, Naik RK, Patil SS and Bharti P (2001) Morphological and physico-chemical characters of ber varieties. *Karnataka J. of Agri. Sci.* **14(2)**: 541-544.

Zielinski QB (1955) Modern systematic pomology. W.M.C. Brown Company, Dubuque, Iowa. p. 82-100.

Evaluation of Exotic Germplasm of Kabuli Chickpea

J Kaul Shiv Kumar and SN Gurha*

Division of Crop Improvement, Indian Institute of Pulses Research, Kanpur 208 024, Uttar Pradesh,
**Division of Crop Protection, Indian Institute of Pulses Research, Kanpur 208 024, Uttar Pradesh,*

The present study was undertaken to identify high yielding, large (>40g/100 seeds) and extra-large (>50g/100 seeds) germplasm accessions of Kabuli chickpea with resistance/tolerance against Fusarium wilt. 150 exotic germplasm accessions belonging to diverse geographical regions were raised in augmented design and studied for phenological and agro-morphological traits.The results indicated high variability for traits, during rabi 2002-03, viz. yield/plant, pods/plant and 100 seed weight, respectively.While moderate variability was detected for plant height.13 accessions found desirable for seed size were further studied during rabi 2003-04, for plant type, yield (kg/ha), 100 seed weight and seed coat characteristics. Four accessions, namely, ICC12033, ICC14199, ICC14197 and ICC14203 demonstrated high yield potential of >18q/ha. Their respective 100 seed weight were recorded as 60.2, 54.73, 58.31 and 46.16. Based on screening in wilt sick nursery, an accession ICC14199 displayed complete resistance whereas ICC14203 showed moderate resistance against Fusarium wilt (race 2).

Key words: Kabuli chickpea, Exotic accessions, Yield potential, Seed size, *Fusarium* wilt

Chickpea is among the major pulse crops in Indian subcontinent. India leads the chickpea producing countries with 75% and 73% as its share in area and production, respectively (FAO, 2005). However, most of the varieties of Kabuli types have low yield potential, small to medium seed size and eventually succumb to various biotic and abiotic stresses. Narrow genetic base is attributed as one of the reasons of non-performance of these varieties. In countries like Turkey, Spain, Canada varieties with 50-60g/100 seed weight are cultivated as these fetch premium price in the market. Hence, exotic material with wider genetic variation for yield and yield contributing traits, resistance/tolerance to fusarium wilt, Ascochyta blight, drought and cold, and plant type which is amenable to mechanical harvesting as well as suitable for different environmental niches is urgently sought. This investigation was an attempt to evaluate the phenological and yield and its component traits in exotic Kabuli accessions as well as screening their reaction against wilt (*Fusarium oxysporum* f. sp. *ciceri)* race 2 so as to identify the promising entries to be utilized in augmenting breeding programmes.

Material and Methods

The investigation was carried out at Indian Institute of Pluses Research, Kanpur (Uttar Pradesh) which falls in northern part of India; its latitude and longitude being 20°27'N and 80°14'E, respectively. A total of 150 Kabuli germplasm accessions (98 from NBPGR, New Delhi and 52 from ICRISAT, Hyderabad), originating from diverse geographical regions were selected. The accessions were sown in November, 2002 and evaluated by a Petersen's augmented design (Petersen, 1985) with three commercial varieties, namely, KAK2, L550 and BG1003 as checks. Therefore, five blocks were formed each one having 30 different genotypes and a replication of the checks. The experimental plots consisted of two rows, 3m long, each with row to row and plant to plant distance of 30cm and 10 cm, respectively. Cultural operations, weed control and fertilizations were made according to standard practices. Observations were recorded on days to flower (50%), days to pod (Ist), days to maturity (95%), % wilt incidence and plant height (cm) upon maturity. On the basis of five competitive plants, information was collected on number of primary branches/plant, secondary branches/plant, pods/plant, and seed/pod and yield/plant (g). Plot yields (g) were converted into kg/ha using the formula (plot yield (g)/ plot size x 10). A total of 27 accessions were designated as promising entries on the basis of their overall performance. However, 13 entries were identified as large to extra-large seeded with low to moderate wilt incidence. These entries along with two checks namely KAK2 and L550 were raised in RBD with two replications during rabi 2003-04. The entries were raised on a plot size of 2.7 sqm with row to row and plant to plant spacings of 30cm, and 10 cm, respectively. The cultural practices, etc. as followed during previous year were resorted to. Information was gathered on various traits as done previously. Recorded data were analysed using the INDOSTAT programme.

Seven most promising lines displaying low wilt incidence under natural conditions were screened for

scoring their reaction against Fusarium wilt (race 2). During rabi 2004-05, the accessions along with three commercial varieties, viz. KAK2 and L550 were sown in a wilt sick plot (WSP) — 15-year old diseased nursery wherein pathogen inoculum was continuously added and followed by growing highly susceptible varieties/ strains every year since 1989-90. The accessions were planted in 4.5 m long rows with row-row and plant to plant spacings of 30 cm and 10 cm, respectively.The susceptible check entry, JG62—a twin podded desi was sown after every test entry. Two rows of each entry alternated with one row of infector JG62 enabling the development of heavy pathogen inoculum and maintenance of high disease pressure in the nursery. The extent of disease incidence in the susceptible infector rows served as a standard check for susceptibility of the test material. The crop was raised as per the recommended cultural practices for the chickpea pathological trials. The wilt incidence in each accession was scored and the lines characterized as per the guidelines of All India Co-ordinated Research Project on improvement of chickpea (Anonymous, 2004). Accordingly, plant count upon emergence was noted and the entries were regularly observed for wilt incidence. A count of wilted plant/s per accession was made and final data was recorded 2-weeks before maturity. The information on plant count upon emergence and maturity and the number of dead plants because of infection were compiled and % FW due to mortality was calculated.

Results and Discussion

Chickpea is a long day plant (van der Maesen, 1972). Its sown during October-November and matures during last week of March-mid April. Under north Indian conditions, the crop thus encounters decreasing temperature and decreasing photoperiod until flowering begins, and increasing temperature as well as day length during pod development and maturity (Khanna-Chopra and Sinha, 1987). During investigation, 20 accessions showed first flush of flowering within 50-60 DAS (date of sowing being 2 November, 2002). This period was an exceptional phase characterized by high day as well as night temperatures which started falling from last week of December with next 30 days being exceptionally cold, humid and foggy, with mean day temperature below 5^{O}C at the time of pod establishment (weather bureau, IIPR, data not given). The flowers /pods degenerated and the lines re-flowered during 103-110 DAS. Such lines produced only a few pods by 117-120 DAS. These lines also displayed 100% wilting at podding stage. Eventually shrivelled seeds were harvested. No further studies could be conducted on these accessions.

The mean values, range and CV (%) for the ten traits recorded, are given in Table 1. All the accessions displayed 50% flowering between 100-126 DAS with the mean of 108.68 DAS. An average of 115.81 DAS were taken for pod initiation. The accessions were found to mature by 152.01DAS.A low coefficient of variation (cv) for these three parameters was discernible (Table1).

Table 1: Phenological and agro-morphological variability in exotic germplasm accessions of Kabuli chickpea

Trait	Mean	Range	CV (%)	Extreme accession/s
DF (50%)	108.68	100-126	4.31	EC 381867-EC382436
DP (Ist)	115.81	102-130	4.57	EC 381867-EC382352
DM (95%)	152.01	150-165	1.39	EC381909-EC381616/ EC381617
Plant height (cm)	48.39	27.3-68.3	20.18	ICC 1969-EC 387190
Primary branches/plant	4.62	2.0-9.0	39.94	ICC16552-ICC4753
Secondary branches/plant	7.92	2.3-18.0	31.22	EC 382383-ICC16673
Pods/plant	33.72	1.0-103.0	74.26	EC 382379-ICC4753
Seed/pod	1.01	1.0-2.0	9.95	ICC9593-ICC16463
Yield/plant	6.46	0.2-36.12	83.87	EC 382379-ICC12033
100 seed weight (g)	24.79	2.5-61.4	64.27	EC381893-ICC12034

The plant height ranged from 27.3 cm to 68.3cm. Futhermore, only two accessions namely, ICC9593 and ICC16463 possessed 2 seeds/pod. Traits, viz.yield/plant, number of pods/plant and 100 seed weight exhibited higher variability, % cv being 83.87, 74.26, and 64.27, respectively, followed by number of primary (39.94) and secondary (31.22) branches. On the other hand, moderate variability (20.18%) was found for plant height. These figures indicated the scope of exercising selection for direct improvement in yield and indirectly through the number of primary and secondary branches. Raju *et al.* (1978) and Sood and Kumari (2000) have reported similar observations in Kabuli chickpea.

Based on yield and its contributing traits, 27 accessions were found promising. In Kabuli types, grain quality determines its desirability for consumption purposes and hence acts as a yard stick for price determination. In

recent times, the demand for large (>40g/100 seeds) and extra-large (>50g/100 seeds) Kabuli varieties is on the rise. Currently, this demand is met through import. Hence, there is a strongly felt need to boost production of large and extra large varieties so as to be self sufficient not only in meeting the domestic need but also having surplus for export by evolving a suitable strategy. In other words, donors possessing target trait/s need to be identified and exploited in developing the target varieties. This implies the intense screening of exotic germplasm from diverse world regions as one of the first steps for varietal development. During this investigation, out of 27 promising Kabuli accessions, 13 were found to be large to extra large seeded and were therefore studied further. These entries were analyzed thoroughly for plant type, grain yield (kg/ha), 100 seed weight(g) and seed coat characteristics. This information is compiled in Table 2. All the entries were found to be taller than both the local checks. Furthermore, seven entries, viz. ICC 12033, 12034, 14197, 14199, 14203, 14204 and 14204 were found to be erect with semi-compact growth habit. Six accessions, namely, ICC 7344, 14214, 14194, 14195 and 14196, and EC381882, displayed open canopy. Three accessions each displayed spreading and semi-spreading canopies, respectively. The study further established four accessions, namely, ICC12033, ICC14199, ICC14197 and ICC14203 as high yielding entries. The yield potential of these accessions was found above 18q/ha. The 13 test entries were also studied for their seed size and testa characteristics (Table 2). Entries namely ICC12033 &12034 displayed 100 seed weight of >60g while nine others viz., ICC 14204, 14214, 14194, 14196, 14197, 14199, 7344, 42051 and EC381882 showed in the range of 50-60g. Two entries, viz., ICC14195 and 14203 displayed 100 seed weight of around 45g. The best check KAK2 showed 100 seed weight of 38g. Additionally, eight accessions displayed milky white testa while rest exhibited beige. However, it was found to be intact (non-bursting type) in seven of these entries, viz.ICC 14195, 14196, 14197, 14199, 14203, 14204 and 14205, respectively. Four accessions exhibited bursting type seed coat, whereas, two accessions ICC12033 and EC 381882 produced both the types.

Wilt caused by *Fusarium oxysporum* f. sp *ciceri* (FOC) is a major biotic factor capable of reducing chickpea yield by 10 to 15 per cent with 100 % loss under specific situations (Singh and Dahiya, 1973; Haware and Nene, 1980). Of the four physiological races reported from India (Haware and Nene, 1982) Kanpur isolate (race 2) is known to be the most aggressive (Gurha and Mishra, 1982). Hence, one of the major breeding objectives is to develop cultivar/s with resistance to FOC race 2. In the present investigation, an attempt has been made to screen exotic Kabuli accessions against Fusarium wilt both under natural as well as sick plot conditions. The results on wilt incidence under natural conditions indicated low (<5%) to high including 100% in exotic material. 20 accessions were found to wilt completely before the on-set of maturity. However, 27 accessions showed upto 40% mortality due to wilt. Based

Table 2: Yield (kg/ha), 100 seed weight (g), plant types and testa characteristics of highly promising exotic Kabuli germplasm accessions

Accession #	Source of origin	Yield kg/ha	g/100 seeds	Plant type	Testa characteristics
ICC 14214	Mexico	250	55.90	Tall, spreading, open canopy	Milky white, bursting type
ICC 14194	Mexico	561	50.01	Tall, semi-spreading, open canopy	Milky white, bursting type
ICC 14195	Mexico	945	45.34	,,	Beige, non-bursting type
ICC 14196	Mexico	800	53.80	Tall, spreading, open canopy	Milky white, non-bursting
ICC 7344	Mexico	1160	51.80	Tall, semi-spreading, open canopy	Milky white non-bursting
ICC 12034	Mexico	1078	61.0	Tall, erect, semi-open canopy	Beige, bursting
ICC 12033	Mexico	2060	60.20	Tall, erect, semi-open canopy	Beige, bursting+non-bursting
ICC 14197	Mexico	1877	58.31	,,	Milky white, non-bursting
ICC14199	Mexico	2020	54.73	,,	Beige,non- bursting
ICC 14205	Mexico	360	52.79	,,	Milky white, non-bursting
ICC 14204	Mexico	880	53.53	,,	Beige,non-bursting
ICC 14203	Mexico	1840	46.16	,,	Milky white, non-bursting
EC 381882	Turkey	501	51.91	Tall, spreading type, open canopy	Milky white, bursting+non-bursting
KAK2		981	38.0	Medium height, semi-spreading, open canopy	Beige, non- bursting
L550 (local check)		1230	18.0	Medium height, erect, semi-open canopy	,,
		CV(%)	CV(%)		
		13.04	5.636		
		CD @5% level	CD @5% level		
		310.43	6.07		

Table 3:Reactions of highly promising exotic Kabuli germplasm accessions against *FOC* race 2 under WSP conditions

Accession #	%FW	Reaction type*
ICC14199	5.6	R
ICC14203	18.7	MR
ICC14195	36.2	S
ICC14196	48.1	S
ICC7344	39.2	S
ICC14197	22.4	S
ICC14205	56.4	S
KAK2 (ch)	23.7	S
L550 (ch)	80.6	S
JG62 (susceptible ch)	100.0	Highly susceptible

* R: resistant, MR: moderately resistant, S: susceptible

Table 4: Highly desirable accessions of exotic Kabuli chickpea germplasm and their useful trait/s

Useful trait(s)	Desirable accession(s)
Primary branches/plant	ICC4753, ICC16541
Secondary branches/plant	ICC5099, ICC16673
Plant height (cm),	IC accessions from Table 2
100 seed weight (g)	ICC 4753, ICC9361, ICC11255
Pods/plant	ICC12033, ICC14199, ICC14197,
Yield (kg/ha)	ICC14203
Resistance against	
Fusarium wilt	ICC14199, ICC14203

on their low wilting (0-20%), 13 large to extra-large seeded accessions were earmarked for screening under sick plot conditions. However, six of these entries exhibited bursting seed coat (Table 2) and could not be studied further. Therefore, seven entries were grown in sick nursery (Rabi 2004-05) and reactions against wilt were scored as per the guidelines of AICRP on chickpea improvement (Anonymous, 2004). The results are presented in Table 3.One entry ICC14199 showed 5.6% mortality (ie %FW) and was thus designated as resistant (R) on account of wilting of plants below 10%. Likewise, an accession ICC14204 exhibited wilt incidence in the range of 10-20% and was thus classified as moderately resistant (MR), its %FW being 18.7. Rest of the four entries were found susceptible, %FW being in the range of 20.1 to 100.0 (Table 3).

Limited genetic variation has been a major constraint in attaining improvement in different pulse crops including chickpea. Use of exotic material is necessary when desired gene/s are not available in local cultivars. All available Kabuli varieties besides being low yielders are susceptible to a number of biotic and abiotic stresses and have small to medium sized seeds. A clear understanding of genetic variability and interrelationship between yield and yield-related traits would complement breeders' efforts in evolving superior varieties. During this investigation some accessions of the exotic germplasm of Kabuli chickpea displayed useful variations for important traits especially wilt, plant height, primary and secondary branches, pods/plant, yield potential, 100 seed weight (Table 4). Accessions ICC14199, 14203, 14197 and 12033 were potential types identified for broadening the genetic base of the local Kabuli cultivars as well as providing a better chance to recover transgressive segregants.

References

Anonymous, (2004). All India Co-ordinated Research Project on Chickpea.Annual Report. IIPR (Indian Institute of Pulses Research), Kanpur.

FAO (2005) FAOSTAT-Agriculture-India.

Gurha SN and DP Mishra (1982) Donors for resistance to *Fusarium oxysporum* f. sp. *ciceri* in chickpea. *Indian. J. Mycol.& Pl. Pathol.***13**: 229-231.

Haware MP and YL Nene (1980) Influence of wilt at different stages on the yield loss in chickpea. *Trop. Grain Leg. Bullet.* **19**: 38-44.

Haware MP and YL Nene (1982) Races of *Fusarium oxysporum* f sp. *ciceri. Pl. Dis.* **66**:809-810.

Khanna-Chopra R and SK Sinha (1983) Chickpea: Physiological aspects of growth and yield.In.Chickpea, Saxena MC and KB Singh (Eds), Cab International, Wallingford, UK, p163-189

Petersen RG (1985) Augmented designs for preliminary yield trials. *RACHIS* **4**: 27-32.

Raju DB, RB Mehra and PN Bahl (1978) Genetic variability and correlation in chickpea. *Tropical legumes Bulletin* **11-14**: 35-39.

Singh KB and BS Dahiya (1973) Breeding for wilt resistance in Bengal gram. *Proc. Symp. on Wilt Problem and Breeding for Wilt Resistance in Bengal Gram.* IARI, New Delhi, 13-14 (abstract).

Sood BC and V Kumari (2000) Genetic variability and character association in Kabuli gram. *Indian. J. Pulses Res.***13**:48-49

Van der Maesen, LJG (1972) *Cicer* L. A monograph of the genus with special reference to the chickpea (*Cicer arietinum* L.), its ecology and cultivation. Communication of the Agricultural University, Wageningen. p 72-100.

Variability for Flower Characters in Cultivated and Wild Species of *Gossypium*, L.

Subhash Mehetre* Gorakh Shinde, Aparna More, Ashwini Thul and Jitendra Patil
All India Coordinated Cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri-413 722, Maharashtra.

Cotton is the most important fibre crop of world, belonging to genus Gossypium. This genus includes approximately 50 species distributed in arid to semi-arid regions. Hybridization and introgression have played important role in the evolution of new world cotton. The success of crossing, i.e. identification of a true hybrid can be established using morphological characters like presence/absence of floral and foliar nectaries, leaf lobbing, petal spot and colour. Hence efforts were made during present investigation for characterization of the cotton species including perennial cotton and other races and wild cotton belonging to the genomes and sub genomes. In case of 'A' genome longest peduncle length was observed in Punaspatti where as flower colour ranged from dark yellow to pink-wish white. In 'B' genome all four species had flowers with varying intensity. In this group the largest petal spot was recorded in *G. anomalum*. In the 'B' genome species the shortest peduncle was observed in *G. aridum* while it was longest in *G. armourianum* whereas the flower colour varies its intensity from cream white to yellow. In the genome E flower colour appears from light yellow to yellow with petal spot. *G. longicalyx* belonging to F genome shows yellow flower without petal spot. The peducle length in A_1D_1 genome was shortest in Seridov and longest in Exotic-3. The flower colour of this genome produced cream to yellow flowers. These results revealed that there is wide range in the floral characters of races and perennial types of cultivated cottons as well as wild species of Gossypium. Qualitative characters are under the control of either single or two genes. The information on flower characters will certainly useful for selecting desired types from the segregation of populations both for improved yield, fibre quality parameters coupled with resistance to diseases and pests.

Key words: *Gossypium*, Flower characters, Wild species, Cultivated species, Variability

Cotton is a leading fibre crop of the world (Murthy and Acharya, 1975; Fryxell, 1992) belonging to genus *Gossypium*. This genus includes approximately 50 species distributed in arid to semi-arid regions of the tropics and sub-tropics. Four species independently domesticated for their fibre in Africa-Asia and the Americas. *Gossypium* species exhibit extraordinary variation ranging from herbaceous perennials to small trees with diverse array of reproductive and vegetative characteristics. Similarly parallel level of cytogenetical and genomic diversity has arisen during the global radiation of the genus leading to the evolution of eight groups (A-G and K) of diploid (n=13) (Wendel and Cronn, 2003) tropical and sub-tropical regions of the world (Percival *et al*,1999 Endrizi *et al*, 1985). Among these species 44, are diploid and fall into A to G and K genomes and the remaining are allotetraploids with progenitors of *G. herbaceum* var. *africanum* (AA) and *G. raimondii* (D_5D_5) (Wendel, 1989). There are four cultivated species, the New World allopolyploids *G. hirsutum* and *G. barbadense* and the old world diploids *G. herbaceum* and *G. arboreum*.

Many of the various species of both diploid and tetraploid provide the most intriguing sources of genetic variability for cotton variety improvement. Difficulties arise in the transfer of wild diploids into tetraploids. These species arise from chromosome structural differences (Niles,1980). Fertility relationship among species is highly variable, and only about two thirds of the interspecific hybrids studied produce fertile F_1 s (Anonymuos,1968).The exotic species are the sources of useful genes (Table 1) for improvement of fibre properties, cold tolerance and resistance to diseases and insects (Fryxell, 1976). Further, nuclear complements of two upland cottons when combined with cytoplasm of seven wild *Gossypium* species; these provide a valuable and unique germplasm source for cotton improvement (Meyer, 1973;1975).

Hybridization and introgression have played important role in the evolution of New World cotton (Hutchinson, 1959). Adoption of standardized systems of introgression, precise evaluation of the selective value of a particular gene complex, sophisticated techniques with suitable adjustments in the breeding system for accelerating the rate of introgression and controlled experimentation are necessary to achieve the desired goals of interspecific gene transfer. The various aspects of introgressive gene transfer in *Gossypium* for diseases and pest resistance (Mehetre *et al.*, 2002 a), for fibre

quality parameters (Mehetre *et al.*, 2004 a), problems of wide hybridization ((Mehetre *et al.*, 2002 b) and embryo rescue as tool to achieve interspecific hybridization (Mehetre *et al.*, 2004 b) are reviewed critically.

The success of a cross, i.e., identification of a true hybrid can be established using morphological characters like presence/ absence of floral and foliar nectaries, leaf lobbing, petal spot and color etc. However, these characters may not be significantly distinct. Cytological data are more reliable for the identification of interspecific cotton hybrids because, the hybrid between tetraploid and diploid is triploid and distinct from its parent for chromosome number and pairing. However, such assessments require laborious experiments. Although isozyme markers are used to identify the hybrids of cultivars (Roxas *et al.*, 1993) the paucity of isozyme loci restricts their usefulness in breeding (Heletjaris *et al.*, 1986). Molecular marker analysis though offers an efficient alternative to this approach requires sophisticated laboratories and trained scientific manpower, which is not readily available everywhere. Hence, for confirmation hybrids, one has to depend upon the expression of morphological characters in the F_1 hybrid in comparison with their parents. Hence efforts were made during present investigation for characterization of the cultivars and species including perennial cottons and other races, wild cotton belonging to genomes and subgenomes. Objective of the present investigation was to utilize this information for confirmation of hybridity of an interspecific hybrid of *Gossypium* L. spp. (Naryanan, *et al., 1984*; Mehetre and Pardeshi, 2004).

Materials and Methods

Various races and perennial types and cultivated diploid and tetraploid cottons and world species maintained in garden of wild species and cytogenetical stocks (Table 1) at Cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri comprised the experimental material. The observations were recorded on three randomly selected plants of each species, for different characters mentioned in Table 1.

The fully opened three flowers were collected for recording observations. The flowers were dissected for recording observations of petals. Area (mm^2) of petal, petal spot, bracteoles, and calyx was measured using area meter-Am-100, Model–SE 213 CE ADC Bio-Scientific Limited, England. Measurements and counts of other floral parts were recorded with help of scale/ ruller. The averages of ten observations were considered for statistical analysis (Syndecor and Cocharn, 1967).

Results

During present studies the variability for different floral characters (Table 1) was studied in species, races and perennial types of diploid (*G. arboreum* and *G. herbaceum*) and a tetraploid (*G. hirsutum*) cotton (Plates I & II).

A Genome

A single race of *G. herbaceum* was available for the study. Peduncle length was 2.1 cm, it produced flower with yellow colour, the petal of 29 mm width and 34 mm length was present. The petal spot area was 166 mm^2 (12.7 mm x 29.7 mm). The average calyx area (196 mm^2) was observed with width (8.9 mm) and length (27.9 mm). It had bract area of 531 mm^2 with the bract width (24.4 mm) and length (58.9 mm) on an average three number of teeth. It produced yellow coloured anther with the anther number 121; style length of (1.90 cm) and ovary length of 0.7 cm having 23 average ovule/ovary.

In *G. arboreum*, two perennial cotton *viz.*, ' Kudaikotti' and 'Punaspatti' and 3 races, *indicum*, *bengalense* and *sinense* were studied. Average peduncle length was 1.32 ± 0.25 cm, shortest (0.9 cm) and longest (1.6 cm) peduncle length was observed in Punaspatti and *bengalense* respectively.

The flower colour ranged from dark yellow (race *Kudaikotti* and *Punaspatti*), pinkish white (race *indicum*) yellow (race *bengalense* and *sinense)*. The average size of petal was 27.86 ± 3.30 mm wide and 36.7 ± 4.40 mm long. Flowers of all the five types studied, showed petal spot of having an average area (150 ± 34.34mm^2) and width 12.66 ± 3.32mm and length 21.42 ± 4.23 mm. The width of petal spot ranged from 9.4 mm (race *indicum*) to 18.3 mm (race *sinense*) and longest petal spot length 24.4 mm (race *Kudaikotti*) and shortest 13.0 mm in *bengalense* was observed.

Calyx had an average area 185 ± 56.40 mm^2 with the width 9.02 ± 1.11 mm and length 32.84 ± 11.90 mm. The area of calyx ranged from 107 mm^2 (race *Punaspatti*) to 275 mm^2 (race *Kudaikotti*). The width of calyx ranged from 7 mm (race *bengalense*) to 10.2 mm (race *indicum*) and longest calyx 51. 8 mm (Kudaikotti) and shortest calyx 19.3 mm (punaspatti) was also observed. Bract had an average area 239.60 ± 31.93 mm^2 with the width 17.16 ± 1.36 mm and length 25.78 ± 3.75 mm. The width of bract ranged

Table 1. Variability in different wild species of cotton for different morphological characters

Characters	Diploid cultivated						
	G. herbaceum	*G. arboreum*, L. (perennials and races)					
	africanum Genome A_1	*Kudaikottii* A_2	*Punaspatti* A_2	*indicum* A_2	*bengalense* A_2	*sinenses* A_2	Average (SD)
Peduncle Length (cm)	2.1	1.5	0.9	1.4	1.6	1.2	1.32 (0.25)
Petal colour	Yellow	Dark yellow	Dark yellow	Pinkish white	Yellow	Yellow	
Petal area (mm^2)	426.0	413.0	789.0	208.0	585.0	598.0	518.60 (195.68)
Petal width (mm)	29.0	27.3	26.0	23.0	31.0	32.0	27.86 (3.30)
Petal length (mm)	34.0	36.5	36.0	29.0	41.0	41.0	36.7 (4.40)
Petal spot	P (+)	P (+)	P (+)	P (+)	P (+)	P (+)	
Petal spot area (mm^2)	166.0	142.0	140.0	110.0	144.0	214.0	150 (34.34)
Petal spot width (mm)	12.7	10.1	14.5	9.4	11.0	18.3	12.66 (3.32)
Petal spot length (mm)	29.7	24.4	24.1	23.4	13.0	22.2	21.42 (4.23)
Calyx area (mm^2)	196.0	275.0	107.0	193.0	148.0	202.0	185 (56.40)
Calyx width (mm)	8.9	9.8	8.9	10.2	7.0	9.2	9.02 (1.11)
Calyx length (mm)	27.9	51.8	19.3	31.5	22.0	39.6	32.84 (11.90)
Bractiole No.	3	3	3	3	3	3	3
Bract area (mm^2)	531.0	291.0	219.0	234.0	198.0	256.0	239.60 (31.93)
Bract width (mm)	24.4	19.5	16.3	15.7	16.5	17.8	17.16 (1.36)
Bract length (mm)	58.9	28.3	25.9	25.7	19.0	30.0	25.78 (3.75)
Teeth No.	5, 3, 2	2,3,3	5,4,3	1,1,1	1,2,2	2,4,3	2.60 (1.02)
Anther colour	Yellow	Yellow	Yellow	R. Yellow	Yellow	Yellow	
Anther Nos.	121	103	86	71	98	112	94 (14.24)
Style length (cm)	1.9	2.1	2.1	2.1	2.4	2.2	2.18 (0.12)
Ovary length (cm)	0.7	0.7	0.8	0.9	0.9	0.7	0.80 (0.09)
Ovule Nos.	23	20	17	21	18	21	19.40 (1.62)

Characters	*Gossypium* species Diploid wild of B genome				
	anomalum B_1	*triphyllum* B_2	*barbasonum* B_3	*capitis viridis* B_4	Average (SD)
Peduncle Length (cm)	0.5	0.3	0.7	0.5	0.50 (0.14)
Petal colour	Dull violet	Dull violet	Dull violet	Light red	
Petal area (mm^2)	642.0	524.0	567.0	617.0	587.50 (45.53)
Petal width (mm)	29.0	21.6	24.0	33.0	26.90 (4.42)
Petal length (mm)	34.0	36.8	43.0	37.0	37.70 (3.28)
Petal spot	P (+)	P (+)	P (+)	P (+)	
Petal spot area (mm^2)	268.0	253.0	290.0	176.0	246.75 (42.91)
Petal spot width (mm)	16.5	28.0	15.7	13.5	18.43 (5.64)
Petal spot length (mm)	44.2	33.0	25.5	34.8	34.38 (6.86)
Calyx area (mm^2)	282.0	223.0	203.0	300.0	252.0 (40.14)
Calyx width (mm)	12.7	15.0	16.0	16.3	15.0 (1.41)
Calyx length (mm)	52.8	33	33.3	64.4	45.87 (13.37)
Bractiole No.	3	3	3	3	3.0
Bract area (mm^2)	120.0	55.0	104.0	101.0	95.0 (24.20)
Bract width (mm)	4.6.0	3.6	4.1	4.3	4.15 (0.36)
Bract length (mm)	40.6	19.8	46.0	46.2	38.15 (10.83)
Teeth No.	3,3,3	3,3,3	3,3,3	3,3,3	3.0 (0.0)
Anther colour	Cream	Yellow	Yellow	Yellow	
Anther Nos.	103.0	97.0	107.0	88.0	98.75 (7.15)
Style length (cm)	1.7	2.2	2.2	1.8	1.97 (0.23)
Ovary length (cm)	0.6	0.5	0.6	0.5	0.55 (0.05)
Ovule Nos.	14	14	16	11	13.75 (1.78)

Characters	*Gossypium* species Diploid wild of D genome						
	thurberi D_1	*armourianum* D_{2-1}	*devidsonii* D_{3-1}	*aridum* D_4	*raimondii* D_5	*trilobum* D_8	Average (SD)
Peduncle Length (cm)	1.4	3.6	2.9	0.2	0.7	1.3	1.68 (1.19)
Petal colour	Cream	Yellow	P.Yellow	Pink	Cream	Cream	
Petal area (mm^2)	462.0	958.0	434.0	535.0	1278.0	441.0	684.67 (321.70)
Petal width (mm)	21.0	35.0	29.9	22.6	44.0	22.3	29.13 (8.28)
8.Petal length (mm)	24.5	42.0	30.9	39.4	48.0	24.8	34.93 (8.84)
Petal spot	P(+)	P(+)	P(+)	P(+)	P(+)	P(+)	
Petal spot area (mm^2)	123.0	211.0	242.0	209.0	672.0	99.0	259.339 (191.38)
Petal spot width (mm)	6.9	14.2	14.3	12.4	32.3	6.1	14.37 (8.66)
Petal spot length (mm)	23.0	33.8	16.8	11.2	38.1	20.6	23.92 (9.34)
Calyx area (mm^2)	110.0	283.0	136.0	319.0	517.0	82.0	241.17 (151.38)
Calyx width (mm)	10.4	15.2	4.2	17.0	21.2	7.6	12.60 (5.78)
Calyx length (mm)	15.5	27.9	21.8	33.5	54.6	15.0	28.22 (13.39)
Bractiole No.	3	Absent	3	3	3	3	3.00
Bract area (mm^2)	175.0	–	–	16.0	497.0	30.0	179.5 (193.59)
Bract width (mm)	12.2	–	17.4	3.3	29.4	4.3	9.60 (12.06)
Bract length (mm)	17.8	–	30.8	9.9	48.3	8.4	17.70 (18.11)
Teeth No.	1,1,1	–	7,8,8	1,1,1	17,14,14	1,1,1	4.30 (7.36)
Anther colour	Cream white	Yellow+ red spot	Yellow	Cream pink	Dark red	Cream white	
Anther Nos.	102	145	46	138	154	98	113.83 (36.88)
Style length (cm)	2.1	3.8	1.9	2.7	4.5	2.1	2.85 (0.97)
Ovary length (cm)	0.5	0.6	0.4	0.5	0.7	0.4	0.52 (0.110)
Ovule Nos.	22	18	20	16	28	22	21 (3.78)

Characters	*Gossypium* species Diploid wild E genome			*Gossypium* species Diploid wild F genome	*Gossypium* species Diploid wild G genome	Tetraploid cultivated *G. babrbadense* race A_2D_2 genome
	stocksii E_1	*somalense* E_2	Average (SD)	*longicalyx* F_1	*Gbiskli* G_8	Kidney cotton A_2D_2
Peduncle Length (cm)	0.7	1.7	1.68 (1.19)	1.2	2.1	2.6
Petal colour	Light yellow	Yellow		Yellow	Pink	Dark yellow
Petal area (mm^2)	185.0	220.0	202.50 (17.50)	474.0	584.0	1164.0
Petal width (mm)	11.4	18.2	14.80 (3.40)	20.3	21.5	42.0
8.Petal length (mm)	26.7	28.7	27.7 (1.00)	29.5	27.2	48.0
Petal spot	P(+)	P(+)		–	P(+)	(P+)
Petal spot area (mm^2)	88.0	136.0	112.0 (24.40)	(Ab)	173.0	92.0
Petal spot width (mm)	5.3	8.9	7.1 (1.8)	(Ab)	9.8	4.8
Petal spot length (mm)	14.6	25.5	20.05 (5.45)	(Ab)	11.8	5.4
Calyx area (mm^2)	149.0	79.0	114.0 (35.0)	143.0	139.0	583.0
Calyx width (mm)	10.2	7.9	9.05 (1.15)	10.7	8.4	17.0
Calyx length (mm)	38.6	22.6	30.60 (8.0)	24.1	28.2	48.3
Bractiole No.	3	3	3.0	3	3	3
Bract area (mm^2)	129.0	411.0	270.0 (9141.0)	208.0	–	1102.0
Bract width (mm)	9.1	20.6	14.85 (5.75)	14.0	10.5	49.5
Bract length (mm)	33.8	56.1	44.95 (11.15)	36.1	12.4	64.0
Teeth No.	8,9,10	15,15,15	12.0 (3.0)	1,1,1	6,7,7	16,14,12
Anther colour	Cream	Yellow		Yellow	Yellow	Yellow
Anther Nos.	50	82	66.0 (16.0)	63	68	116.0
Style length (cm)	1.3	2.1	1.70 (0.40)	1.5	1.1	4.8
Ovary length (cm)	0.4	05	0.45 (0.05)	0.5	0.4	1.0
Ovule Nos.	9	10	9.50 (0.50)	8	20	27

Characters	Tetraploid cultivated *G. hirsutum* races A_1D_1 genome						
	Palmeri A_1D_1	Punctatum A_1D_1	Morilli A_1D_1	Yellow.spotted A_1D_1	Exotic -3 A_1D_1	Seridov A_1D_1	Average (SD)
Peduncle Length (cm)	1.7	1.3	2.0	1.2	2.3	1.2	1.62 (0.42)
Petal colour	Cream to yellow	Cream to yellow	Cream to yellow	Cream to yellow	Cream to yellow	Cream to yellow	
Petal area (mm^2)	482.0	597.0	644.0	582.0	516.00	674.0	582.50 (66.94)
Petal width (mm)	22.0	32.0	28.0	32.1	29.0	32.0	30.85 (6.01)
Petal length (mm)	31.5	48.9	34.3	34.7	42.2	39.0	38.43 (5.82)
Petal spot	P(+)	P(+)	(P+)	(Ab)	(Ab)	P(+)	
Petal spot area (mm^2)	44.0	93.0	86.	(Ab)	(Ab)	156.00	94.75 (40.02)
Petal spot width (mm)	4.6	5.1	5.00	–	–	8.8	5.88 (1.70)
Petal spot length (mm)	15.5	18.6	17.4	–	–	12.6	16.03 (2.27)
Calyx area (mm^2)	352.0	425.0	226.0	250.00	196.0	179.0	271.33 (88.35)
Calyx width (mm)	17.50	15.5	9.4	11.9	9.4	6.8	11.75 (3.71)
Calyx length (mm)	46.0	76.4	26.2	32.3	32.0	25.0	39.65 (17.79)
Bractiole No.	3	3	3	3	3	3	3.0 (0.0)
Bract area (mm^2)	548.0	512.0	415.0	573.0	445.0	278.0	461.83 (98.80)
Bract width (mm)	23.1	24.1	22.4	27.7	21.6	17.9	22.80 (2.93)
Bract length (mm)	48.5	52.3	36.3	36.8	47	31.3	42.03 (7.61)
Teeth No.	8,6,7	8,9,7	11,10,9	10,9,9	2,3,3	5,5,5	7.0 (2.38)
Anther colour	Pale Yellow	Yellow	Pale Yellow	Pale Yellow	Yellow	Yellow	
Anther Nos.	77	101	98	84	107	112	96.50 (12.31)
Style length (cm)	2.1	2.5	2.3	2.8	2.2	2.6	2.42 (0.24)
Ovary length (cm)	0.8	0.8	0.9	0.8	0.8	0.8	0.82 (0.04)
Ovule Nos.	28	28	24	30	24	28	27.0 (2.24)

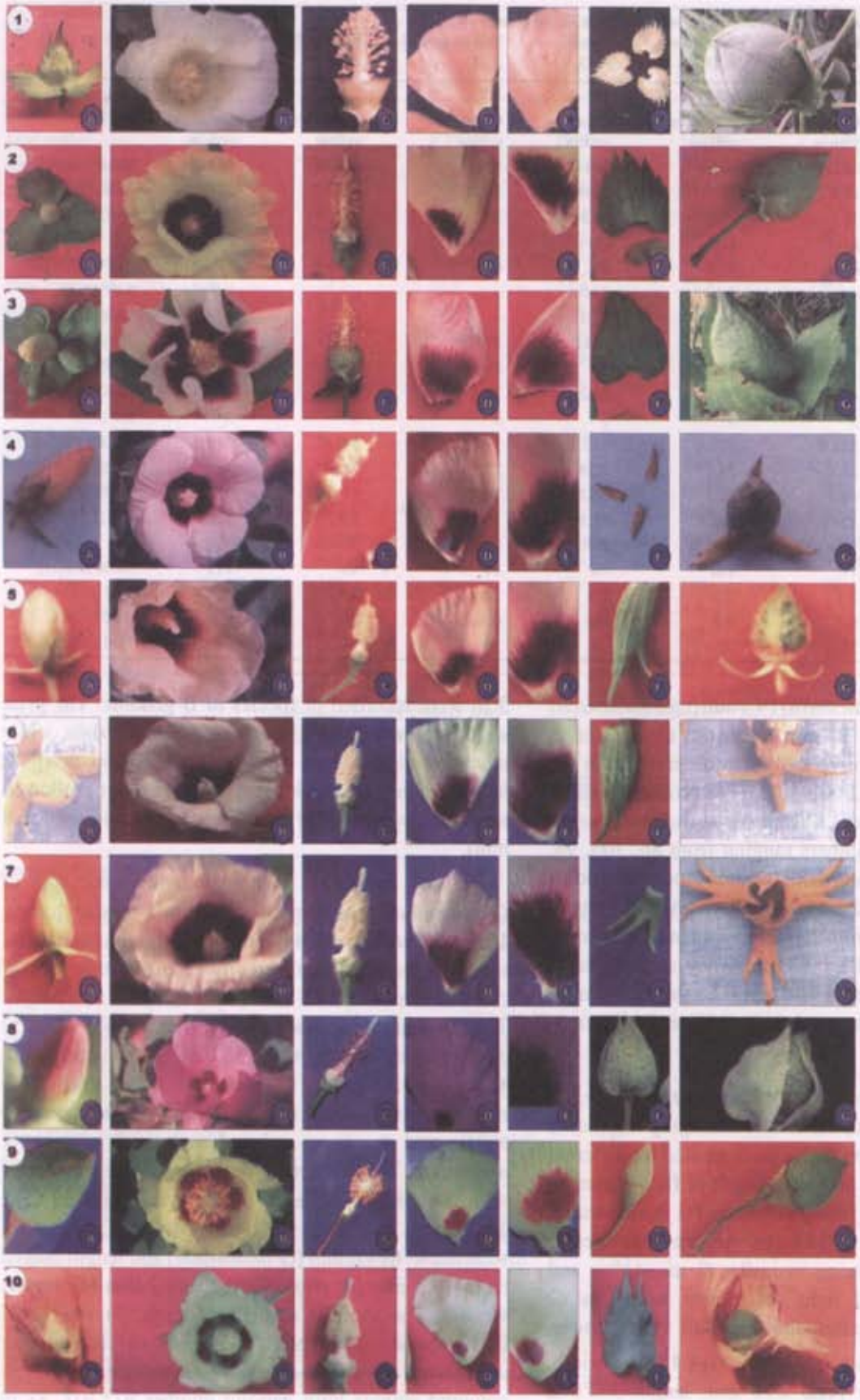
from 15.7 mm (race *indicum*) to 19.5 mm (race *Kudaikotti*) and longest bract of 30 mm (*sinense*), shortest bract of 19.0 mm (*bengalense*) were also observed with the average teeth number 2.60 ± 1.02. They produced yellow anthers (races *Punaspatti, Kudaikotti, bengalense, sinense* with the number of anthers ranging from 86, 103, 98, 112, respectively, among them *indicum* produced reddish yellow anthers with the number 71. They had varying style length ranging from 2.1 cm to 2.4 cm. The average style length was 2.18 ± 0.12 mm. They also produced average ovule numbers 19.40 ± 1.62, ranging from 17 to 21 and average ovary length 0.80 ± 0.09 cm.

B Genome

Four species namely G. anomalum, G. triphyllum, G. barbasonum and *G. capitis viridis* belonging to genome B_1, B_2, B_3 and B_4, respectively were studied for different floral characters. The peduncle length of flower ranged from 0.3 cm (*G. triphyllum*) to 0.7 cm (*G. barbasonum*) with average of 0.5 ± 0.14 cm. All the four species had flowers with varying intensity. *G. anomalum* and *G.capitis viridis* had light red flower where as *G. triphyllum* and *G. barbasonum* had dull violet flower.

Average petal size (mm), 26.90±4.42 mm width, 587.50 ± 45.53 mm^2 petal area and, length 37.70 ± 3.28 were recorded in species of B genome. The petal width was maximum (33 mm) in *Capitis viridis*, while it was minimum in a *G. triphyllum* (21.60 mm). *G. barbasonum* produced longest petal (43.0 mm) followed by *capitis viridis* (37.0 mm) and *G. trypymullum* (36.8 mm).

It was interesting to note that the petal spot of *G. anomalum* was largest (268 mm^2) in size having 16.5 mm width and 44.2 mm length. Smallest petal spot was recorded in *G. capitis viridis* having area of 176 mm^2 and size 13.5 mm width and 34.8 mm length. The average calyx area of four given species was 252 ± 40.14 mm^2, with the width 15.0 ± 1.41 mm and length 45.87 ± 13.37 mm. The maximum calyx width 16.3 mm and length 64.4 mm was observed in *G.capitis viridis* and minimum calyx length 12.7 mm in *G. anomalum*. The average bract area was 95 ± 24.20 mm^2 with the width 4.15 ± 0.30 mm and length 38.15 ± 10.83 mm. The bract width ranged from 3.6 mm (*G. triphyllum*) to 4.6 mm (*G. anomalum*) and length ranged from 19.8 mm (*G. triphyllum*) to 46.2 mm (*G. capitis viridis*). The average number of teeth (3) was equal in all species. They produced cream coloured anther with anther no. 103 in case of *G. anomalum* and yellow coloured anthers with varying number 97, 107, 88 in



S.N.	Gossypium, L.spp
1.	G. hirsutum, L. varJLH-168
2.	G.herbaceum, var GBHV.2
3.	G.arboreum var., Y-1
4.	G.anomlum, Waw. & Peyr.
5.	G.capitis viridis, Mauer
6.	G. barbosanum, Phill & Chem.
7.	G. triphyllum, (Harv.) Hochr.*
8.	G.sturtianum, J.H.Willis
9.	G.armourianum Kearney
10.	G.davidsonii Kell

a = Flower bud one day before blooming showing shape, size, colour, calyx and bracteole shape, size etc.

b = Fully opened flower showing size, colour, presence/absence of petal spot and size and colour intensity of petal spot

c = Androecium colour of anthers, filaments and exertion of stigma etc.

d = Individual petal showing colour, and size and colour intensity of petal spot

e = size and colour intensity of petal spot

f = calyx and bract:type, shape and size of bracteoles

g = bolls showing coverage of calyx and bracteoles

Plate 1

S.N.	*Gossypium, L.spp*
11.	*G. aridum (Rose & Standl.) Skov*
12.	*G. thurberi Tod.*
13.	*G. raimondii Ulbr*
14.	*G. trilobum (Moc. & Sess. ex DC) Skov Kearney*
15.	*G. stocksii Mast ex. Hook*
16.	*G. stocksii, Mast ex. Hook.**
17.	*G. bickii Prokh *
18.	*G.longicatyx Hutch & Lee.**
19.	*G.australe F. Muell *
20.	*G. nelsonii Fryx.**
21.	*G. areysianum Deflers*

a = Flower bud one day before blooming showing shape, size, colour, calyx and bracteole shape, size etc.

b = Fully opened flower showing size, colour, presence/ absence of petal spot and size and colour intensity of petal spot

c = Androecium colour of anthers, filaments and exertion of stigma etc.

d = Individual petal showing colour, and size and colour intensity of petal spot

e = size and colour intensity of petal spot

f = calyx and bract:type, shape and size of bracteoles

g = bolls showing coverage of calyx and bracteoles

Plate 1

case of *G. triphyllum*, *G. barbasonum* and *G. captis viridis*, respectively. The average number of anthers was 98.75 ± 7.15 having maximum in *G. barbasonum* (107) and minimum in *G. capitis viridis* (88). They having average style length of 1.97 ± 0.23 cm ranged from 1.7 cm (*G. anomalum* to 2.2 cm (*G. triphyllum* and *G. barbasonum*) and average ovary length was 0.55 ± 0.05 cm with the average number of ovules 13.75 ± (1.78), which ranged from 11 (*G. capitis viridis*) to 16 (*G. barbasonum*).

D Genome

Six wild *Gossypium* species of D genome were studied namely *G. thurberi*, *G. armourianum*, *G. davidsonii*, *G. aridum*, *G. raimondii*, *G. trilobum* belonging to the genome D_1, D_{2-1}, D_{3-1}, D_4, D_5 and D_8 respectively.

Average peduncle length of D genome species was 1.68 ± 1.19 cm. The shortest peduncle of 0.2 cm was observed in *G. aridum* while it was longest in G. *armourianum* (3.6 cm). The cream flowers were produced by *G. thurberi*, *G. trilobum* and *G. raimondii* while *G. armourianum*, *G. davidsonii* and *G. aridum* produced yellow, purple yellow and pink flowers, respectively. The maximum petal width (44 mm) and length (48mm) was observed in *G. raimondii* while shortest petals 21.0 mm width and 24.5 mm length in *G. thurberi*. The smallest (434 mm^2) and largest (1278 mm^2) flowers were produced by *davidsonii* and *raimondii*, respectively. All the D genomic species have dark petal spot. Petal spot of *G. raimondii* is largest with area of 672 mm^2, 32.3 mm wide and 38.1 mm length while *G. thurberi* (123 mm^2) and *G. trilobum* (99 mm^2) had smallest petal spot. Average calyx area of D genome was 241.17 ± 151.38 mm^2 with width 12.60 ± 5.78 mm and length 28.22 ± 13.39 mm. The maximum width (21.2 mm) and length (54.6 mm) was observed in *G. raimondii* and minimum width (4.2 mm) in *G. davidsonii* and length (15.0 mm) in *G. trilobum*. Maximum bract area (497 mm^2) was observed in case of *G. raimondii* and minimum bract area (16 mm^2) in *G. aridum*. The average bract width 9.60 ± 12.06 mm and length 17.70 ± 18.11 was observed and the bract width ranged from 3.3 mm (*G. aridum*) to 29.4 mm (*G. raimondii*) and bract length ranged from 8.4 mm (*G. trilobum*) to 48.3 (*G. raimondii*). The average teeth number was 4.30 ± 7.36 which was maximum in *G. raimondii* (15) and minimum in *G. thurberi*, *G. aridum and G. trilobum* (1). The various colors of anthers were also observed with varying number of anthers such as creamy white in *G. thurberi* (102), as well as in *G. trilobum* (98), yellow with red spots in *G. armourianum* (145), pink/reddish in *G. aridum* (138), and dark red or violet in case of *G. raimondii* (154), which having maximum number of anther among all species of D genome. The average number of anthers was 113.83 ± 36.88. The average style length 2.85 ± 0.97 cm and average ovary length 0.52 ± 0.11 cm was observed with the average number of ovule 21 ± 3.78, the style length ranged from 1.9 cm (*G. davidsonii*) to 4.5 (*G. raimondii*) and ovary length from 0.4 (*G. davidsonii*) and (*G. trilobum*) to 0.7 (*G. raimondii*). The maximum number of ovules is observed in *G. raimondii* (28) and minimum in *G. aridum* (16).

E Genome

Two species namely *G. stocksii* (E_1) and *G. somalence* (E_2) were studied for different flower characters. They had length of flower peduncle of length 0.7 and 1.7 cm respectively. Light yellow and yellow flowers were produced with the width of petal (11.4 mm and 18.2 mm) and length of petal (26.7 mm and 28.7 mm) respectively. Both the species had a petal spot. The petal spot of *G. somalence* was larger (136 mm^2) than *stocksii* 88 mm^2). Similar trend was observed for petal spot width (8.9 and 5.3 mm) and length (25.5 and 14.6 mm) respectively. The average calyx area of genome was 114 ± 35.0 mm^2 with the width 9.05 ± 1.15 mm and length 30.60 ± 8 mm. Among two species of E genome, the maximum calyx width (10.2 mm) and length (38.6 m) was observed in case of *G. stocksii* and minimum width (7.9 mm) and length (22.6 mm) in *G. somalense*. The average bract area was 270 ± 141 mm^2 with the width 14.85 ± 5.75 mm and length 44.95 ± 11.15 mm. The maximum bract width (20.6 mm) and length (56.1 mm) was observed in *G. somalense* while minimum bract width (9.1 mm) and length (33.8 mm) in *G. stocksii*. They had average no. of teeth 12.0 ± 3.0, the maximum teeth number observed in *G. somalense* (15) and minimum in *G. stocksii* (9). They produced cream coloured anthers (50) and faint yellow anthers (82) in *G. stocksii and G. somalense*, respectively. The average number of anthers was 66 ± 16. They had average style length 1.70 ± 0.40 cm and average ovary length 0.45 ± 0.05 cm with average number of ovule 9.5 ± 0.5.

F Genome

A single specis. *G. longicalyx* belonging to F genome studied which produced yellow flowers having peduncle length 1.2 cm and without petal spot. The area of petal was 474 mm^2 with the length and width of petal 29.5

and 20.3 mm respectively. The average calyx area was (143 mm^2) with width (10.7 mm) and length (24.1 mm) and average bract area 208mm^2 with the width (14 mm) and length (36.1 mm). It had average teeth number (1). It produced 63 yellow coloured anthers with the style length (1.5 cm) and ovary length (0.5 cm). The average number of (8) ovules.

G Genome

G bickii belonging to G_g genome, studied for its different floral characters produced pink flower having 2.1 mm peduncle length and area of petal was (584 mm^2) with, the length and width of 27.2 and 21.5 mm respectively, while the length and width of petal spot was 11.8 and 9.8 mm, respectively. The single G genome species i. e. *G bickii* had average calyx area of 139 mm^2 with width 8.4 mm and length 28.2 mm. The bract area in this species could not be measured because of very minute nature of the bracteoles. However, bract had length of 12.4 mm and width 10.5 mm. It produced an average 68 anthers/flower having yellow colour, style length (1.1 cm) and ovary length (0.4 cm). The average number of ovules in *G bickii* was 20/flower.

A_1D_1 Genome

Three races namely *Palmeri, Puntactum, Morilli* and three perennial types *viz.*, Yellow Spotted, Exotic-3, Seridov had average peduncle length 1.62 ± 0.42. The shortest (1.2 cm) peduncle length was recorded in Seridov and yellow spot while it was longest (2.3 cm) in Exotic-3. All of them were produced cream to yellow flowers. The average petal area of all species was 582.50 ± 66.94mm^2, among them Seridov had maximum petal area 674 mm^2 and Palmeri had minimum 482 mm^2. The maximum average petal width 32.1 mm was recorded in yellow spotted and minimum 22.0 mm was observed, in *Palmeri*, similarly the, longest petal was observed in *Punctatum* (48.9 mm) while shortest in palmeri (31.5 mm). *Palmeri, Punctatum, Morilli* and Seridov having petal spot while other do not have petal spot. The width of petal spot was maximum (8.8 mm) in Seridov and was minimum (4.6 mm) in *Palmeri*. Minimum length 11.8 mm in *Palmeri* and maximum (18.6 mm) in *Punctatum* was observed.

The average calyx area 271.33 ± 88.35 mm was observed with the length 39.65 ± 17.79 mm and width 11.75 ± 3.71mm^2. The width of calyx ranged from 6.8 mm (*Seridov*) to 17.5 mm (*Palmeri*) and longer calyx 76.4 mm was observed in *G punctuatum* and shorter (25.0 mm) in Seridov. They had average bract area 461.83 ± 98.80 mm^2 with the average length 42.03 ± 7.61 mm^2 and width 22.80 ± 2.93 mm. The various species had varying number of teeth, the *G morilli* was maximum (10) in number of teeth and exotic – 3 was minimum (3). The average number of teeth was 7.0 ± 2.38. The three species *G punctatum*, exotic – 3 and Seridov produced yellow coloured anthers with respective number 101, 107, 112 and *G palmeri, G morilli* and yellow spotted produced pale yellow coloured anthers such as 77, 98 and 84 in number, respectively. The average style length 2.42 ± 0.24 cm, average ovary length 0.82 ± 0.04 cm was observed with average number of ovules 27 ± 2.24. The yellow spotted was maximum (2.8 cm) in style length and *G palmeri* was minimum (2.1 cm). Similarly *G morilli* was maximum (0.9 cm) in ovary length and while rest of anthers having minimum (0.8 cm) ovary length. The yellow spotted having maximum (30) number of ovules.

A_2D_2 Genome

One perennial type of *G barbadense* under the name Kidney Cotton was studied, its yellow flower had peduncle length was 2.6 cm having dark yellow petals of size 42 mm width and 48 mm long. The petal area 1164 mm^2 was presented having petal spot area 92 mm^2. The length and width of petal spot was 5.4 mm and 14.8 mm respectively. It had calyx area 583 mm^2 with the width 17 mm and length 48.3 mm. The kidney cotton had larger bract area of 1102 mm^2 (64 mm x 49.5 mm) with 14 number of teeth. It produced yellow coloured 116 anthers and 27 ovules. Its style length and ovary length was 4.8 cm and 1 cm, respectively.

Corolla/Petal Colour

Corolla colour in the species of *Gossypium* studied is dependent upon the presence or absence of two distinct classes of sap soluble pigments-anthocyanin and flavonoids (Stephens, 1954). These two classes of pigments are controlled by independent genetic system and with few exceptions; there is little physical interaction between them (Hutchinson, 1931, Harland, 1937) established i) full yellow, pale and white constitute a multiple allelomorph series designated as **(y), (y/p)**, ii) The correlation between petal colour and petal size holds good for minor factors affecting corolla colour as well as for three members of the multiple allelomorph series and iii) The occurrence of plants with short petals and yellow flowers, or long petals and white flowers is

due to the reshuffling of modifying factors, their being a physiological relationship between petal colour and size.

Petal Spot

Petal spot in new world cottons is due to a series of basal spot, genes differing from species to species in i) relative potency on standard genetical background and ii) mutability. Spot in *G barbadense* is controlled by gene S^B. It is accompanied by series of genes modifier. The Y gene (yellow corolla) also acts as a strong modifier of S^B. Spot in *G hirsutum* is due to S^H (a relatively rare gene) which is an allele of S^B and spotless S (Harland, 1936; Harland, 1937; Harland, 1939 and Leake, 1911); size and colour of corolla found correlated (Leake, 1911).

Pollen Colour

The genes symbol Pa and Pb have been assigned to *G herbaceum* cream and *G arboreum* pale pollen respectively. Genotypes of *G anomalum* are reported to be *Pa Pb*, pollen colour being cream (Silow,1941; Ramanathan and Balasubrmanium, 1933).

Pollen varies among cotton breeding lines ranging from a near white colour to yellow or orange that favour food source for many adult insects. Variability in larval growth has been reported for tobacco budworm fed diets including yellow pollen (Hanny *et al.*, 1979; Bailey, 1981), such reduction in larval development is a additional source of insect pests resistance in cotton.

Boll weevil resistance associated with the frego bract trait (Bailey, 1981) which affect the feeding and oviposition behaviour of the boll weevil (Jones, 1972; Jones *et al.*, 1969). It is tolerant to *Heliothis zea* (Hedin, *et al.*, 1983; Jones *et al.*, 1978) to boll weevil (Ramanathan and Balasubramanium, 1933) and to bollworms (Karve *et al.*, 1977).

The narrow bract is also known as frego bract and is of twisting nature. In frego bract, the bracteole surface in greatly reduced. Hence such bracts do not provide shelter to bollworm larvae (Jones *et al.*,1964) on the other hand normal bract provides shelter to bollworm larvae. Moreover, it also contributes less trash in the lint. Contrary normal bracts, have large surface and cover more than half portion of the boll and hence contribute more trash in the lint.In addition frego bract genotypes have less boll rot (Jones *et al.*, 1969) and permit better penetration of insecticides on the flower buds. Thus frego bracts genotypes confer non-preference type of resistance to bollworms (Hunter *et al.*, 1965).

Caducous Bract

In cotton, persistent bracts remain till harvesting while caduceus bract fall before opening of bolls. Trait caduceus bract is governed by oligogenes hence, can be easily manipulated. The problems of disease can be controlled to some extent by developing cotton varieties with caduceus bract. Caducous bract is found in two wild species *G armourianum* and *G harknessii* both belonging to D genome (Muramoto, 1978).

Pedicel Length

Long pedicel is a desirable character which confers non preference type of resistance to bollworm, a long pedicel makes the movement of larvae more difficult from one boll to another. Cotton varieties with longer pedicel are more resistant to bollworms than those with shorter ones (Kadapa, 1988; Kadapa *et al.*, 1983).

From the date presented in Table 1, and Figures included plate 1 revealed that there is wide range in the floral characters of races and perennial types of cultivated cottons as well as wild species of *Gossypium*. Qualitative characters are under the control of either single or two genes (Sikka and Joshi,1960) and are included in the linkage groups. The information will certainly useful for selecting desired types from the segregation of populations both for improved yields, fibre quality parameters coupled with resistance to diseases and pests. Our attempts of preheating and handling of segregating material of *G arboreum x G anomalum* (Saitwal *et al.*, 2003 and Amolic, 2005), *G arboreum x G capitis viridis* (Amolic 2005), *G herbaceum x G anomalum* (Mehetre *et al.*, 2003) and *G arboreum x G thurberi* (Mehetre *et al.*, 2003 and Kale, 2005) has resulted in development of germplasm with promising germplasm lines marker characters *viz.*, ghost spot (Silow,1941), corrupted with pinkish petal colour, bract size and shape and improved fibre qualities of *G anomalum* (Deodikar, 1950) and boll size, shape and yield of *G arboreum* cotton(Amin, 1940). In addition introgression lines with white flower colour and naked seed of *G thurberi* introgressed into *G arboreum* cotton are also in F_5 generations. In these lines the chemical present in petals of *G thurberi* repel the pink bollworm moth from egg laying is expected (Ganesan, 1947; Hutchinson *et al.*, 1938; Squire, 1939). If confirmed, these lines will be a source of pink as well as Heliothis resistance. Further, studies are in progress.

Acknowledgement

Authors are thankful to ICAR for sanctioning Cotton Technology Mission Project under the Technology Mission on Cotton Mini Mission 1.3 where this work was carried out.

References

Amin KC (1940) Interspecific hybridization between Asiatic and new world cottons *Indian J Agric Sci* **10(3)**: 404-413.

Amolik VL (2005) Evaluation of progenies of interspecific hybrids of *Gossypium* spp. for sucking pests complex, bollworms and fibre quality parameters. *Ph D thesis submitted to the Mahatma Phule Krishi Vidyapeeth, Rahuri 413 712 (MS).*

Anonymous (1968) Genetics and cytology of cotton 5th Co-op *Ser Bull* **139**: 84.

Bailey JC (1981) Growth comparision of *Helithois virescene* (F) larvae fed white, yellow and orange cotton pollen. *Proc Beltwide cotton prod Res Conf* 79.

Deodikar GB(1950) Cytogenetic studies on crosses of *Gossypium anomalum* with cultivated cotton II. Substitution and addition of *Gossypium anomalum* chromosomes in the genome of the cultivated tetraploid cottons. *Indian J Agric Sci* **20**: 399-414.

Endrizi TE, EL Turcotte and RJ Kohel (1985) Genetics, cytology and evolution of *Gossypium. Adv Genet,* **23**: 272-327.

Fryxell PA (1992) A revised taxonomic interpretation of *Gossypium* L. (Malvaceae) *Rheedea* **2**: 108-165.

Fryxell PA (1976)*Gossypium*, a case history. USDA-ARS-S-137. US Government Printing Office, Washington, DC.

Ganesan D(1947) Interspecific hybridization in cotton. *3rd Conf. Cotton Gr Prob India, ICCC, Bombay,* 80-86.

Hanny BW, JC Bailey, and JR Meredith (Jr) (1979) Yellow cotton pollen suppress growth of tobacco budworm. *Environ Entomol* **8**: 706-707.

Harland SC (1937) The genetics of cotton XVII increased mutability of a gene in *Gossypium purpurascens* as a consequences of hybridization with *Gossypium hirsutum. J Genet* **34**: 153-168.

Harland SC (1939) The genetics of cotton. Jonathan Cape, London 193.

Harland SC(1936) The genetical conceptionof the species. *Biol Rev* **11**: 82-112.

Hedin PA, JN Jenkin, DH Collum, WH White and WL Parrot (1983) Multiple factors in cotton contributing to resistance to the tobacco budworm *Heliothis viresences* (F.) in PA Hedin (ed), Plant Resistance to Insects. American Chemical Society, Washington, DC 347-365.

Helentjaris T, M Slocum, S Wright, A Schaeffer, J Nienhuis (1986) Construction of genetic linkage maps in maize and tomato using restriction fragment length polymorphism. *J Theor Appl Genet* **72**: 761-769.

Hunter RC, TF Leigh, C Lincoln, BA Waddle, and LA Bariola. (1965) Evaluation of a selected cross section of cottons for resistance to the Boll Weevil. *Arkansas Agriculture Experiment Station Bulletin* 700.

Hutchinson JB (1931) The genetics of cotton.Part IV the incidence of corolla colour and petal size in Asiatic cottons. *J Genet* **24**: 325-353.

Hutchinson JB (1959).The application of genetics to cotton improvement. Cambridge Univ Press London

Hutchinson JB, PD Gadkari and MAA Ansari (1938) The genetics of Gossypium & its application to cotton breeding. *I^st Conf Sci Res Wrkrs Cott India, ICCC,* Bombay. p. 296-312.

Jones JE (1972) Effect of morphological characters of cotton on insects and pathogens. *Proc Beltwide Cotton Prod Res Conf* p 88-92

Jones JE, JA Andries, LW Sloane, SA Phillips and JG Marshall (1969) Effects of frego bracts on boll rot, yield and other important characters of Upland cotton. *Proc Beltwide Cotton Prod Res Conf* p 111-112

Jones JE, LD Newsom and KW Tipton (1964) Differences in boll weevil infestation among several biotypes of upland cotton. *Proc Sixteenth Annu Cotton Improvement Conf* p 48-55.

Jones JE, JA Andries, LW Sloane, SA Phillips and JG Marshall (1969) Effects of frego bract on boll rot, yield and other important characters of upland cotton. *Proc Beltwide cotton prod Res Conf* 111-112.

Jones JE, BR Williams, JW Brand, DF Clower, and DT Bowman (1978) Interacting effects of the okra leaf, frego bract and glabrous traits on pest resistance and agronomic performance. *Proc Beltwide Cotton Prod Res Conf* p 84-85

Kadapa SN, G Thimmaiah, and BM Khadi (1983) Seminar on "Cotton productivity Challenges In 80s". Karnataka Chambers of Commerce and Industry, Hubli,27-29th Oct.27-29 pp 1-8.

Kadapa SN (1988) The role of morpho-histological attributes in bollworm resistance. *"Bollworm" Seminar, Nagpur, India* 32-243.

Kale MB (2005) Morphological, Cytological and RAPD analysis of Parents, F_1,F_2 and Backcross (BC_1) Generations of Interspecific Cross *Gossypium arboreum, L.* X *Gossypium thurberi*, Tod. *M.Sc. thesis submitted to the Mahatma Phule Krishi Vidyapeeth, Rahuri (Maharashtra).*

Karve AC, AG Zirpe and AC Bhalerao (1977) Bollworm resistance in hirsutumcotton. *Nimbkar Agricultural Research Institute, Phaltan (Satara)*

Leake HM (1911a) Studies on Indian cotton *J Genet* **1**: 205-272.

Leake HM (1911a) Experimental studies in Indian cotton. *Proc. Roy Soc Ser B* **83**: 447-451.

Mehetre SS and SU Pardeshi (2004) Cotton improvement through interspecific hybridization of *Gossypium spp* – potential, problems, remedies and achievements. *National Symposium on Cotton held at Hyderabad,* 49-63.

Mehetre SS, VL Gawande, and AR Aher (2002a) Incompatibility in wide hybridization of *Gossypium* species causes and remedies A Review. *J Cotton Res Dev* **16(2)**: 111-124.

Mehetre SS, SD Patil and VL Gawande (2002b) Introgression of disease and pest resistance from wild to cultivated species of *Gossypium* – A Review *J Cotton Res Dev* **16(2)**: 178-181.

Mehetre SS, VL Gawande, AR Aher and AS Mokate (2003) Cytomorphology of an interspecific hybrid involving *G. herbaceum* and *G. anomalum Nucleus* **6(3)**: 138-146.

Mehetre SS, SD Patil, and AR Aher (2004 a) Improvement of fibre properties through interspecific hybridization (A Review) *J Indian Soc Cotton Improv* **29(2)**: 55-64.

Mehetre SS, VR Patil, AR Aher and GC Shinde (2003) Interspecific hybrids involving Genetic Male Sterile Line of *Gossypium arboreum* and *Gossypium thurberi*. *SABRAO J Breed Genet* **35(2)**: 71-79.

Mehetre SS, M Gomes, S Eapen, AR Aher and GC Shinde (2004b) RAPD and Cytomorphological Analysis of F1,F2 and Amphidiploid (A_1) Generation of *Gosspiym arboreum x Gossypium capitis viridis*. *Cytologia* **69(3)**: 367-369.

Meyer VG (1973) Registration of sixteen germplasm lines of upland cotton. *Crop Sci* **13**: 778-779.

Meyer VG (1975) Male sterility from *Gossypium harkensssii J Hered* **66(1)**: 23-27.

Muramoto H(1978) Cadicous bracts in cotton.In *Proc. Beltwide cotton production-Mechanization Conference, January 9-12, 1978, Dallas, Texas, USA* :17-18.

Murthy MS, and KT Achaya (1975) Cotton seed chemistry and Technology. *Publication and Information Directorate, Council of Scientific and Industrial Research, New Delhi.*

Narayanan SS, J Singh and PK Varma (1984)). Introgressive gene transfer in *Gossypium* Goal, Problems, strategies and achievements. *Cot Fib Trop* **390**: 123-135.

Niles GA (1980) Plant breeding and improvement of the cotton plant. *Outlook an Agric*. **10(4)**: 152-158.

Percival AE, JF Wendel and JMcD Stewart (1999) Origin, history, technology and production (eds). Smith CW and Cothern, JT John Willey and Sons, Inc. USA: 33-64.

Ramnathan V. and R Balsubrahamanyam (1933) Inheritance of pollen colour in Asiatic Cottons. *Indian J Agric Sci* **3**: 1116-1123.

Roxas NJL, Y Tashiro, S Miyazali, A Takeshita, T Oshima (1993) Isozyme analysis in *Chrysanthemums grandiflora* Tzvelvev *J Jpn Soc Hortic Sci* **61**: 919-924.

Saitwal VM, SS Mehetre, AH Sonone and VL Gawande (2003) Cytomorphology of F_1, F_2 Backcross generations of interspecific cross *Gossypium arboreum x Gossypium anonalum*. *Cytologia*. **68(4)**: 317-327.

Sikka SM and AB Joshi (1960) Genetics In Cotton Monograph-I (eds. Sethi *et al.*) *Indian Central Cotton Committee (ICCC), Mumbai* 403-466.

Silow RA (1941) The comparative genetics of *Gossypium anaomalum* and the cultivated Asiatic cottons *J Genet* **42**: 259-358.

Squire FA (1939) A note on the resistance of *Hibiscus esculentus* and *Gossipium trloum II. Emp Cott Gr Rev* **16**: 268-271.

Stephens SG Genetic (1954) Interspecific homologies between gene loci in Gossypium. *I Pollen colour II Corolla colour*. **739:** 701-711 and 712-723.

Syndecor GW and WG Cochran (1967) Statistical methods (6th ed.) *Oxford and IBH Co., New Delhi.*

Wendel JR (1989) New tetra plod cotton contains old world cytoplasm. *Proc Natl Acad Sci USA* **86:** 4132-4136.

Wendel JF and RC Cronn (2003) Polyploidy and the evolutionary history of cotton. *Advn Agron* **78**: 139-186.

Characterization of *Sesbania* Accessions Based on Isozyme System

Poonam Rani, Subhadra Singh, O.P. Yadav[1] and Jaivir Singh[1]
Department of Genetics, [1]Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, (Haryana) India

A set of 40 accessions of *Sesbania* belonging to 13 *Sesbania* species were characterized by fractionating 6 isozyme systems on polyacrylamide gel electrophoresis (PAGE). The isozyme systems studied were: acid phosphatase, amylase, catalase, glutamate dehydrogenase, peroxidase and malate dehydrogenase. These isozyme systems produced 193 polymorphic bands. A dendrogram was obtained using Jaccards similarity co-efficient and Unweighted Paired Group Method with Arithmetic Average (UPGMA) clustering method. Accessions were grouped into 11 clusters. Four accessions from *S. rostrata* species grouped together in the same cluster. Similar pattern of grouping was observed for *S. aculeata* accessions. An accession from *S. macrantha* species was uniquely isolated from rest of the clusters. However, there was no strict one to one relationship between botanical origin of accessions and their location in the dendrogram. The diversity analysis based on isozyme system may be used to identify diverse parents for inter and intraspecific hybridization in *Sesbania.*

Key words: *Sesbania*, Isozyme, Cluster analysis, Genetic diversity, UPGMA

The genus *Sesbania* is one of the important genera of legumes with multifarious benefits for mankind. It is an organic rich biofertilizer due to its heavy root nodulation. *Sesbania* species have also been used as indigenous folk and Ayurvedic, Unani and Siddha systems of medicines. Besides, it has many other uses like ruminant fodder, firewood, wood product, human food (Veasey *et al.*, 1999) and fibre as substitute for jute (Data and Bachi, 1991). With the alarming depletion of natural resources, continuing energy crisis, growing ecological concern from intensive cultivation and use of chemical fertilizers, pesticide and other inputs led to a renewal interest in the activities of research and utilization of *Sesbania* in the recent years, particularly in tropics and sub-tropics (Qadir *et al.*, 2002).

Considering the immense importance of the *Sesbania* species, systematic breeding efforts are required to improve the plant type and economic traits of the crop. Breeding programmes are contingent on germplasm resources. Accordingly, detailed genetic characterization of the *Sesbania* species is desired both for high efficiency of breeding strategy and for commercial seed production. Collection that has not been systematically characterized may contain many duplicates (Steiner and Poklemba, 1994).

Morphological characters have been generally used to study genetic diversity (Tanksley, 1983), but these characters are influenced by environmental factors. Protein markers including seed storage protein and isozyme are among the first group of molecular markers (Cooke, 1984) exploited for genetic diversity assessment. These markers are easy to screen, relatively simple to perform and the cost per sample is low. Isozymic markers have not been completely explored for the study of genetic diversity in the *Sesbania* species. Few reports are available on electrophoretic protein profile and isozymic characterization of *Sesbania.* Sarswati *et al.* (1993) analysed seed protein profile of 17 *Sesbania* species using sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE). The authors reported species-specific protein profiles for 15 of the 17 species. Recently, 22 accessions belonging to seven species of *Sesbania* were evaluated for isozyme electrophoretic patterns (Veasey *et al.*, 2002). They used eight isozymes: acid phosphatase (ACP), isocitrate dehydrogenase (IDH), phosphoglucomutase (PGM), malate dehydrogenase (MDH), phosphoglucoisomerase (PGI), glutamate oxaloacetate transaminase (GOT), peroxidase (PRX) and catalase (CAT) and classified the accessions in eight groups corresponding to the seven species and separate group for an accession of *S. exasperata.*

This study was intended to assess genetic diversity among 40 *Sesbania* accessions using six polymorphic isozyme systems *viz.*, acid phosphatase, amylase, catalase, glutamate dehydrogenase, peroxidase and malate dehydrogenase.

Materials and Methods

Plant Material

A set of 40 accessions representing a cross-section of variability among *Sesbania* species were obtained from National Bureau of Plant Genetic Resources (NBPGR),

New Delhi. These include 16 indigenous and 24 exotic collections belonging to 13 species from four different countries (Table 1). These accessions were coded: T1, T2 ....T40 to have brief text in their description.

Seeds of the accessions were imbibed on moist filter paper in petridishes at a constant temperature of 30± 2°C in an incubation.

Isozyme Assay

The following six isozyme systems were studied: acid phosphatase (E.C.3.1.3.2), amylase (E.C.3.2.1.1), catalase (E.C.1.11.1.6), glutamate dehydrogenase (E.C.1.4.1.2), peroxidase (E.C.1.11.1.7) and malate dehydogenase (E.C. 1.1.1.3.7).

Extraction of Enzymes from the Seeds

About 500 mg of 24 h imbibed seeds were used to prepare the enzyme extracts in 1.5 ml of appropriate buffer containing 5mM 2-mercaptoethanol and 5 mM EDTA using hand grinding method in chilled pestle and mortar by keeping in ice bucket. Crude extract was centrifuged at 10,000 rpm for 30 minutes at 4°C temperature. The supernatant was collected, stored in refrigerator at 4°C and used the same day for enzyme studies. Samples for catalase, peroxidase, glutamate dehydrogenase and malate dehydrogenase were extracted in 0.05 M sodium phosphate buffer (pH 7.4). Amylase and acid phosphatase were extracted in 0.05 M acetate buffer (pH 5.0). Enzymes were fractionated on polyacrylamide gels (8% running and 2.5% stacking gel) in anionic system using vertical electrophoretic apparatus. Tris buffer (pH 8.3) was used as an electrode buffer. The electrophoresis was allowed to begin with

Table 1. Details of 40 accessions of *Sesbania*

Coded Acc. No.	National Identity (IC/EC)	Species	Source
T1	EC 331970	*S. rostrata*	IRRI, Philippines
T2	EC 331973	*S. rostrata*	IRRI, Philippines
T3	IC 277784	*S. rostrata*	PAU, Ludhiana (Punjab), India
T4	EC 223312	*S. rostrata*	IRRI, Philippines
T5	EC 178342	*S. rostrata*	IRRI, Philippines
T6	EC 218472	*S. rostrata*	IRRI, Philippines
T7	EC 213472-A	*S. rostrata*	IRRI, Philippines
T8	EC 213473	*S. sesban*	IRRI, Philippines
T9	IC 277791	*Ses.PDCSR-1*	PDCSR, Modipurum (UP), India
T10	IC 27777	*S. aculeata*	PAU, Ludhiana (Punjab), India
T11	IC 277786	*S. aculeata*	PAU, Ludhiana (Punjab), India
T12	IC 277782	*S. aculeata*	PAU, Ludhiana (Punjab), India
T13	IC 277775	*S. aculeata*	PAU, Ludhiana (Punjab), India
T14	EC 509439	*S. sesban*	Brazil
T15	EC 509434	*S. exasperata*	Brazil
T16	EC 509442	*S. virgata*	Brazil
T17	IC Ses H-9	*S. aculeata*	Haryana, India
T18	IC Ses. H-1	*S. aculeata*	Haryana, India
T19	IC Ses. H-6	*S. aculeata*	Haryana, India
T20	IC 277789	*S. aculeata*	PAU, Ludhiana (Punjab), India
T21	EC 493668	*S. simplicuscula*	Australia
T22	EC 493666	*S. simplicuscula*	Australia
T23	EC 493664	*S. exaltala*	Australia
T24	EC 493681	*S. bispinosa*	Australia
T25	EC 493687	*S. exasperata*	Australia
T26	EC 493676	*S. leptocarpa*	Australia
T27	EC 493695	*S. campylocarpa*	Australia
T28	EC 493688	*S. exasperata*	Australia
T29	EC 493667	*S. simplicinscula*	Australia
T30	EC 493662	*S. exaltala*	Australia
T31	EC 493700	*S. cannabina*	Australia
T32	EC 493701	*S. macrantha*	Australia
T33	EC 493702	*S. macrantha*	Australia
T34	EC 493706	*S. speciosa*	Australia
T35	IC Pant-1	*S. aculeata*	Uttranchal, India
T36	IC Pant-3	*S. aculeata*	Uttranchal, India
T37	IC NBPGR3	*S. aculeata*	Najafgarh, New Delhi, India
T38	IC Ses.PDCSR2	*S. aculeata*	Modipurum (UP), India
T39	IC NIC-4149	*S. aculeata*	India
T40	IC NIC-4223	*S. aculeata*	India

15 mA current and supplied till tracking dye entered the gel and subsequently the current was increased to 40 mA for the plates till the marker dye recorded.3.5 mm from the other end of the plate. The enzymes acid phosphatase, amylase, GDH and MDH were detected using the staining methods of Stoddart (1971), Pearse (1972), Malik and Singh (1980) and Soltis *et al.* (1983), respectively. The methods of Robinson (1966) were used to detect catalase and peroxidase enzymes. Binary data matrix was generated taking '1' as presence and '0' as absence of a band. The genetic similarity for all possible pairwise combinations among 40 accessions were estimated using Jaccard's similarity index (1908). The distance measures were computed as complement of Jaccard's similarity index. Accessions were grouped by unweighted paired group method with arithmetic average (UPGMA) using the distance matrix (Romesburg, 1984).

Results and Discussion

Abundance of polymorphism for isozymic bands from six isozymic systems was present in *Sesbania* accessions. A total of 193 polymorphic bands were generated from 6 isozymic systems, namely acid phosphatase, amylase, catalase, GDH, peroxidase and MDH. Isozyme markers-based dendrogram grouped *Sesbania* accessions into 11 clusters (Fig. 1). The groups are presented in Table 2. Cluster 1 consisted of 7 accessions, and all were from Australia. Cluster 2 was the largest cluster containing 9 accessions: 3 from Brazil and 6 from India. Cluster 3 contained 6 accessions all from Philippines except one from Australia. Four accessions were included in cluster 4, three were from Australia and one was indigenous. Cluster 5 contained only two accessions, one from Australia and another from India. Three accessions were included in the cluster 6, two accessions were indigenous and one from Philippines. Cluster 7 and 8 contained only one accession each and both were from India. Cluster 9 consisted of 4 accessions, all were from India. The clusters 10 and 11 contained two and one accession, respectively and all were from Australia.

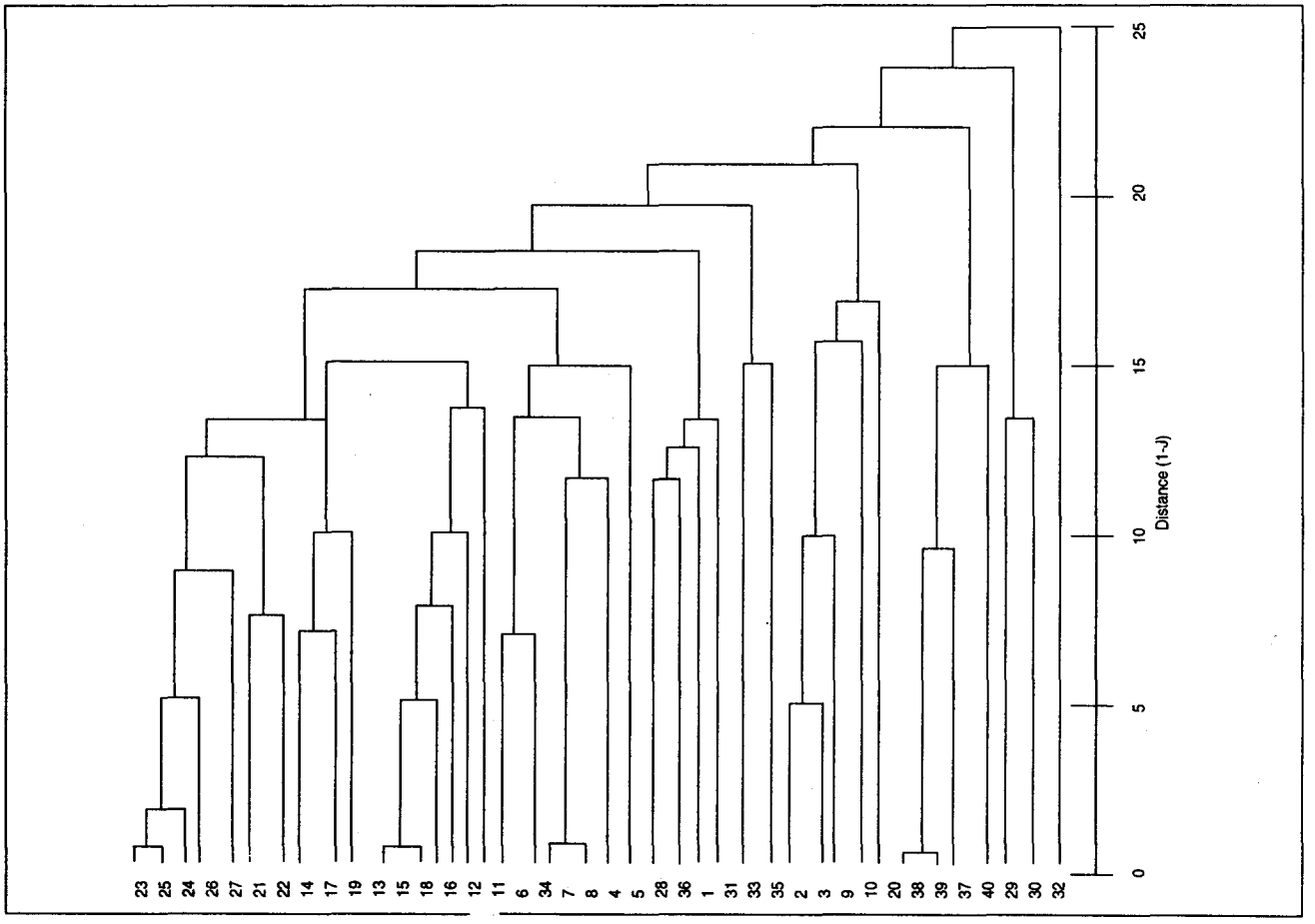


Fig. 1: Dendrogram from the cluster analysis with presence/absence of band (193 bands) from six isozymatic systems, using Jaccard index (J) and UPGMA method

Interestingly, four accessions from *S. rostrata* species grouped together in the same cluster (Cluster number 3). More or less, similar pattern of grouping was observed for *S. aculeata* accessions. However, overall grouping of the accessions did not exhibit one to one relation between botanical origin of accessions and their location in the dendrogram. For example, accessions of *S. exaltala*, *S. bispinosa*, *S. exasperata*, S. *leptocarpa*, *S. campylocarpa*, and *S. simpliciuscula* were not separated in the dendogram and were present together in cluster number 1. Similar results have also been reported by Samec *et al.* (1998) in pea and Veasey *et al.* (2002) in *Sesbania*. To the best knowledge of the authors, there is only one report on isozymic characterization in *Sesbania* by Veasey *et al.* (2002). The accession T32 from *S. macrantha* species was uniquely isolated from rest of the clusters and located in cluster number 11. The dendrogram produced from isozymic profiling revealed larger interspecific variation than intraspecific variation. The diverse accessions selected from isozymic based dendrogram may be used to exploit potential parents for inter and intraspecific crossing in *Sesbania*. Similar to grouping pattern in isozymic-based dendrogram, the accessions of *S. rostrata* and the accessions belonging to *S. aculeata* also grouped in their respective clusters in the dendrograms produced from morphological data (Poonam, 2005). However, there were some differences in dendrogram pattern generated from morphological and isozymic data. This may be due to several reasons, such as lack of some of the important morphological/ taxonomic characters related to botanical origin of accessions; isozymic profiles from six isozymic systems

Table 2. Composition of isozyme based clusters and the geographical origin of *Sesbania* accessions

Cluster	No. of Accessions	Coded Acc.	Species	Accession	Origin/Source
1	7	T 23	*S. exaltala*	EC 493664	Australia
		T 25	*S. exasperata*	EC 493687	Australia
		T 24	*S. bispinosa*	EC 493681	Australia
		T 26	*S. leptocarpa*	EC 493676	Australia
		T 27	*S. campylocarpa*	EC 493695	Australia
		T 21	*S. simpliciuscula*	EC 493668	Australia
		T 22	*S. simpliciuscula*	EC 493666	Australia
2	9	T 14	*S. sesban*	EC 509439	Brazil
		T 17	*S. aculeata*	IC Ses H-9	Haryana (India)
		T 19	*S. aculeata*	IC Ses H-6	Haryana (India)
		T 13	*S. aculeata*	IC 277775	PAU, Ludhiana (India)
		T 15	*S. exasperata*	EC 509434	Brazil
		T 18	*S. aculeata*	IC Ses H-1	Haryana (India)
		T 16	*S.virgata*	EC 509442	Brazil
		T 12	*S. aculeata*	IC 277782	PAU, Ludhiana (India)
		T 11	*S. aculeata*	IC 277786	PAU, Ludhiana (India)
3	6	T6	*S. rostrata*	EC 218472	IRRI, Philippines
		T34	*S. speciosa*	EC 493706	Australia
		T7	*S. rostrata*	EC 213472-A	IRRI, Philippines
		T8	*S. sesban*	EC 213473	IRRI, Philippines
		T4	*S. rostrata*	EC 223312	IRRI, Philippines
		T5	*S. rostrata*	EC 178342	IRRI ,Philippines
4	4	T28	*S. exasperata*	EC 493688	Australia
		T36	*S. aculeata*	IC Pant-3	Uttranchal (India)
		T1	*S. rostrata*	EC 331970	Australia
		T31	*S. cannabina*	EC 493700	Australia
5	2	T33	*S. macrantha*	EC 493702	Australia
		T35	*S. acuelata*	IC Pant-1	Uttranchal (India)
6	3	T2	*S. rostrata*	EC 331973	IRRI, Philippines
		T3	*S. rostrata*	IC 277784	PAU, Ludhiana
		T9	*S. aculeata*	IC 277791	Modipurum (U.P.)
7	1	T10	*S. aculeata*	IC 277777	PAU, Ludhiana
8	1	T20	*S. aculeata*	IC 277789	PAU, Ludhiana
9	4	T38	*S. aculeata*	IC PDCSR2	Modipurum (U.P.)
		T39	*S. aculeata*	IC NIC-4149	India
		T37	*S. aculeata*	IC NBPGR-3	Najafgarh, New Delhi
		T40	*S. aculeata*	IC NIC-4223	India
10	2	T29	*S. simpliciuscula*	EC 492667	Australia
		T30	*S. exaltala*	EC 493662	Australia
11	1	T32	*S. macrantha*	EC 493701	Australia

may have covered only part of whole of the genome; genotype x environment interaction for morphological characters, and variables are standardized (mean zero and variance one) while Euclidean distances among accessions are calculated from agromorphological data. This made all variables (15 agromorphological characters) equally important in determining these distances. Thus, standardization has the effect of minimizing group differences, because if groups are separated well by X_i variable, then the variance of X_i will be large (Manly, 1994). Therefore, inbuilt mechanism of the computation procedure adopted for field data may be one of the factors for observed discrepancy between clustering patterns from field observations via-a-vis isozymic electrophoresis data. This requires a further detailed study for its confirmation. Despite the increasing significance of DNA markers in cultivar identification and phylogenetic studies, the use of isozymes in combination with DNA markers and morphological traits may be still very useful and important (Havey and Muehlbauer, 1989; Chase *et al.*, 1991; Gepts, 1995; Torres *et al.*, 1994; Hoey *et al.*, 1996; Samec *et al.*, 1998). The study established the utility of isozymes for assessing genetic diversity and in grouping of *Sesbania* accessions. However, further investigations using DNA based molecular markers are required to establish the phylogenetic relationship of botanical origin of *Sesbania* accessions.

References

Chase CD, VM Ortega, and CE Vallejos (1991) DNA restriction fragment length polymorphism correlate with isozyme diversity in *Phaseolus vulgaris* L. *Theor Appl Genet* **81:** 806-811.

Cooke RJ (1984) The characterization and identification of crop cultivars by electrophoresis. *Electrophoresis* **5:** 59-72.

Data RM and S Bachi (1991) Intercropping between two fibre producing species of *Sesbania* (*S beuthomiania* and *S brachycarbia*). *Agri and Agro Industries J* **4:** 21-22.

Gepts P (1995) Genetic markers and core collections. In: T Hodgkin, AHD Brown, TJL Van Hintun and EAV Morales (Eds), Core collections of plant genetic resources. pp. 127-146. J Wiley and Sons, Chichester.

Havey MJ and FJ Muehlbauer (1989) Linkages between restriction fragment length, isozyme and morphological characters in lentil. *Theor Appl Genet* **77:** 395-401.

Hoey BK, KR Crowe, VM Jones and NO Polans (1996) A phylogenetic analysis of *Pisum* based on morphological characters, and allozyme and RAPD markers. *Theor Appl Genet* **92:** 92-100

Jaccard P (1908) Nouvelles recherches sur la distribution florale. *Bull Soc Vaud Sci Nat* **44:** 223-270.

Malik CP and MB Singh (1980) Plant Enzymology and Histo-enzymology: A Text Manual. Kalyani Publishers, New Delhi. 137.

Manly BFJ (1998) Multivariate Statistical Methods A Primer. 2nd edition, Chapman & Hall/CRC.

Pearse AGE (1972) Histochemistry, Theoretical and Applied. Vol. III London: Churchill.

Poonam Rani (2005) Genetic variability among the accessions of *Sesbania* species for morphological and biochemical markers. M Sc Thesis, CCS HAU, Hisar.

Qadir M, RH Qureshi and N Ahmad (2002) Amelioration of calcareous saline sodic soils through phytoremediation and chemical strategies. *Soil Use and Management* **18(4):** 581-585.

Robinson K (1966) An examination of *Corynebacterium* spp. by gel electrophoresis. *J Appl Bact* **29(1):** 179-184.

Romesburg HC (1984) Cluster Analysis for Researchers. Lifetime Learning Publications, Belmont, California.

Samec P, Z Posvec, J Stejskal, V Nasinec and M Griga (1998) Cultivar identification and relationships in *Pisum sativum* L. based on RAPD and isozymes. *Biol Plant* **41(1):**39-48.

Saraswati R, T Matoh, T Sasai, P Phupaibul, TA Lumpkin, M Kobayashi and J Sekiya (1993) Identification of *Sesbania* species from electrophoretic patterns of seed proteins. *Trop Agric* (Trinidad) **70(3):** 282-285.

Soltis DE, CH Hanfler, DC Darrow and GJ Gastony (1983) Starch gel electrophoresis of ferns: A compilation of grinding buffers, gel and electrode buffers and staining schedules. *Amer Fern J* **73:** 9-27.

Steiner JJ and CJ Poklemba (1994) Lotus corniculatus classification by seed globulin, polypeptides and relationship to accession pedigrees and geographic origin. *Crop Sci* **34:** 255-264.

Stoddart JL (1971) Sequential changes in amylase isoenzymes during grains maturation in barley. *Planta* **97**: 70-82.

Tanksley SD (1983) Molecular markers in plant breeding. *Plant Mol Biol Rep* **1:** 3-8.

Torres AM, J Satovic, J Canovas, A Martin and JI Cubero (1994) Faba bean mapping with trisomic. Linkage among morphological, isozyme and RAPD markers. In: JV van Ooijen and J Jansen (Eds). Biometrics in Plant Breeding: Applications of Molecular Markers. pp. 259-260. CPRO-DLO, Wageningen, the Netherlands, 1994.

Veasey EA, EA Schammass, R Vencovsky, PS Martins and G Bandel (1999) Morphological and agronomical characterization and estimates of genetic parameters of *Sesbania* scop (Leguminosae) accessions. *Genet and Molecular Biol* **22(1):** 81-93.

Veasey EA, R Vencovsky, PS Martins and G Bandel (2002) Germplasm characterization of *Sesbania* accessions based on isozyme analyses. *Genet Resour and Crop Evolution* **49**: 449-462.

Molecular Characterization of Genetic Diversity in Glutinous Rice of Assam using RAPD Marker

RN Sarma* and D Barooah
Department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat-785013

The genetic diversity of 60 glutinous rice accessions of Assam was analyzed using 17 RAPD primers. Out of the 160 reproducible bands, 145 found to be polymorphic. The number of polymorphic bands ranged from 4 (OPL-17) to 18 (OPB-07). With an average of 88.75% polymorphism between the accessions, a high degree of molecular variation was detected in the rice collection. The average Jaccard's similarity co-efficient based on RAPD data was found to be 0.446, indicating a high level of diversity in the glutinous rice of Assam. The cluster analysis grouped the accessions in to nine sub clusters. Implications of these findings in indigenous glutinous rice conservation and improvement are discussed.

Key words: Glutinous rice, Bora rice, Chakuwa rice, Genetic diversity, Assam rice, RAPD

Among different classes of rice available in Assam, glutinous or waxy rice (locally known as 'Bora' rice) is an important class. This class, with higher amylopectin than amylose, is considered as soft rice because of its soft cooking consistency. Based on amylose content, the glutinous rice of Assam has been classified into two groups, Bora and Chokuwa. The amylose content of Chokuwa varieties varies between 15 and 20%, while that in Bora varieties found to be in trace (Dutta and Barua, 1978). Glutinous rice or Bora rice of Assam has significance in social and religious ceremonies and forms a popular daily breakfast diet in rural Assam. The local people use Bora rice in the preparation of snacks, flat rice, puffed rice, sweet rice beer and other dishes. The Bora rice of Assam has the potential of greatly increasing exports into this market, owing to its cooked stickiness (i.e. low amylose content), which is preferred by the South East Asian market.

Bora rice germplasm of Assam constitute an important source of genetic variation for breeding of improved Bora variety/hybrid, and their conservation and characterization is an important component in this direction. Though some of the germplasm of this important class of rice has been maintained in Assam Agricultural University (AAU) and elsewhere, no effort has been made to study the nature and extent of diversity along with possibility of redundant accessions in *ex-situ* conserved materials (Barooah and Sarma, 2004). The difficulty of studying diversity based on morphological data is well demonstrated in various studies (Ahmed and Das, 1990; Das and Ahmed, 1992). Barooah and Sarma (2004) reported the use of molecular marker in diversity analysis of Assam rice, particularly in sali rice (winter rice). The use of molecular marker data alone or in combination with morphological characterization is considered as best to characterize the genetic diversity.

There is very little information available on the nature and extent of genetic diversity of Bora rice of Assam, particularly at the molecular level. Hence the present study was conducted to characterize and document the genetic variation by identifying the DNA profile in few glutinous rice accessions of Assam using RAPD marker.

Material and Methods

Sixty glutinous rice accessions, including Bora and chokuwa types, were obtained from Regional Agricultural Research Station, Assam Agricultural University, Titabar. The list of the accessions with their place of collection is given in Table 1. Some of the accessions with same name have been maintained because of inability to distinguish them on the basis of morphology.

Genomic DNA was isolated from seeds following Plaschke et al (1995) with minor modification. Two to three seeds of each accession were crushed with a mortar and pestle to a fine powder for DNA extraction using 1000 ul of extraction buffer (1M Tris-Cl, pH 8.0, 5M NaCl; 500mM Na_2 EDTA; 20%SDS). The homogenate was centrifuged to remove cell debris. The supernatant was treated with RNase and DNA was precipitated with chilled 95% alcohol. The quality and quantity was assayed by running DNA on a 0.8% agarose gel alongside a known quantity of lambda uncut DNA.

*Author for correspondence: E-mail: masarma@aau.ac.in,ramen5in@yahoo.co.in

Table 1. Glutinous rice accessions used in the study

Sl. No.	Name	Place of collection	Sl. No.	Name	Place of collection
1.	Aghoni Bora	High yielding variety	31	Kmj B 2	Karimganj
2	Bao Bora	Dhakuakhana, Lakhimpur	32	Kmj B 48	Karimganj
3	Beji Bora	Dhakuakhana, Lakhimpur	33	Kmj B 9	Karimganj
4	Boga Bora 1	Rowraih, Jorhat	34	Kola Bora	Titabar, Jorhat
5	Boga Bora 2	Nagaon	35	Malbhog Bora	Jorhat
6	Bogachokua	Titabar, Jorhat	36	Memon Bora	Lakhimpur, Lakhimpur
7	Bor Bora	Golaghat, Golaghat	37	Moju Chokua	Titabar, Jorhat
8	Bor Chokua	Jorhat, Jorhat	38	Mon Bora 1	Saraibahi, Jorhat
9	Bora 1	Nalbari, Kamrup	39	Mon Bora 2	Borhola, Titabar
10	Bora 2	Silghat, Nagaon	40	Nae lace Bora	Golaghat, Golaghat
11	Bora 3	Jagiroad, Morigaon	41	Nalia Bora	Kampur, Nagaon
12	Bora 4	Dibrugarh	42	New Bora 2	Nagaon
13	Bora 5	Sibsagar	43	New Bora 5	Nagaon
14	Bormalbhog	Goalpara	44	New Bora 6	Kampur, Nagaon
15	Chandra Bora	Jorhat, Jorhat	45	New Bora 7	Lakhimpur, Lakhimpur
16	Chokua Bora	Titabar, Jorhat	46	New Bora 8	Nagaon
17	Ghew Bora	Batadrava, Nagaon	47	Poita Bora	Rangajan, Golaghat
18	Goruckokua Bora	Janji, Jorhat	48	Ranga Bora	Titabar, Jorhat
19	Helochi Bora	Dergaon, Jorhat	49	Rangali Bora	Titabar, Jorhat
20	Jangoni Bora	Jorhat	50	Runohi Bora	Bokakhat, Golaghat
21	Joha Bora	Sibsagar	51	Rupahi Bora	Batadrava, Nagaon
22	Jota Bora	Golaghat	52	Sam Chokua	Dergaon, Jorhat
23	Kajoli Bora 1	Rupahi, Nagaon	53	Saudung Bora	Borhola, Titabar
24	Kajoli Bora 2	Sibsagar	54	Sukoni Bora 1	Borhola, Jorhat
25	Kakhichakua Bora	Nagaon	55	Sukoni Bora 2	Titabar, Jorhat
26	Kauri Bora	Titabar, Jorhat	56	Tagun Bora	Kochajan, Titabar
27	Khaldhor Bora	Jorhat	57	Til Bora 1	Golaghat
28	Khamti Bora	Arunachal Pradesh	58	Til Bora 2	Dergaon, Jorhat
29	Kmj B 10	Karimganj	59	Titanhulia Bora	Dhemaji, Lakhimpur
30	Kmj B 13	Karimganj	60	Tulasi Bora	Rupahi, Nagaon

Amplification reaction was carried out in a 25ul reaction volume containing 10ng of template DNA, 50pM of primer, 200μM of dNTPs, 0.5 unit of Taq polymerase (Bangalore Genei Pvt. Ltd, Bangalore, India) and 1XPCR Buffer (50mM KCl, 10mMTris-Cl, 2mM, 0.01% gelatin). Initially thirty decamer random primers (Operon Technologies, Inc., Alamanda, CA, USA) were used for RAPD amplification as described by Williams *et al.* (1990) with minor modification. Amplification reaction was performed in a thermal cycler (Gene amp PCR2400, Applied Biosystem, USA) for 35 cycles. Each cycle consisted of denaturation for 1 minute at 94°C, 1 min annealing at 37°C, followed by a 5 min for primer elongation at 72°C, and final elongation for 1 min at 72°C. The PCR products were resolved by electrophoresis in 1.5% agarose gel in 1XTBE buffer, ethidium bromide stained gel was photographed with a digital gel documentation system (Ultra-violet products, UK). Reproducibility of RAPD assay was tested by performing duplicate reactions at different times using identical genotypes and primer combinations under strict control of experimental conditions and only the reproducible bands were scored.

The RAPD bands were scored as present (1) or absent (0) for each genotype-primer combination of all the 60 glutinous rice accessions, considering each amplified band as unique locus. Band-sharing data were used to calculate genetic similarities using Jaccard's coefficient (Jaccard, 1908). The similarity matrices were analyzed using NTSYS-PC 2.10 (Rohlf, 2002) and clustered with UPGMA (un-weighted pair group methods using arithmetic average) algorithm to determine the genetic relationships of the 60 Bora rice accessions and the dendrogram was constructed using NTSYS-PC. The average similarity index for all pair wise comparison ($\bar{X}_D$) was calculated and used to estimate the probability of DNA fingerprints of two genotypes being identical by chance (Wetton et al. 1987, Ramkishna et al. 1994) with the formula $(\bar{X}_D)^n$, where $(\bar{X}_D)$ = average similarity index and n= the average number of bands per accession.

Results and Discussion

Out of the 30 primers tested, 17 primers were selected to detect polymorphism in glutinous rice accessions based on their reliability of amplification profile. The amplification profile, generated by the 17 primers, is summarized in Table 2. The number of polymorphic

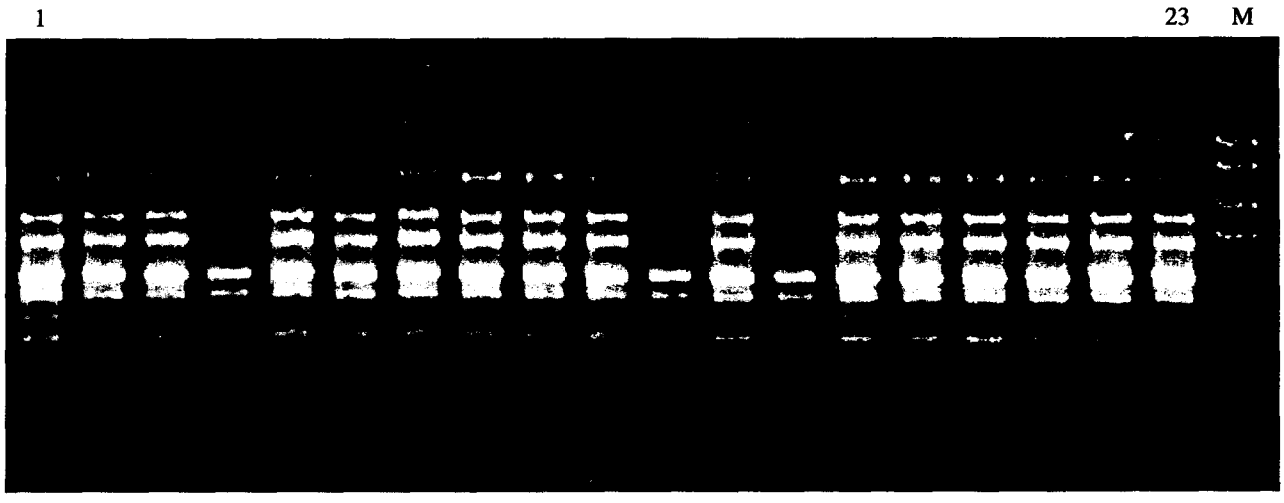


Fig.1. A representative RAPD amplification profile in glutinous rice of Assam with primer OPB08. Numbers (from 1to 23) represent the accessions as per Table 1.

Table 2. Summary of RAPD data of 60 glutinous rice accessions

Primers	Total band	Polymorphic bands	Polymorphism (%)
OPB 07	18	15	83.33
OPB 08	9	8	88.89
OPB 10	11	10	90.91
OPD 01	7	7	100.00
OPD 03	8	8	100.00
OPD 18	9	8	88.89
OPD 20	13	11	84.62
OPH 04	7	7	100.00
OPH 05	9	8	88.89
OPH 07	13	12	92.31
OPH 19	9	8	88.89
OPH 20	9	9	100.00
OPK 14	6	2	33.33
OPK 19	8	8	100.00
OPL 17	4	3	75.00
OPM 16	10	9	90.00
OPP 02	10	9	90.00
Total	160	142	88.75

bands ranged from 4 (OPL-17) to 18 (OPB-07) with an average of 88.75% polymorphism. The size of amplified products ranged from 0.05 kb to 2.5 kb.

The average similarity index, based on Jaccard co-efficient, was 0.446, indicating that existing diversity was sufficient to distinguish any given two accessions. The similarity co-efficient ranged from 0.275 (between 'Titanhulia Bora' and 'Bor Bora') to 0.840 (between 'New Bora 8' and 'Bora 2'). The place of collection revealed that the two most dissimilar accessions were collected from two different districts on either side of Brahamputra valley, whereas, the two most similar accessions came from same district. The phenetic representation of similarity co-efficient among 60 glutinous rice accessions is presented in Figure 2. The dendogram classified 60 glutinous rice genotypes into two major clusters (A and B) with 42 and 18 accessions, respectively. The major group A could be classified into seven sub clusters. The sub cluster A1 comprised of seven genotypes, in which 'Bora 2' and 'New Bora 8' (from Nagaon district with 0.84% similarity) was grouped together, indicating close genetic similarity between these accessions. The sub cluster A2 comprised of 11 accessions, out of which six were semi-glutinous or chokuwa accessions ('Sam Chokua', 'Bor Chokua', 'Chokua Bora', 'Goruckokua Bora', 'Moju Chokua' and 'Bogachokua'). The clustering pattern in this sub cluster revealed that semi-glutinous accessions showed some difference from glutinous accession. Despite most of accessions were collected from same district, the average similarity of 0.465 among the chokuwa accessions indicated sufficient genetic differences among themselves. The sub-clusters A3 and A4 consisted of nine genotypes each. In thse two sub-clusters, the accessions from Borak valley of Assam were included. The three sub clusters, A5, A6 and A7, were comprised of two genotypes each.

The cluster B comprised of two sub-clusters, and the 'Bora 3' showed sufficient genetic divergence from the other genotypes in this cluster. Seven accessions form another sub cluster B1, in which 'Nalia Bora' (collected from Nagaon) and 'Kauri Bora' (collected from Golaghat) were grouped together with 0.834% similarity revealing some genetic similarity between them. In this sub cluster 'Aghoni Bora' and 'Bora 1' showed divergence from the rest. It is worthwhile to

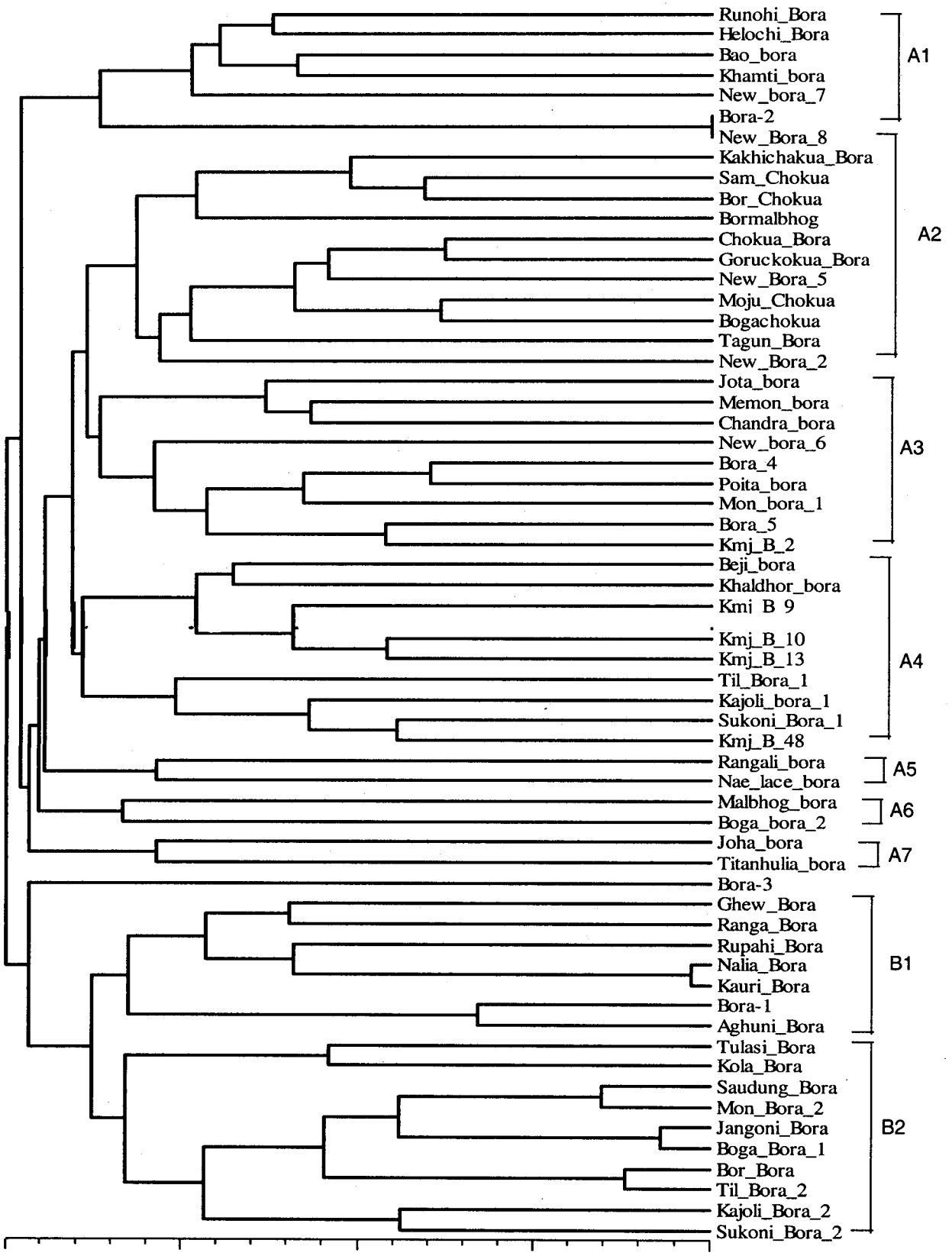


Fig.2: Dendrogram of 60 glutinous rice genotypes constructed using UPGMA based on 160 RAPD bands using Jaccard's coefficient of similarity

mention that 'Aghoni Bora' is a high yielding variety developed in AAU (pedigree 'Gandhi Bora' x 'Kmj-1-52-2') (Pathak, 2001). The sub cluster B2 includes ten accessions, in which 'Kajoli Bora 2' and 'Sukoni Bora 2' showed genetic divergence from the rest of accessions. Some of accessions with common names (e.g. 'Kajoli Bora 1' and 'kajoli Bora 2' with 43% similarity); ('Boga Bora 1' and 'Boga Bora 2' with 44% similarity) were found to be different, based on RAPD data.

This study revealed existence of sufficient genetic variation at DNA level in Bora rice collection maintained in Assam Agricultural University. This clustering pattern was not associated with geographic locations. Genetic drift and unconscious selection from original land races might have contributed to this situation. The probability of banding pattern being identical by chance in any two Bora accession was 4.39×10^{11}, suggesting that about 10^{11} Bora accession can be distinguished with the 17 primers used. This indicates the high resolving power of RAPD markers to distinguish Bora rice accession of Assam. Knowledge about the distribution of genetic variation among the Bora landraces plays crucial role in their conservation and utilization in breeding programme. However, accessions that are found similar based on molecular genetic data may differ in just one important trait. So before declaring similar accessions as redundant, evaluation data and end user request should be considered or otherwise molecular data should be considered to identify those as redundant (Treuren *et al.*, 2001).

Acknowledgement

This work was carried out under the Department of Biotechnology, Govt of India funded project. We are grateful to the Chief Scientist, RARS, AAU, Titabar for providing the seeds of the accessions used in the study.

References

Ahmed T and GR Das (1992) Inheritance of anthocyanin pigmentation and endosperm character of glutinous rice. *Oryza.* **27:** 220-223.

Barooah D and RN Sarma (2004) Genetic diversity analysis of traditional Sali rice germplasm of Assam through RAPD marker. *Ind. J. of Genet. and Plant Breed.* **64:** 5-8.

Das GR and TAhmed (1982) Distribution of pigments in glutinous rice. *Oryza.* **19:** 114-116.

Dutta L and JN Barua (1978) Nutrient composition of glutinous & nonglutinous rice varieties grown in Assam. *Indian J. of Agric. Sci.* **48:** 610-613.

Jaccard P (1908) Nouvelles réchèrches sur la distribution florale. *Bull. Soc. Vaud. Sci. Nat.* **44:** 223-270.

Pathak P K (2001) Major cereal crops of Assam. *In*: Agriculture in Assam, (eds) by AC Thakur, H Bhattacharya and DK Sarma. p 53-77 Directorate of Extension Education, Assam Agricultural University, Jorhat.

Plaschke J, MW Ganal and MS Röder (1995) Detection of genetic diversity in closely related bread wheat using micro satellite markers. *Theor. Appl. Genet.***91:** 1001-1007.

Ramkshina W, MD Lagu, VS Gupta and PK Ranjekar (1994) DNA fingerprinting in rice using oligonucleotide probes specific for simple repetitive DNA sequences. *Theor. Appl. Genet.* **88:** 402-406.

Rohlf FJ (2002) NTSYSpc: Numerical Taxonomy System, ver. 2.1. Exeter Publishing, Ltd.: Setauket, NY.

Treuren van R, JM van Soest and Th.JL van Hintum (2001) Marker assisted rationalization of genetic resource collection: a case study in flax using AFLP. *Theor. Appl. Genet.* **103:** 144-152.

Wetton JH, RE Carter, DT Parkin and D Walters (1987) Demographic study of the wild house sparrow population by DNA fingerprinting. *Nature.* **327:** 147.

Williams JGK, AR Kubelik, KJ Livak, JA Rafalski and SV Tingery (1990) DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. *Nucl. Acid Res.* **18:** 6231-6235.

Studies on Genetic Diversity for Growth, Yield and Quality Traits in Chilli (*Capsicum annuum* L.)

AD Munshi, B Krishna Kumar, AK Sureja[1], Subodh Joshi and Ravinder Kumar
Division of Vegetable Science, Indian Agricultural Research Institute, Pusa, New Delhi 110 012
[1]Department of Vegetable Science, College of Horticulture & Forestry, Central Agricultural University, Pasighat 791 102 (Arunachal Pradesh)

The genetic diversity was studied in 30 genotypes of chilli using 14 quantitative traits. D^2 analysis using Tocher's method resulted in eight clusters representing the genetic diversity among the genotypes studied. The cluster I (ACS 2000-02, Green Wonder, Motikeera 39) representing genotypes with highest fruit length, fruit width, fruit weight and ascorbic acid could be selected if the aim of the breeding programme is to improve any of these traits. The cluster VIII having a single genotype Pusa Sadabahar, possesses either higher or lower value for most of the traits, justifying its inclusion as a separate cluster. Cluster VII (DCL 228, DCL 335, DCL 901, DCL 001, DCL 268, Red Star, Soldier, DCL 344 and DCL 266) topped in having maximum number of genotypes among clusters formed, while maximum inter-cluster distance was noticed between cluster I and cluster VIII. Cluster I and VIII were identified as important clusters with respect to various traits. Therefore, the genotypes in these two clusters may be utilized in multiple breeding programmes to recover transgressive segregants with desirable combinations. The genotypes in cluster VI (RC 1-1,DCL-008) exhibiting high yield might be tested for their stability for few years in multilocation trials and if found suitable, may be directly adopted as high yielding varieties. Cluster VII topped in having maximum number of genotypes among clusters formed, while maximum inter-cluster distance was noticed between cluster I and cluster VIII. Cluster I and VIII were identified as important clusters with respect to various traits. Therefore, the genotypes in these two clusters may be utilized in multiple breeding programmes to recover transgressive segregants with desirable combinations.

Key words: *Capsicum annuum*, Genetic diversity, Cluster, Chilli

Chilli (*Capsicum annuum* L.) is a popular vegetable and spice crop in India and many parts of the world. It provides a wide range of variability and diversity with a tremendous scope for genetic studies and improvement by breeding. The selection of parents for the purpose of breeding depends on the existence of genetic diversity necessitating its assessment for improvement of quantitative traits. Several workers have evaluated germplasm of chilli for yield and its component traits (Singh and Singh 1976; Mehra and Peter 1980; Pandey and Dobhal 1994; Roy and Sarma 1996; Oliveira *et al.*, 1999).

Materials and Methods

The experimental material comprised of thirty genotypes of chilli assembled from various parts of India (Table 1). Genotypes were grown in three replications in a randomized block design during *Kharif* season of 2001. Spacing was maintained at 60 cm between the rows and 30 cm between the plants. Observations were recorded on five randomly selected plants in each replication for fourteen traits *viz.*, plant height (cm), number of primary branches, number of secondary branches, days to flowering, days to first fruit harvest, fruit length (cm), fruit width (cm), number of fruits

Table 1. Chilli genotypes used for evaluation

Genotype(s)	Place of collection
ACS 2000-02	Anand (Gujarat)
ACS 98-9	Anand (Gujarat)
DCL 408	Lam (Andhra Pradesh)
DKC 8	Sirmour (Himachal Pradesh)
Phule Sai	Rahuri (Maharashtra)
KDCS-810	Kalyanpur (Uttar Pradesh)
RC 1-1	Durgapura (Rajasthan)
DCL 228	Bhubaneshwar (Orissa)
DCL 236	Bangalore (Karnataka)
DCL 335	Jabalpur (Madhya Pradesh)
DCL 006	Bhatinda (Punjab)
DCL 358	Lam (Andhra Pradesh)
DCL 901	Rahuri (Maharashtra)
DCL 001	Akola (Maharashtra)
DCL 268	Lam (Andhra Pradesh)
DCL 270	Rahuri (Maharashtra)
Red Star	Delhi
DCL 008	Durgapura (Rajasthan)
Soldier	Delhi
Green Wonder	Delhi
PMR 57	Bangalore (Karnataka)
K 1	Kovilpatti (Tamil Nadu)
A 8	Almora (Uttaranchal)
DCL 344	Jalna (Maharashtra)
DCL 266	Coimbatore (Tamil Nadu)
DCL 271	Rahuri (Maharashtra)
Rajasthan Local	Jodhpur (Rajasthan)
Sel. 5	Jodhpur (Rajasthan)
Motikeera 39	Jodhpur (Rajasthan)
Pusa Sadabahar	Delhi

per plant, fruit weight (g), yield per plant (g), ascorbic acid (mg/100g), total carotenoids (µg/100g), capsicin (%) and TSS (%).

Genetic diversity was analysed using Mahalanobis D^2 statistics with Tocher's method (Rao 1952). All possible D^2 values between thirty genotypes were computed utilizing the genotypic mean with respect to fourteen traits.

Results and Discussion

The thirty genotypes (Table 1) were grouped into eight clusters based on their D^2 values. Four clusters *viz.*, cluster VII (9), cluster II (5), cluster III (5) and cluster IV (4) were having maximum number of genotypes. While cluster I had 3 genotypes and cluster VI comprised 2 genotypes. Cluster V and cluster VIII were solitary with one genotype in each cluster (Table 2). The genotypes Rajasthan Local and Pusa Sadabahar comprising individual clusters with valuable traits open up the chance of having new genetic combinations when hybridized with other genotypes of different clusters and may be used to broaden the genetic base among the selected germplasm pool.

The grouping (Table 3) showed that maximum divergence existed between cluster I and VIII (D^2=108.22), while closer proximity existed between cluster II and cluster VII (D^2= 6.52). Cluster VIII had maximum distance in six out of the seven combinations, indicating that it had wide diversity among all the clusters. Greater the genetic distance between the clusters, wider is the genetic diversity between genotypes. Maximum intra-cluster distance was recorded for cluster III (6.46).

The cluster means for the fourteen traits revealed considerable differences among all the clusters (Table 4). The cluster VIII having a single genotype Pusa Sadabahar, possesses either higher or lower value for most of the traits, justifying its inclusion as a separate cluster. Cluster I and cluster VIII among them, had the maximum values for the yield related traits and quality traits. Cluster I had late flowering genotypes with maximum fruit length (12.09), fruit width (1.59), fruit weight (5.57) and ascorbic acid content (175.89) whereas cluster VIII had genotype with maximum number of primary branches (4.60), secondary branches (22.53), number of fruits per plant (137.51), total carotenoids (3879.50) and capsicin content (0.45) with considerably high yield per plant. Incidentally these two clusters were also the most genetically divergent. Hence, the genotypes from these two clusters could be used as parents to obtain better recombinants and widen the genetic base of the germplasm pool (Edang *et al.*,1971).

For breeding programmes aimed at earliness coupled with high yield, Pusa Sadabahar exhibiting minimum days to flowering (47.00) and days to first fruit harvest (80.67) could be used as a parental source. Additionally it also possesses maximum number of fruits per plant, total carotenoids and capsicin content. However, this variety had lowest fruit length, fruit width, fruit weight and TSS. On the other hand cluster I representing genotypes with highest fruit length, fruit width, fruit weight and ascorbic acid could be selected if the aim of the breeding programme is to improve any of these traits. But genotypes in this cluster were late in maturity and comparatively low yielder. Hence, backcross breeding involving genotypes from both these clusters could be done to develop an early as well as high yielding cultivar with higher capsicin and/or ascorbic acid content. Edang *et al.* (1971) stated that the clustering pattern could be utilized for choosing parental combinations for generating maximum possible variability for various economic traits. The genotypes in cluster VI exhibiting high yield might be tested for their stability for few years in multilocation trials and if found suitable, may be directly adopted as high yielding varieties.

Table 2. Cluster classification of 30 genotypes

Cluster	Genotypes (No.)	Genotype(s)
I	3	ACS 2000-02, Green Wonder, Motikeera 39
II	5	DCL 408, DKC 8, Phule Sai, DCL 006, DCL 358
III	5	KDCS 810, DCL 236, PMR 57, K 1, A 8
IV	4	ACS 98-9, DCL 270, DCL 271, Sel. 5
V	1	Rajasthan Local
VI	2	RC 1-1, DCL 008
VII	9	DCL 228, DCL 335, DCL 901, DCL 001, DCL 268, Red Star, Soldier, DCL 344, DCL 266
VIII	1	Pusa Sadabahar

Table 3. Inter- and intra-cluster distance of 8 clusters in 30 genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**4.87**	35.89	54.36	16.43	33.64	20.66	33.29	108.22
II		**3.87**	10.75	14.88	27.87	37.05	6.52	56.45
III			**6.46**	23.15	25.20	33.27	9.03	25.28
IV				**2.99**	26.83	10.39	10.18	70.09
V					**0.00**	24.94	27.81	53.46
VI						**5.15**	25.00	67.86
VII							**4.66**	41.22
VIII								**0.00**

Bold figures indicate the intra-cluster distance.

Table 4. Cluster means for various characters of chilli

Character	Cluster							
	I	II	III	IV	V	VI	VII	VIII
Plant height (cm)	44.16	47.70	54.75	60.86	44.40	56.18	49.80	51.73
Number of primary branches	2.70	2.76	3.51	3.40	3.20	4.00	3.40	4.60
Number of secondary branches	6.38	8.85	11.96	7.47	19.60	12.05	9.55	22.53
Days to flowering	64.11	58.93	48.47	61.83	60.00	58.67	53.93	47.00
Days to first fruit harvest	97.44	83.47	81.00	91.75	91.33	93.83	84.44	80.67
Fruit length (cm)	12.09	7.20	7.01	9.96	8.26	11.95	9.35	6.44
Fruit width (cm)	1.59	0.96	0.98	1.21	1.30	1.30	0.97	0.78
Number of fruits per plant	26.86	49.07	78.77	43.41	44.83	48.22	56.09	137.51
Fruit weight (g)	5.57	2.24	2.22	3.82	3.70	5.00	2.71	1.70
Yield/plant (g)	151.56	110.27	166.87	165.08	165.33	238.17	156.41	233.00
Ascorbic acid (mg/100g)	175.89	124.20	100.60	149.50	90.67	159.17	125.70	110.33
Total carotenoids (mg/100g)	2873.47	2391.02	2032.96	2576.16	2058.67	1687.44	3512.91	3879.50
Capsaicin (%)	0.38	0.44	0.43	0.37	0.33	0.35	0.42	0.45
TSS (%)	6.83	7.82	7.48	8.22	6.47	7.77	8.12	6.80

References

Edang S, Iam Sudin, Sri Andani and H Nasoetion (1971) Multivariate classification of some rice (*Oryza sativa L.*) varieties and strains on yield components. *Intl Rice Comm Newsl* **20:** 68-71.

Mehra CS and KV Peter (1980) Genetic divergence in chilli. *Indian J Agril Sci* **50:** 477-481.

Oliveira VR, VWD Vasali and CD Cruz (1999) Assessment of genetic diversity in sweet pepper using multivariate analysis. *Horticultura Brasileira* **17:** 19-24.

Pandey G and VK Dobhal (1994) Multivariate analysis in chilli (*Capsicum annuum* L.). *J Spices Aromatic Crops* **2:** 71-74.

Rao CR (1952) *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons, Inc., New York, USA.

Roy A and RN Sarma (1996) Multivariate analysis in chilli (*Capsicum annuum* L.). *Ann Agril Res* **17:** 130-132.

Singh A and HN Singh (1976) Genetic divergence in chilli. *Indian J Genet Pl Breed* **36:** 425-430.

Genetic Divergence for Yield and Biochemical Characters in Snapmelon (*Cucumis melo* L. var. *momordica* Duth. and Full.)

AN Krishna Reddy[1], AD Munshi[1], TK Behera[1] and Rajender Parsad[2]
[1]*Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi 110 012*
[2]*Division of Agricultural Statistics, Indian Agricultural Research Institute, New Delhi 110 012*

Genetic divergence was studied among 30 indigenous genotypes of snap melon (*Cucumis melo* L. var. *momordica*) for 19 important quantitative and qualitative characters using D^2 statistics. The genotypes were grouped into five clusters based on D^2 values, which exhibited no association between geographical distance and genetic divergence. Maximum divergence was observed between clusters I and III followed by I and V. The clusters showing high genetic divergence could be effectively utilized in heterosis breeding programme.

Key words: Snap melon, Genetic divergence, Biochemical characters

Snapmelon (*Cucumis melo* L. var. *momordica*) is one of the important cucurbitaceous crops grown in India. Its tender fruits are used as vegetable and ripe fruits as dessert. Fruits are rich source of vitamins and minerals. Besides, it has got enormous medicinal values. India being secondary centre of origin, snap melon has accumulated wide range of genetic variability (Alcazar and Gullick, 1983). Despite its nutritional and medicinal importance, no information is available on genetic parameters, specifically, magnitude of genetic diversity in this crop. Divergence analysis is a potent tool in divulging the diversity among the genotypes based on multiple characters. Mahalanobis (1936) generalized distance estimated by D^2 statistics has been used as an efficient tool in the estimation of genetic diversity for a rational choice of potential parent in a breeding programme. In the present investigation, an attempt has been made to assess the genetic divergence in a set of 30 genotypes of snap melon.

Materials and Methods

The present investigation was carried out at the research farm of Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi, during the spring-summer season of 2003. The experimental material consisted of 30 indigenous genotypes of snap melon. The experiment was laid out in a randomized block design with three replications. Each treatment comprised ten hills and two plants were allowed to grow per hill. The observations were recorded on five randomly selected plants per replication for each treatment on nineteen quantitative and biochemical characters *viz.*, first male flower node number, first female flower node number, days to first male flower appearance, days to first female flower appearance, days to first fruit set from anthesis, number of fruits per plant, maturity period (days), fruit length (cm), average fruit weight (g), fruit diameter (cm), flesh thickness (cm), length of fruit cavity (cm), yield per plant (kg), vine length (m), ascorbic acid (mg/100g), total carotenoids (μg/100g), reducing sugars (%), non reducing sugars (%) and total soluble solids (%).

D^2 statistics was estimated by the method of Mahalanobis (1936). The D^2 values between each pair of varieties were estimated after confirming that the varietal differences were highly significant for all the characters. The genotypes were grouped into distinct clusters according to Tochers Method (Rao, 1952).

Results and Discussion

Based on D^2 values, the 30 genotypes were grouped into five highly divergent clusters (Table1). The cluster divergence is proved by the high inter cluster and low intra cluster distance values. The intra cluster divergence ranged from 0.00 in cluster I to 3.917 in cluster III. The intra cluster divergence value in cluster I is zero because it had only one genotype. The inter cluster was maximum between cluster I and cluster V (7.715) followed by cluster I and cluster III (7.385).

The genotypes were so divergent that only 6 genotypes were grouped in cluster IV, 3 genotypes in cluster V. The genotype AP-6 was so divergent in all the characters

Table 1: Inter and intra cluster distance (D^2 values) for 5 clusters

Cluster	I	II	III	IV	V
I	**0.000**				
II	5.922	**3.030**			
III	7.385	4.141	**3.917**		
IV	6.131	3.221	5.533	**3.231**	
V	7.715	4.295	4.804	4.602	**3.232**

Intra cluster distances in bold figures

that it formed a separate cluster i.e. cluster I. Cluster II had maximum genotypes of 12 and cluster III had 8 genotypes. Different genotypes, their respective clusters and source of collections are presented in Table 2. which clearly showed that the genotypes usually did not cluster according to geographical distributions. This is in agreement with the results obtained by Kalloo *et al.* (1982) and More and Sheshadri (2002) in muskmelon and Krishna Prasad *et al.* (1993) in cucumber. The absence of relationship between genetic diversity and geographical distance indicated that forces other than geographical origin, such as exchange of genetic stocks, genetic drift, spontaneous variation, natural and artificial selection were responsible for genetic diversity. It might also be possible that causes for clustering pattern were much influenced by environment and genotype x environment interaction resulting in differential gene expression.

Table 2: Cluster classification and source of collection of 30 genotypes

Cluster	No. of genotypes	Name of Genotypes	Source of collection
I	1	AP-6	Baraut (U.P.)
II	12	SM-11, SM-81, DBSM 2-1-2, SM-56, SM-16, SM 25-1, SM60(0), DBSM-7, DBSM-5, DBSM 9-2, SM-4, NBPGR-35	Keonjhar, Keonjhar, Bagpat, Phulbani, NBPGR, NBPGR, NBPGR Bagpat, Bagpat, Bagpat, Phulbani, NBPGR
III	8	SM-18, SM-2, SM-7, DBSM 8-3, SM-5, SM-22, SM-14, DBSM-3	Balangir, Mayurbhanj, NBPGR, Bagpat, Panipat, NBPGR, NBPGR, Bagpat
I V	6	AP-8, SM 15-1, SM-1, SM-13, SM-40, AP-1	Baraut, Mayurbhanj, NBPGR, Phulbani, Sonepat, Baraut
V	3	SM-25, SM-6, SM-42	NBPGR, Balangir, Mayurbhanj

NBPGR: National Bureau of Plant Genetic Resources, New Delhi

The cluster means for 30 genotypes (Table 3) showed that mean value for the clusters varied in magnitude for all the 19 characters. Lowest values for first male flower node number (1.27), first female flower node number (3.20), days to first male flower appearance (32.13), days to first female flower appearance (36.47), and maturity period (21.60) were exhibited by cluster I. Cluster IV showed maximum value for number of fruits per plant (4.86), while cluster III exhibited maximum values for fruit length (17.88), average fruit weight (795.96), fruit diameter (9.84), flesh thickness (1.94), length of fruit cavity (6.13), yield per plant (2.83), and vine length (2.06). Cluster V showed maximum values for ascorbic acid (13.04) and total carotenoids (762.80) while maximum values for reducing (2.75) and non-reducing sugars (3.05) were exhibited by cluster I. Cluster IV showed highest value for total soluble solids (7.21).

Cluster means in Table 3, revealed the best cluster for various characters. Depending upon the aim of breeding, the potential lines could be selected from different clusters as parents in hybridization programme. The selection of parents to be included in hybridization programme should be based on genetic distance. If a breeding programme is aimed at higher yield then genotypes from cluster III can be selected as parent in hybridization programme as it showed highest mean yield per plant along with higher fruit length, average fruit weight, fruit diameter, flesh thickness and vine length. Even this cluster had medium maturity period. If a breeding programme is aimed at earliness, then genotype AP-6 (cluster I) showing lowest maturity period and other characters contributing towards earliness can be selected. But it was evident from the table 3 that it was a low yielder. Hence a convergent improvement

Table 3: Cluster means of 30 genotypes of snap melon for 19 characters

Cluster	FMFNN	FFFNN	DFMFA	DFFFA	DFA	No. of fruits / plant	Maturity period (days)	Fruit length (cm)	Av. fruit weight (g)	Fruit diameter (cm)	Flesh Thickness (cm)	Length of fruit cavity (cm)	Yield / plant (kg)	Vine length (m)	Ascorbic acid (mg/ 100g)	Total carotenoids (μg/100g)	Reducing sugars (%)	Non-reducing sugars (%)	Total soluble solids (%)
I	1.27	3.20	32.13	36.47	2.33	3.27	21.60	10.83	318.6	8.97	1.93	5.10	1.05	1.10	4.42	203.73	2.75	3.05	4.93
II	1.41	3.62	34.48	41.45	2.27	3.81	21.83	13.06	365.6	7.55	1.30	4.95	1.39	1.47	6.61	649.41	1.52	1.52	5.58
III	1.35	3.88	33.31	42.83	2.08	3.67	23.47	17.88	795.9	9.84	1.94	6.13	2.83	2.06	7.10	592.49	1.64	1.47	6.05
IV	1.42	3.42	34.19	42.53	2.08	4.86	23.44	9.96	305.2	6.50	1.28	3.93	1.42	1.46	8.36	327.46	2.01	1.77	7.21
V	1.58	3.87	36.56	45.59	2.73	4.11	25.31	13.83	598.8	7.27	1.46	4.36	2.46	1.77	13.04	762.80	1.92	1.89	5.66

FMFNN- First male flower node number
FFFNN - First female flower node number
DFMFA - Days to first male flower appearance
DFFFA - Days to first female flower appearance
DFA - Days to first fruit set from anthesis

or double back cross can be suggested between the lines of two clusters (I and III) by simultaneously selecting for higher yield along with earliness to develop an early high yielding cultivar. If a breeding programme is aimed at improving nutritional characters then cluster V showing maximum ascorbic acid and total carotenoids content can be utilized in breeding programme. Even this cluster had genotypes with good yielding habit. Cluster IV can be utilized in breeding programme to improve the total soluble solid content. The genotypes of highly divergent cluster may also be utilized in a diallel or line x tester fashion for effective exploitation of heterosis.

References

Alcazar-Equinas JT and Gullick PJ (1983) Genetic resource of cucurbitaceae – A Global Report. IBPGR, Rome.

Kalloo G, Dixit J and Sidhu AS (1982). Genetic divergence is musk melon (*Cucumis melo* L.), *Genet Agr*, **36**: 1-8.

Krishna Prasad VSR, Singh DP and Singh RP (1993). Biological divergence in the land races of Indian cucumber (*Cucumis sativus* L.). *Ind J Hort*, **50(1)**: 57-63.

Mahalanobis PC (1936) On the generalized distance in statistics. *Proc Nat Inst Sci*, India **12**: 49-55.

More TA and Seshadri VS (2002) Studies on genetic divergence in musk melon (*Cucumis melo* L.). *J Maharashtra Agric Univ*, **27(2)**: 127-131.

Rao CR (1952) Advanced Statistical Methods in Biometrical Research. John Wiley and Sons Inc. New York

Genetic Diversity Analysis of Field Bean (*Lablab purpureus* L.) Sweet Through RAPD Markers

BN Gnanesh, M Reddi Sekhar, K Gopal, K Raja Reddy and NP Eswara Reddy
Department of Genetics and Plant Breeding, SV Agricultural College, Tirupati 517 502 (Andhra Pradesh)

RAPD analysis based on six random primers detected a high level of genetic variation among the 15 field bean genotypes of southern India. A total of 46 bands were generated of which 42 were polymorphic. A high degree of polymorphism was obtained with the primers OPM 20 (11 bands), OPM 1 (9 bands) and OPM 3 (9 bands). The similarity index values ranged from 0.286 to 0.897 indicating a wide range of genetic diversity. The dendrogram consisted of four close-knit groups having 6, 5, 2 and 2 genotypes in groups 1, 2, 3 and 4, respectively. Based on RAPD marker analysis, MAC 8, GA 100 and GA 74-4 were found to be diverse when compared to other genotypes.

Key words: Field bean, *Lablab purpureus* (L.) Sweet, Clustering, Diversity, RAPD markers

In India to date, field bean remains an important but minor pulse crop. Field bean is used as a vegetable and pulse crop for human consumption, as fodder for cattle and as cover crop. The species is extremely diverse (Verdcourt, 1970 and Duke *et al.*, 1981) with two subspecies namely *typicus,* the perennial garden type and *lignosus,* the annual field type. Genetic diversity is an important factor for heritable improvement in any crop and knowledge of genetic diversity, its nature and degree of variability would be useful for selecting desirable parents from available germplasm for a successful breeding programme. The efforts of improving the field bean utilizing indigenous germplasm have been useful in breaking the yield barriers resulting in compact plant type, reduced duration and photo-insensitive types. The present study was undertaken to elicit information on nature and extent of genetic diversity among promising field bean genotypes using Random Amplified Polymorphic DNA (RAPD) markers.

Materials and Methods

Fifteen genotypes from different districts of Karnataka, Andhra Pradesh and Tamil Nadu, were drawn from germplasm collection of field bean being maintained at UAS, GKVK, Bangalore. 18-days old healthy leaf samples from the plants grown in green house were used for DNA extraction as per modified CTAB (Cetyl Trimethyl Ammonium Bromide) method given by Murray and Thompson (1980). Healthy leaves were taken, weighed and cut into small pieces and were ground in liquid nitrogen with pre-chilled pestle and mortar and the powder was transferred into eppendorf tubes and suspended in a pre-heated (65°C) 900 μ l of extraction buffer containing (2% CTAB, 100 mM Tris-HCl, 20mM EDTA, 1.4M NaCl and 1% PVP). The tubes were incubated at 65°C for an hour followed by addition of chloroform: isoamyl alcohol (24:1) and spunned at 14000 rpm for 10 minutes. Upper aqueous phase was precipitated with 200 l of 95% ethanol and 10 l of 3M sodium acetate (pH 5.2) and centrifuged at 14,000 rpm for 10 minutes. DNA recovered as pellet was washed with 70% ethanol. The concentration and quality of DNA was estimated using spectrophotometer at 260nm and verified by running sample on one per cent agarose gel along with 1 Kb DNA ladder.

Amplification reaction was carried out in a 25 l reaction volume containing 25ng of template DNA, 20ng of random primer (Operon, USA), 0.1mM dNTPs, 0.5U of Taq polymerase (Bangalore Genei Pvt. Ltd., Bangalore, India) and 2.5 l of 1 x PCR buffer (10mM Tris-HCl, pH 8.0; 50mM KCl, 1.8mM $MgCl_2$ and 0.01 mg/ml gelatin). Amplification was carried out on Corbett Research Thermocycler following one cycle of initial denaturation at 94°C for 2 min; 45 cycles of 92°C for 1 min, 37°C for 1 min and 72°C for 2 min then closed by 72°C for 5 min, for post extension. The PCR products were separated on 1% agarose gel stained with ethidium bromide. The gels were visualized with UV transilluminator and photographed. Only reproducible and clear RAPD bands were scored as present (1) or absent (0). The sizes of different DNA fragments were revealed with reference to 1 Kb DNA ladder. The estimates of genetic similarity were calculated following Jaccard (1908). The similarity coefficients were subjected to un weighted pair-group method on arithmetic average (UPGMA) method of cluster analysis to group the genotypes based on their overall similarities. SPSS

package was used for the cluster analysis and subsequent dendrogram preparation.

Results and Discussion

Out of the 20 random primers tested, six primers were selected ultimately to detect the variation among the genotypes, which gave on an average 6-7 clear bands with fragment size varying from 100bp to 3000bp. A total of 46 bands were obtained among which 42 bands were polymorphic (91.30%) in nature (Table1). A high degree of polymorphism was obtained with the primers OPM 20 (11 bands), OPM 1 (9 bands) and OPM 3 (9 bands) indicating a wide range of diversity (Fig.1). The similarity index values ranged from 0.286 to 0.897, indicating the presence of wide range of genetic diversity at molecular level among the 15 genotypes (Table 2). Similarly, Renu and Mishra (2003) noticed a wide range of genetic diversity by RAPD markers in germplasm lines of pea.

The clustering pattern using RAPD data resulted in four major groups (Fig.2). The dendrogram of similarity coefficients indicated that genotypes GA 100 of the group-1 and genotype GA 40-2 (white) of the group-4 were clustered at the two extremes based on their similarity coefficients. Even though they belong to same ecological region (Mysore), they exhibited only 36.7 per cent of similarity. This clearly indicates diversity is mainly because of inherent genetic differences at DNA level. While genotype Co 1 from Tamil Nadu was genetically similar (88.0%) to GA 60-15, which is a local selection from Belur (Karnataka). Similarly RDT from Andhra Pradesh were closely associated (47.4%) to GA 2-27, which is a local selection from Bangalore (North). The tendency of accessions occurring in clusters irrespective of geographic boundaries demonstrates that geographical isolation is not the only factor causing genetic diversity. Liu (1996) also indicated in field bean that the existing variation in cultivated materials has no geographic basis and corroborated the results of the present study.

The first group comprising of 3 sub-clusters (1a, 1b, 1c), had a minimum similarity of around 57.1 per cent and maximum of 89.7 per cent. The genotypes GA 100 and GA 14-1 (black) of group 1a were closely related having 89.7 per cent similarity, while group 1b consisted of GA 60-15 and Co 1, which were genetically closer with 88.0 per cent similarity. Group 1c consisted only single genotype GA 20-6. Group 2 included 2 sub-clusters within which the maximum similarity is 80.0 per cent and minimum is 50.0 per cent. Group 3 included only 2 genotypes *viz.* GA 2-27 and RDT having similarity of 47.4 per cent indicating that they are moderately related. While group 4 included 2 genotypes i.e., MAC 8 and 40-2 (white) with only GA 42.9 per cent similarity. Sub-clustering pattern indicated

Table 1. List of Primers selected for DNA amplifications in Field bean

Primer code	Nucleotide Sequence	Total bands	Polymorphic bands	% Polymorphism
OPM-01	5'-GTTGGTGGCT-3'	11	9	81.8
OPM-03	5'-GGGGGATGAG-3'	9	9	100.0
OPM-05	5'-GGGAACGTGT-3'	3	2	66.6
OPM-12	5'-GGGACGTTGG-3'	6	5	83.3
OPM-18	5'-CACCATCCGT-3'	6	6	100.0
OPM-20	5'-AGGTCTTGGG-3'	11	11	100.0
	Total bands	46	42	91.3

Table 2. Similarity matrix of 15 field bean genotypes using Jaccard's coefficient of similarity

Genotypes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
GA 74-4	1														
HA 3	.630	1													
MAC-8	.478	.500	1												
GA 49	.533	.800	.375	1											
GA 40-2 (White)	.455	.429	.429	.355	1										
Adagur-II	.593	.700	.464	.710	.444	1									
GA 16-3	.500	.686	.485	.743	.343	.657	1								
GA 2-27	.409	.345	.381	.323	.421	.407	.353	1							
GA 100	.364	.514	.303	.618	.367	.529	.622	.429	1						
GA 14-1 (Black)	.353	.459	.294	.556	.355	.559	.564	.414	.897	1					
RDT	.500	.367	.348	.344	.381	.481	.371	.474	.448	.483	1				
Devegowdana doddi I	.448	.515	.333	.529	.407	.581	.541	.542	.821	.733	.560	1			
GA 60-15	.448	.563	.333	.576	.462	.581	.500	.423	.759	.677	.500	.846	1		
CO-1 .414	.531	.345	.545	.480	.600	.514	.500	.786	.700	.520	.880	.880	1		
GA 20-6	.286	.514	.303	.447	.323	.405	.463	.379	.636	.571	.313	.645	.645	.613	1

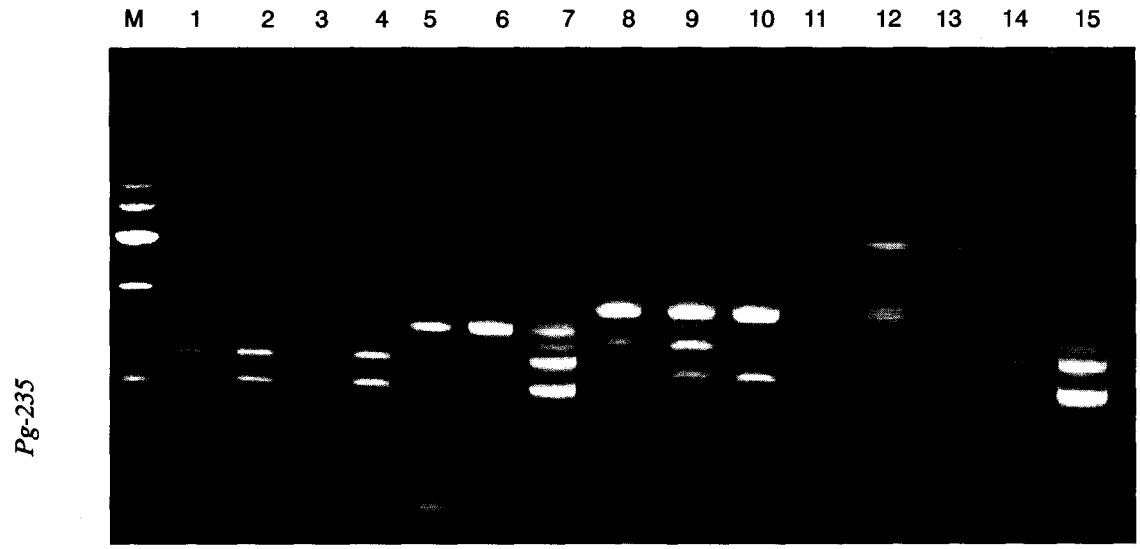


Fig. 1. Arepresentive RAPD banding patterns of 15 Field bean genotypes obtained with primer OPM-20. M=marker

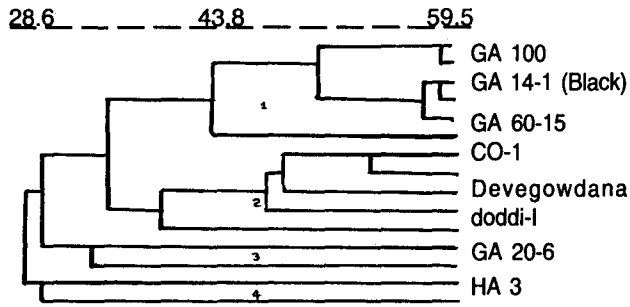


Fig. 2. Association among field bean genotypes revealed by UPGMA cluster analysis of Jaccard genetic similarity coefficients based on RAPD data

low variation within the cluster and high variation between the clusters.

In spite of more intensive cultivation and more concentrated breeding work in India, *Lablab purpureus* collections from Asia seem to possess a higher level of variation (Liu, 1996). Hence, the utilization of available local germplasm resources in hybridization programme is advocated to evolve high yielding and photo-insensitive cultivars of field bean.

References

Duke JA, Kretschmer AE, Junior Reed CF and Weder JKP (1981) *Lablab purpureus* (L.) Sweet. In: Duke J A (Ed.) *Hand Book of Legumes of World Economic Importance.* Plenum Press, New York, USA pp. 102-106

Jaccard P (1908) Nouvelles réchèrches sur la distribution florale. *Bull Soc. Vaud Sci Nat* **44:** 223-270.

Liu CJ (1996) Genetic diversity and relationships among *Lablab purpureus* genotypes evaluated using RAPD as markers. *Euphytica* **90:** 115-119.

Murray M and Thompson W (1980) The isolation of high weight plant DNA. *Nucleic Acids Res* **8**: 4321-4325.

Renu and Mishra SK (2003) Characterization of *Pisum* germplasm based on molecular markers. *Indian J Pulses Res* **16**: 84-91.

Verdcourt B (1970) *Lablab adans. In:* Studies in the *Leguminosae–Papilionoideae* for the 'Flora of Tropical East Africa III Kew *Bull* **24**: 409-411.

Genetic Variability Studies in *Lasora* (*Cordia myxa* Roxb.)

DK Samadia
Central Institute Arid Horticulture Bikaner 334 006 (Rajasthan)

Lasora is an under-exploited fruit and an important herbal tree in rural India. Two extensive explorations were made during 2000 and 2001 for the surveys and collections of *lasora* variability in Rajasthan. The germplasm was collected from 95 sites having varied agro-climatic conditions. The analysis of variance revealed that there were high and significant differences among the thirty groups of *lasora* population. A wide range of variation was observed for important characters on plant growth, leaf size, fruit size and fruit quality and yield components. The estimation of GCV and PCV for fruit weight and leaf size was high and therefore, good scope for improvement through selection. Genotypes with large sized leaves are potential source of bigger sized fruits and *vice-versa*.

Key words: Lasora, *Cordia*, Genetic variability, Arid region

In spite of environmental constraints, arid region has a great fruit production potential by exploiting the native rich gene reserves in a number of fruit yielding species. The region is endowed with rich variability in minor fruit yielding species like *ker* (*Capparis decidua*); *khejri* (*Prosopis cineraria*); *jharber* (*Ziziphus nummularia*); *pilu* (*Salvadora oleroides*); *lasora* (*Cordia myxa* Roxb.), etc. in the natural forms (Pareek and Samadia, 1999). Owing to drought hardiness, these species are not only adapted but also have high productivity under extremes of environmental stresses (Pareek and Sharma, 1993). The genetic resource of these fruit species is under severe threat of erosion due to manifold reasons of social and economic nature. The shrinkages of *Orans* (a type of natural resources management systems on community land for harvesting of indigenous fruits and for animal grazing in the Indian desert) and high profit making crops are the important reasons. These indigenous species are playing significant role in the life of desert dwellers, not only in their cultural values but also for subsistence economy to the rural people. On the other hand, modern communication network has already increased the awareness in the world community about rich potentiality in the under exploited horticultural species (Samadia, 2003). *Lasora*, *lehsua*, *gunda*, sebesten or Indian cherry (*Cordia myxa* (Roxb.) syn. *C. dichotoma* Forst) is as important herbal tree in rural India. It belongs to family Boraginaceae probably originated in India and has about 300 species (Rai and Gupta, 1996). It is distributed throughout the country especially in warmer regions of northwest and central India. Realizing the importance of native genetic resources, intensive crop specific exploration programmes were made during 2000-2002 under National Agricultural Technology Project (NATP) on Sustainable Management of Plant Biodiversity by CIAH, Bikaner (Rajasthan). Thus the present piece of work discussed here was undertaken to explore and conserve the natural seedling originated landraces and variability of *lasora* (*Cordia myxa* Roxb.) from arid and semi-arid regions of northwestern India. Long-term strategies for the conservation of genepool and its utilization has been discussed.

Materials and Methods

Rajasthan (23°3'-30°12' N and 69°3'-78°17' E) is the largest state in the country covering approximately 34.2 million hectare of geographical area, out of which an area of 27.1 m ha (79.08 % of total state area) is lying in arid and semi-arid region spreading over 21 out of 32 districts. Over a large part of the state, agriculture is a struggle against inhospitable nature. Low precipitation, extremes of temperatures and high vapour deficit are the important restrictions imposed by the nature. The annual rainfall is low (185-600 mm) and is confined from July to September. Uncertainty, scanty and erratic nature of monsoon rains, result in drought conditions once every three years in eastern region and once every two years in the western regions. The state has no perennial river. The water table lies very deep and much of the water is brackish and saline.

Two explorations were undertaken during May 2000 and 2001. Both the explorations were formulated and conducted in the districts of Ajmer, Jaipur, Alwar, Bharatpur, Pali, Dausa, Sikar, Bhilwara, Chittorgarh, Udaipur, Rajsamand, Jalore, Barmer, Jodhpur, Nagour, Bikaner, Churu and Jaisalmer. Germplasm was collected from a wide range of locations in eighteen districts falling under arid, semi-arid and sub-humid agro-climatic zones of Rajasthan. Visits were performed to farming villages where *lasora* cultivation had been practiced

sporadically and in target core variability hot pockets. Beside the Old kingdom State's farm (*Bari*), Government's nurseries/farm and forest houses were also visited where it is maintained in the form of amateur plantations. Interactions were held with farmers and agricultural workers, individually or in groups for the collection of information on *lasora* cultivation, areas of cultivation and availability of natural or cultivated seedling population, etc.

A total 95 sites were visited and 65 fruit samples were collected, selectively or randomly from the seedling population of 5 to 50 (or more) years age group. Both individual and population sampling was adopted. The potential individual trees were marked for the collection of bud wood for the conservation and direct use in evaluation. Thirty groups were formed from the 65 collected samples to assess the extent of genetic variability in the population of the specific agro-climate of the target variability pockets of district boundaries in the state. Tree age and size (primary and secondary sources of population) and distinct fruit size (big and small) and specific micro-climatic conditions of the district were the criteria used for developing core groups.

In depth discussions were held with the farmers/ growers to assemble realistic information on plant growth, flowering and fruiting behaviour, fruit yield and quality traits, fertilization and water management, specific practices on harvesting and post-harvest practices, marketing, socio-economic and medicinal uses. Tree size and annual fruit production and returns per tree were estimated from the potential core sites. Passport information was compiled on agro-climate, soil and topography, extent of population variability, productivity and farming system, etc. During the surveys, quantitative data were collected on important aspects such as plant growth, leaf, fruit and seed characters. The main objective of quantitative analysis was to find out extent of variability in the seedling population of *lasora* in relation to localities and micro agro-climatic conditions and also to work out the relationship for the identification and selection of elite trees on the basis of any specific component. Data were analyzed to quantify the extent of *lasora* variability in the state of Rajasthan.

Results and Discussion

Greater variability in the initial breeding material ensures better chances of producing desired forms of a crop plant. Thus the primary objective of germplasm conservation is to collect and preserve the genetic variability in indigenous fruit producing crop species to make it available to present and future generation. The indigenous horticultural species like *ker*, *lasora*, *khejri*, *pilu*, *jharber*, etc. are naturally growing fruits in the arid and semi-arid regions of Rajasthan. Fruits of these species have nutritional and medicinal values apart from being delicious and wholesome fruits at immature, mature or ripe stages. Being drought hardy and xerophytic adaptive mechanism, they can be exploited for regular cultivation in the vast arid and semi arid lands provided support is extended by processing industries since these fruits are used to make excellent pickles, *chutney* and vegetable curries, jam, jelly, squash or converted into dried forms for off season uses (Pareek and Samadia, 1999 and Samadia, 2004).

The *lasora* populations in the arid and semi-arid areas of Rajasthan have sprung up through natural regeneration and seedling plantations. The observed variability occurs in *lasora* is with regard to tree size and fruit size, shape and quality etc. The *lasora* plants are tolerant to drought and stressed conditions. It is not grown as orchard under cultivation but grows abundantly and unsystematically on non-cultivable lands, backyard or near the houses (*Vada*), along with farm boundaries or roadside or in farm land as scattered trees in the arid and semi arid areas of Rajasthan. Several arid zone fruit crop workers (Pundir, 1987, Singh, 1989, Pareek *et al.*, 1999, Samadia, 2003 and Kaushik and Dwivedi, 2004) also reported the importance and availability of *lasora* in Rajasthan. It has lot of variations and so far there is no named variety for the cultivation. A wide range of variability was explored and variation in size and spread of tree, leaf size, fruit maturity, flowering and fruiting behaviour, fruits per cluster, fruit size, seed size, pulp: seed ratio, fruit quality and fruit yield potential of *lasora* under varying agro-climatic sub region of the Rajasthan were recorded (Table 1-4). Among the locations screened for the variability studies, Pushker valley of Ajmer, Sadri area of Pali, parts of Jodhpur, Barmer, Jalore, Jaipur, Bhilwara, and Nagour were core hot spots and exhibited the rich variability in *lasora*. During the surveys elite plants were identified and marked for collecting the budwood for *ex situ* clonal conservation.

A wide range of variations was observed in the

lasora population for the plant growth parameters and fruit yield potential (Table 1). The plant height and spread ranged from 3.48-13.34 m and 2.84 to 10.05 m with a population mean of 7.08 and 6.08, respectively. Tree canopy volume was quantified and very high range of variations was obtained (11.5 to 596.3 m^3) for this character. The wide range of variations for tree characters among the groups of *lasora* might be due to two reasons. Of them the first is genetically heterogenous population and age of the seedlings and second one may be environmental condition and crop management practices at the production sites. During the survey, for realistic information from the locations of core hot spots, uniform age group individuals of seedling population were observed for plant growth and yield characters. In general there were two forms of trees, tall and vigorous growth habit and another medium sized and wide spread. In hot core variability pockets, there were three groups in population of which the first group belongs to very old (>50 years) seedling at the village common places, forest nurseries or near the houses located in the field or near to open wells. These plants were in few numbers. These were probably originator of the secondary (full grown or mature trees of 20-25 age group) and the third generation new seedling populations (<10 years age) which is now at the farmers field and in orchards.

The analysis of variance revealed high and significant difference among the thirty groups of *lasora* population for the characters studied which indicated that all the groups were highly diverse (Table 4). The leaf size could be the one of the marker character as observed during the course of explorations. In general, there were two typical leaf sizes *i.e.* small and big. A relative pattern was observed in the size of leaves and fruits in a tree. Therefore, leaf characters were recorded for length, width and size to find out the extent of variations and relationship between the size of leaf and fruits in *lasora*. The leaf length and width in the population ranged from 8.98-20.14 and 5.21-17.18 cm respectively. The calculated leaf size (length x width) ranged between 47.5-346 cm^2. It was noted that the maximum seedling trees were of big sized leaf where as very few trees were of smaller leaf size. While interacting with the growers, two points emerged out; the first one is that the plant having bigger sized leaves produces commercially important fruits. The tree with smaller leaf size produces smaller fruits, which have no consumer preference. Therefore, the farmers were not allowing in the field to grow it. The scattered smaller leaf sized trees were available at few forest and government nurseries, near open wells or community places in the villages or as trees shade yard (*e.g.*, open dense shaded animal yard for buffaloes in Jalore and Barmer area).

Table 1. Extent of variability in plant characters of *lasora* population in Rajasthan

Characters	Range values
Plant height (m)	3.48 – 13.34
Plant spread (m)	2.84 – 10.05
Plant canopy volume (m^3)	11.55 – 596.37
Fruit yield potential (q/tree) of 5 – >50 years old age seedling trees, practically maintained with zero inputs.	0.12 – 10.12
Returns / tree from the 5 to >50 years age group trees, annually (whole sale market rate @ Rs 4=00 per kg).	48 – 4049

The data in Table 4 revealed a wide range of variation for fruit characters studied and it was for weight (1.84-11.50 g), length (1.51-2.82 cm) and diameter (1.23-2.86 cm) of fruits. Variations were also recorded for weight of five seeds (1.30-2.79 g), seed length (0.99-1.52 cm) and width (1.04-1.72 cm) from the mature fruits and these are important characters for the fruit quality in *lasora*. Fruit size, quality and productivity are the major attributes to select the superior seedlings from the natural population which could be multiplied clonally for *ex situ* germplasm evaluation and conservation. Considering the growers experiences and their justifications on the fruit quality and yield components, some elite trees were marked and observations were recorded in the potential *lasora* growing core locations. Among the observations recorded, wide variations were observed for number of fruit per cluster and bunch, fruit yield per plant, duration of harvesting of tender fruits and period of availability etc. (Tables 2 and 3).

Genotypic and phenotypic coefficient of variation (GCV and PCV) studies indicated that there is an ample scope for the improvement of this crop (Table 4). In general, the estimates of PCV were higher than GCV for all the characters but the differences were generally negligible. In such situations, selection can be effective on the basis of the phenotype alone. The estimation of GCV and PCV for three important characters *i.e.* fruit weight and leaf size and width were high and thus have greater scope for improvement through selection. The estimates of heritability act as a predictive instrument in expressing the reliability of phenotypic value. Therefore, it helps to make selection for a particular character

Table 2. Plant growth and fruit yield of potential *lasora* seedling trees from the core variability pockets in the districts of Ajmer, Pali, Jalore and Barmer

Age groups (years)	Plant height (m)	Plant spread (m)	Plant canopy volume (m^3)	Fruit yield potential (q/tree)
< 5	3.96	3.44	12.91	0.114
5-10	4.95	5.42	44.15	0.825
10-20	6.82	6.26	96.81	1.268
20-30	8.51	8.42	202.75	2.285
>30	10.21	9.64	334.12	4.355

Plant spread (m)=Average of East-west + North-south: Plant canopy volume (m^3)= 4/3 a^2 b, where a is half of the tree height and b is tree spread

Table 3. Fruit yield and quality contributing characters of potential *lasora* seedling trees from core variability pockets in the districts of Ajmer, Pali, Jalore and Barmer

Characters	Mature unripe fruits	Ripen fruits
Period of availability of fruits	First week of April to third week of May	Second week of May to second week of June
Number of fruits per cluster	3.2 – 8.5	–
Number of clusters per bunch	2.5 – 4.7	–
Number of fruits per bunch	15.5 – 25.7	–
Marketable fruit yield (kg/ cu m)	0.88 – 1.86	–
Fruit weight (g)	9.21- 11.42	12.84 – 14.22
Fruit length (cm)	2.51 – 2.84	2.75 – 3.11
Fruit diameter (cm)	2.64 – 2.93	2.87 – 3.27
Seed length (cm)	1.21 – 1.35	1.24 – 1.45
Seed width (cm)	1.21 – 1.47	1.24 – 1.56
Seed thickness (cm)	0.78 – 0.95	0.78 – 0.98
Weight of seed (g)	0.654 – 0.722	0.702 – 0.741
Weight of pulp/ fruit (g)	8.54 – 10.61	12.09 – 13.45
Pulp: seed ratio	13.05 – 14.77	17.22 – 18.15
TSS (^{0}Brix)	–	5.55 – 18.24

when heritability is high. In the present study, all the characters exhibited very high heritability. The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. The genetic advance expressed as percentage of mean ranged from 21.46 to 89.72 and the important character like fruit weight (79.95), leaf size (89.72) and leaf width (53.73) recorded higher estimates. In the present study, fruit weight was found to be highly variable and an important character that might be responsible for variations in fruit size and other yield related components in *lasora*. Based upon variability and habitability estimates it is concluded that improvement by direct selection in *lasora* is possible for traits like fruit weight and leaf size. In general, the character that shows high heritability with high genetic advance are genetically controlled by additive gene action (Panse and Sukhatme, 1957), and can be improved through simple or progeny selection methods. Whereas, the character showing high heritability along with moderate or low genetic advance, can be improved by intermitting superior genotypes of segregating population developed from combination breeding, beside with the advantages of clonal propagation of desirable types and individuals in *lasora*.

Conclusions

A seedling tree of about 10-12 year old yields 250-300 kg fruits and can easily generate Rs. 1000/- annually. Being tolerating to biotic and abiotic stresses, this species is suitable for arid and semi-arid and drought prone areas of tribal region of the northern western part of the country. Because of pre-dominance of seed propagation, great variability exists in *lasora,* scattered almost through out the arid and semi-arid areas. In spite of wide variability there is no named cultivars for systematic orchard development and organized farming. Hence, the naturally occurring variations need to be exploited by offering selection as a method for improvement of *lasora*. An oval-round shaped fruit, green to dark green colour at unripe mature stage and big size (9-12 g) producing genotype would be ideal that can be recommended. The small size seed stone

Tables 4. Components of genetic variability in *lasora* seedling population in Rajasthan

Characters	Range	Mean (%)	GCV (%)	PCV (Broad sense)	Heritability (5%SI)	GA as % mean
Leaf length (cm)	8.98-20.14	14.60	22.36	22.38	99.9	46.04
Leaf width (cm)	5.21-17.18	11.84	26.10	26.12	99.9	53.73
Leaf size (cm^2)	47.52-346.01	182.03	43.58	43.60	99.9	89.72
Fruit weight (g)	1.84-11.50	7.33	39.10	39.39	98.5	79.95
Fruit length (cm)	1.51-2.82	2.24	15.36	15.59	97.0	31.16
Fruit diameter (cm)	1.23-2.86	2.35	18.39	18.58	98.0	37.51
Weight of 5 seeds (g)	1.30-2.79	2.00	22.00	22.03	99.7	45.26
Seed length (cm)	0.99-1.52	1.26	10.46	10.50	99.1	21.46
Seed width (cm)	1.04-1.72	1.33	13.22	13.25	99.4	27.15
Seed thickness (cm)	0.56-1.32	0.89	22.25	22.30	99.6	45.73

and high pulp content with better quality fruits for processing, besides higher fruit yielding and longer harvesting period genotypes would be considered potential in *lasora*. There is also need for commercializing this fruit in arid and semi-arid regions by exploring the possibilities of its uses in gums, confectionery and processing industries.

References

Kaushik RA and NK Dwivedi (2004) Genetic diversity in *lasora* *Indian Hort* **49**: II.

Panse VG and PV Sukhatme (1957) Genetics and quantitative characters in relation to plant breeding *Indian J Genet* **17:** 312-328.

Pareek OP and DK Samadia (1999) Breeding for sustainable fruit production in arid zone: present status and future strategies. In: Crop improvement for food security (Eds RK Behl, MS Punia and BPS Lather) SSARM, Hisar, 213-223p.

Pareek OP and S Sharma (1993) Under-utilized fruits *Indian Hort* **38:** 47-56.

Pareek OP, BB Vashishtha, Vishal Nath, DK Samadia and RS Singh (1999) Horticultural Resources in *Thar* desert. In: Proceedings of National Seminar on Management of Natural Resources in Rajasthan (Eds Anil Kumar, Rajesh Sharma and Madhu Sharma). Rajasthan Agricultural University, Bikaner, 4-9 p.

Pundir JPS (1987) Studies on growth, flowering and fruiting behaviour of *lehsua* (*Cordia dichotoma* Forst 'F'). Ph D Thesis submitted to Sukhadia University, Udaipur (Rajasthan).

Rai Mathura and PN Gupta (1996) Distribution and diversity of indigenous tropical fruits. In: Genetic Resource of Tropical fruits: Collection, evaluation and conservation strategies. (Eds PN Gupta, Mathura Rai and KPS Chandel). NBPGR, New Delhi.

Samadia DK (2003) Genetic resource management for sustainable horticultural development in arid regions of India. In: Sustainable Resource Management (Eds BBS Kapoor and Ahemad Ali), Madhu Publications, Bikaner (India) 163-173 p

Singh SP (1989) *Cordia dichotoma* Forst. In Wasteland Development. Agricole Publishing Company, New Delhi.

Identification of Groundnut (*Arachis Hypogaea* L.) Varieties through Biochemical Markers

BN Motagi, MVC Gowda*, GK Naidu and J Salim

Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Dharwad-580005, Karnataka

Sixteen groundnut cultivars were assessed for protein (seed and hypocotyl) and glutamate oxaloacetate transaminase (GOT) polymorphism. Seed protein profiles produced six (S1-S6) electrophoretic phenotypes compared to three (G1-G3) of GOT, while, hypocotyl proteins produced twelve (H1-H12) electrophoretic patterns. Individually, the seed and hypocotyl proteins can identify three and nine cultivars, respectively. However, combination of protein (seed and hypocotyl) and GOT isozyme profiles differentiated all the sixteen cultivars.

Key words: Groundnut, Varietal identification, Biochemical markers

Electrophoresis of storage and functional proteins has emerged as an efficient, simple and reliable tool supplementing traditionally used morphological parameters (Picket and Jarman, 1994). ISTA has adopted standard SDS (sodium dodecyl sulphate), PAGE (Poly acryl amide gel electrophoresis) and IEF (Iso Electric Focusing) methods into the international rules (ISTA, 1996) for cultivar identification. Seed proteins and isozymes because of their stability and reproducibility have potential to serve as tools for fingerprinting of genotypes. Therefore, the present study was carried out to determine the protein (seed and hypocotyl) and isozyme (GOT) variation in groundnut cultivars and their potential for finger printing.

Materials and Methods

Sixteen groundnut varieties belonging to Spanish bunch (Spanish Improved, TMV 2, S 206, Dh 3-30, JL 24, KRG 1, K 134, Dh 8, R 8808, Dh 40, TAG 24 and GPBD 4), Virginia runner (S 230 and DSG 1) and Valencia (ICGV 86590 and mutant 28-2) botanical types released for cultivation were assessed for protein (seed and hypocotyl) and isozyme (GOT) polymorphism.

The analysis of proteins and isozyme was performed by polyacrylamide gel electrophoresis (PAGE) technique. Gels were prepared according to the method of Hames and Rickwod (1984). To study seed protein polymorphism, one-dimensional SDS-PAGE (12.5% separating gel and 2.5% stacking gel) was carried out following the procedure given by Laemmli (1970) in a vertical gel system. For this purpose total protein was extracted after suspending seed flour for 1 hour in an extraction buffer (65mM Tris-HCl, pH 6.8) followed by centrifugation at 10,000 rpm at 4 °C for 20 minutes. Then the protein sample was heated for 3 min in boiling water and gradually cooled. 100μg of protein was loaded with micropipette along with 10mL sample buffer containing bromophenol blue in each sample well. The gel was run at 70 Volts for 3 h followed by staining in Coomassie Brilliant Blue R 250 for 6-8 h. Relative mobility (Rm) of the protein band was determined. For hypocotyl protein and GOT, native PAGE was done with 7.5% separating gel. One gm of fresh hypocotyl sample from 6 days old seedling was macerated in phosphate buffer (pH 8.0) at 4 °C. The homogenate was centrifuged at 10,000 rpm for 10 min and the gel was run at 70 Volts for 3 h. Staining was done according to Tankslay and Orton (1983) using Coomassie Brilliant Blue for total protein and Fast Blue BB salt for GOT.

Results and Discussion

Hypocotyl Proteins

A total of 15 bands with Rm values ranging from 0.218 to 0.945 were resolved. Of these, seven bands (0.345; 0.545, 0.600, 0.625, 0.636, 0.691 and 0.945) were polymorphic. Based on presence/absence of these bands, 12 electrophoretic phenotypes (H1-H12) were identified (Plate 1 and Table1). Nine cultivars (K 134, KRG 1, Dh 40, DSG 1, Dh 3-30, TMV 2, ICGV 86590, Mutant and GPBD 4) exhibited unique banding pattern. Two groups had two cultivars each {Spanish Improved and JL 24 (H3), and S 206 and S 230 (H6)} and one group (H12) had three cultivars [Dh 8, R 8808 and TAG 24].

Seed Proteins

SDS-PAGE of seed proteins showed differences in number and intensity of bands for different groundnut cultivars. A total of 17 bands appeared with Rm values

*Corresponding Author: E-mail: mvcgowda@satyam.net.in

Table 1. Pattern of Polymorphic bands for proteins (hypocotyls and seed) and Glutamate Oxaloacetate Transaminase (GOT) isozyme in groundnut cultivars

Variety	Hypocotyl protein							Seed protein				GOT	
	0.345	0.545	0.600	0.625	0.636	0.691	0.945	0.529	0.567	0.739	0.962	0.338	0.385
Spanish Improved	+	+	+	+	+	+	–	–	+	–	–	–	+
TMV 2	+	+	–	+	–	+	–	–	+	–	–	–	–
S 206	+	+	+	–	+	+	–	–	+	–	–	–	+
Dh 3-30	+	+	–	–	+	+	–	–	+	–	–	–	+
JL 24	+	+	+	+	+	+	–	–	+	–	–	–	–
KRG 1	+	+	–	+	+	+	+	–	+	–	+	–	+
K 134	+	–	+	+	+	+	+	–	+	–	–	–	+
Dh 8	+	+	–	–	–	–	–	–	+	–	–	–	–
S 230	+	+	+	–	+	+	–	–	+	+	+	+	+
R 8808	+	+	–	–	–	–	–	+	–	–	+	+	+
Dh 40	+	–	–	+	+	+	+	–	+	–	–	–	+
DSG 1	+	–	+	–	+	+	+	–	+	+	+	+	+
TAG 24	+	+	–	–	–	–	–	–	+	+	–	+	+
ICGV 86590	–	+	–	–	+	–	+	–	+	+	+	–	+
Mutant (28–2)	–	+	–	–	–	–	+	+	+	+	+	+	+
GPBD 4	–	+	–	+	–	–	–	–	+	–	+	–	+

ranging from 0.300 to 0.970. Of these, only four bands with Rm values 0.529, 0.567, and 0.962 were polymorphic forming six electrophoretic phenotype patterns (S1-S6; Plate 1 and Table 1). Among the 16 cultivars, three (Mutant, R.8808 and TAG 24) exhibited unique banding patterns and thus could be identified solely by the cultivar specific electrophoretogram. Pattern I (S1) had Valencia Mutant; Pattern II (S2) had Virginia runner (S 230 and DSG 1) and Valencia (ICGV 86590) cultivars. While, other electrophoretic patterns (S3-S6) had Spanish bunch cultivars. GPBD 4 and its female parent KRG1 showed similar banding pattern and formed a separate group (S5). Hartzook *et al.* (1969) also observed differences in seed protein content among three botanical types and concluded that PAGE of seed proteins could be used as tool in establishing cultivar identification.

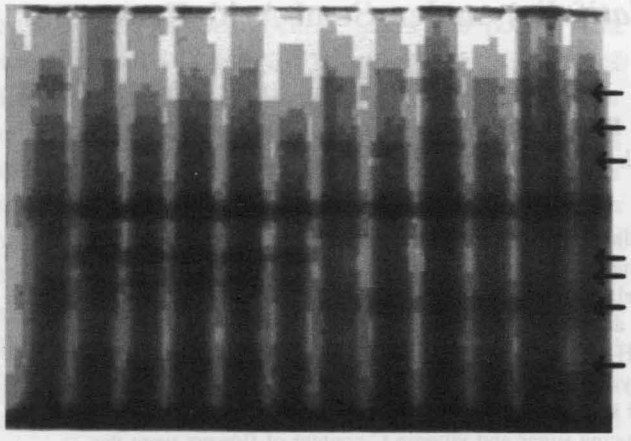
GOT Isozyme

GOT revealed four bands (Rm values 0.338, 0.385, 0.431 and 0.492). Presence and/or absence of first two bands resulted in three banding patterns (G1-G3; Plate 1 and Table1). The pattern I (G1) comprised five cultivars having both the polymorphic bands (0.338 and 0.385). Grieshammer and Wynne (1990) and Lacks and Stalker (1993) reported that, these two polymorphic bands were present only in Virginia types. Pattern II (G2) with eight genotypes had only one polymorphic band (0.385); while, pattern III (G3) comprised three genotypes lacked both the polymorphic bands.

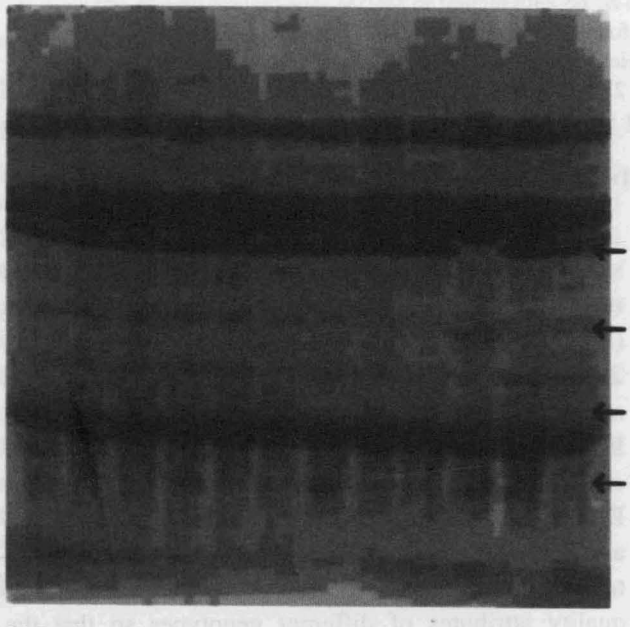
Pattern I that is specific to Virginia botanical type had cultivars belonging to Virginia (S 230 and DSG 1) with some Spanish cultivars (R 8808, TAG 24 and Mutant 28-2). TAG 24 is a cross derivative from two mutants TGE 1 and TGS 2, which in turn derived from Virginia cultivars *viz.*, TG 1 and M 13, respectively. R 8808 had ICGS 11 in its pedigree, which is a selection from Robut 33-1, a Virginia bunch cultivar. 28-2 is a secondary mutant of Dharwad Early Runner (DER). While pattern II and III had Spanish bunch cultivars.

Cultivar Fingerprinting

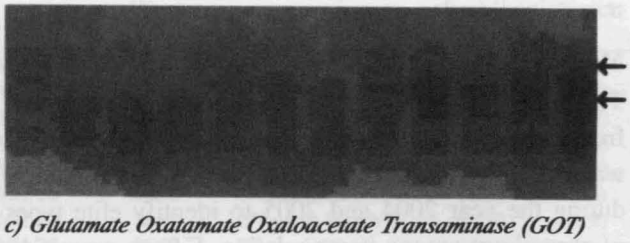
Hypocotyl protein profile has an advantage of twelve (H1-H12) electrophoretic phenotypes compared to six (S1-S6) of seed protein and three (G1-G3) of GOT, which can be used to identify the groundnut cultivars. Hypocotyl and seed protein together identified 14 cultivars. While, Spanish Improved could not be differentiated from JL 24 as they formed a separate group (H3S6). Combination of hypocotyl protein and GOT profiles formed fifteen groups and identified 14 cultivars. Cultivars R 8808 and TAG 24 formed a single group (H12G1). Seed protein and GOT profiles together resulted in eight groups identifying four cultivars. Two groups (S2G1 and S5G2) had two cultivars each, one



a) Hypocotyl proteins



b) Seed proteins



c) Glutamate Oxatamate Oxaloacetate Transaminase (GOT)

Fig. 1: Banding patterns with polymorphism for protein (hypocotyl and seed) and GOT Isozyme

Table 2. Protein fingerprint of groundnut cultivars

Protein fingerprint	Cultivar
H1 S6 G2	K 134
H2 S5 G1	KRG 1
H3 S6 G2	Spanish Improved
H3 S6 G3	JL 24
H4 S6 G2	Dh 40
H5 S2 G1	DSG 1
H6 S2 G1	S 230
H6 S6 G2	S 206
H7 S6 G2	Dh 3-30
H8 S6 G3	TMV 2
H9 S2 G2	ICGV 86590
H10 S1 G1	Mutant (28-2)
H11 S5 G2	GPBD 4
H12 S3 G1	R 8808
H12 S4 G1	TAG 24
H12 S6 G3	Dh 8

group each with three (S6G3) and five (S6G2) cultivars. However, proteins (seed and hypocotyl) and GOT profiles together identified all the sixteen groundnut varieties (Table 2). The multiple enzyme system was used for complete cultivar fingerprinting in soybean. Thus, electrophoresis can be used successfully as a tool for varietal identification in groundnut.

References

Grieshammer U and JC Wynne (1990) Isozyme variability in mature seeds of U.S. peanut cultivars and collection. *Peanut Science* **18**: 72-75.

Hames BD and D Rickwood (1984) *Gel Electrophoresis of Proteins: A Practical Approach*. IRL Press, Washington DC, USA. 91p.

Hartzook A, T Birk and S Hurwitz (1969) Electrophoretic investigation of proteins from three groundnut (*Arachis hypogaea* L.) types. *Isralian Journal of Agricultural Research* **19**: 135.

ISTA (1996) International Rules for Seed Testing, 1996. *Seed Science and Technology* **24** (Supplement): 253-270.

Lacks GD and HT Stalker (1993) Isozyme analyses of *Arachis* species and interspecific hybrids. *Peanut Science* **20**: 76-82.

Laemmli UK (1970) Cleavage of structural proteins during the assembly of head of bacteriophage T_4. *Nature* **227**: 680-685.

Rajgopal K, K Chandran, A Bandyopadyay, HB Lalwani, NR Ghetia and PK Bhalodia (2000) Pattern of distribution of morphological trades among the released groundnut (*Arachis hypogaea* L.) cultivars vis-à-vis the DUS requirements. In: *National Seminar on Oilseeds and Oils-Research and Development Needs in the Millennium*, 2-4 February 2000, Directorate of Oilseeds Research, Rajendranagar, Hyderabad, Andhra Pradesh, India. 16-17 p.

Genetic Divergence in Mahua (*Bassia latifolia*) under Semi-Arid Ecosystem of Gujarat

Sanjay Singh, AK Singh, VV Apparao, BG Bagle and DG Dhandar
Central Horticultural Experiment Station, Vejalpur (Godhra), Panchmahals 389 340 (Gujarat)

Survey was carried out in the district Panchmahals and adjoining areas to identify the elite genotypes among its population. The study revealed that there was a wide variation among the genotypes. Peak period of flowering was earliest (1st week of March) in MH 25, while it was delayed in MH 26, MH 29, MH 31 and MH 32 (1st week of April). MH 32 recorded maximum number of flowers and fruits per fascicle. Early ripening i.e. 4th week of May was recorded in MH 21, MH 22 MH 27, MH 31 MH 32, and MH 33, while it was noted late (3rd week of June) in MH 23, MH 28, MH 34 and MH 35. Dry flower yield ranged from 27-48 kg /plant being highest in MH 32. Fruit yield was found to be highest in MH 32 (98.00 kg /plant). The flower Juice was found to be highest (67.00 %) in MH 32. Total soluble solids, total sugar, reducing sugar and vitamin C content of flowers were the highest in MH 32. Weight of mahua fruit was found to be maximum in MH 34. The seed per cent was found to be maximum in MH 35 (42.91). The total soluble solids, total sugar and vitamin C contents of the fruits were maximum in MH 32.The kernel per cent varied from 74.13-82.68 with highest in MH 24. The highest protein and mineral contents were recorded in MH 34. Fruit yield was found to be positively and significantly associated with flowers and fruits per fascicle, flower weight and flower yield per plant.With respect to all traits studied in these genotypes, MH 32, MH 34, MH 35, MH 26, MH 27, MH 23 and MH 33 were found to be promising and would be exploited as potential parents to develop high yielding stable genotypes.

Key words: Mahua, Flowering, Fascicle, Genetic diversity, Kernel, Minerals, Protein

Mahua (*Bassia latifolia* Roxb.) is an economically multipurpose tree of the family Sapotaceae. The tree is well known to the rural folk since ages in India. It is very hardy and thrives well on rocky, gravelly, saline and sodic soils, even in pockets of soil between crevices of barren rock (Singh, 1998). Its flowers, fruits and seed oil are consumed in various ways. The corolla commonly called mahua flower is a rich source of sugar containing appreciable amount of vitamins and minerals and may be used for preparation of distilled liquors and potable spirits (Singh *et al.*, 1999). The fruit pulp may be utilized as source of sugar for alcoholic fermentation. The oil obtained from kernel is used for edible purpose and permitted for preparation of vegetable oil. Mahua oil is used in manufacture of soap, lubricating grease, fatty alcohols and candles. Cake obtained after extraction of oil is used as manure and has insecticidal properties. In tribal belt of Gujarat, Mahua trees are found growing naturally as stray plantation on wasteland. It is highly heterozygous, cross-pollinated fruit crop and as such seedlings exhibit a wide range of variations, which aids in the selection of the superior desirable genotypes. Due to cross pollination and predomination of seed propagation over a long period of time, it gives immense opportunity to locate elite trees having positive horticultural traits. Wide variations were observed in sweetness, acidity, size, shape and bearing habits in mahua under Uttar Pradesh and Gujarat conditions (Singh *et al.*, 1999; Anonymous, 2002; Singh and Singh, 2005). Considerable genetic diversity under various agro-climatic conditions in different under-utilized fruits like tamarind, jamun has also been reported (Keskar *et al.* 1989a, Keskar *et al.*, 1989 b; Karale *et al.*, 1999; Devi *et al.*, 2002,; Rai and Mishra, 2005 and Singh and Singh, 2005). Present investigation was carried out to find out variability in flowering, fruiting and fruit quality attributes of different genotypes so that the valuable germplasm could be protected from being eroded and at the same time their utilization is also maximized under crop improvement programme.

Materials and Methods

The mahua trees are found scattered throughout Gujarat from cultivable land to waste lands. An extensive survey was made in Panchamahal district and adjoining areas during the year 2004 and 2005 to identify elite types of germplasm among its population. Fifteen promising genotypes from different locations and age group were selected, which had fairly wide spectrum of variability of various characters and they were considered as experimental materials. The observations were recorded on tree characters, flowering, fruiting and fruit quality

attributes for two consecutive years and pooled data were presented (Tables 1-4). Twenty healthy fascicles from each tree were randomly selected to record number of flowers and fruits per fascicle. The ripe fruits differing in shape, size and appearance were collected to study the variability in physico-chemical attributes. The trees were free from pests and diseases. Healthy fruits were harvested and experiment was laid out in completely randomized design with three replications. Flower and fruit yield per tree was recorded on different dates and at the last total yield was calculated. Total soluble solids and titratable acidity were determined by standard methods. Protein, minerals, Vitamin C and sugars were analyzed by the method advocated by AOAC, 1980. Oil content in kernel was determined by the method described by Rangana, 1986.

Results and Discussion

Perusal of the data, collected from the studies on the genetic diversity of mahua in Gujarat revealed that the different trees varied widely in flowering, fruiting and fruit quality attributes. The tree age ranged from 35.00 to 48.00 years in different genotypes (Table 1). Peak period of flowering was earliest (1st week of March) in MH 25, while it was delayed in MH 26, MH 29, MH 31 and MH 32 (1st week of April). There was marked variation in average number of flowers per fascicle in most of the genotypes and MH 32 recorded maximum number of flowers per fascicle (33.50) and fruits (12.50) per fascicle followed by MH 27, MH 26, MH 35 and MH 24 while, it was found least in MH 31. Wide range of variability in different mahua genotypes was recorded under Uttar Pradesh conditions and recorded 66.00,54.60, 64.30 and 78.50 flowers per fascicle were observed in collection number 2,4, and 8 respectively. The leaf area (cm^2) varied from 90.00-122.00 cm^2 and MH 30 being at the top followed by MH 26, MH 31, MH 25 and MH 35. Early ripening (4th week of May) was recorded in MH 21, MH 22 MH 27, MH 31, MH 32 and MH 33, while it was noted late (3rd week of June) in MH 23, MH 28, MH 34 and MH 35. Dry flower yield ranged from 27-48 kg/plant and it was found to be highest in MH 32 followed by MH 27, MH 26, MH 24, MH 35 and MH 25. Wide range of variability was observed in fruit yield per plant. It was found to be highest in MH 32 (98.00 kg /plant) followed by MH 27, MH 26, MH 35 and MH 24, while lowest fruit yield was recorded in MH 31(68.00 kg/ plant). Singh (1998) also recorded the variability in fruit yield attributes on 5-7 year old grafted plants of mahua under Uttar Pradesh conditions. Variation in soil and climatic conditions might have caused wide range of variability in different genotypes. Karale *et al.*, 1999; Keskar *et al.*, 1989a; Devi *et al.*, 2002; Kundu *et al.*, 2001; Mitra, 1998; Pareek and Awasthi, 2002; Maiti and Mitra, 2002 and Sakhyan *et al.*, 2004 observed variability in under-utilized fruits like tamarind, jamun, jackfruit and sea buckthorn under various agro-climatic conditions.

Variability recorded in physical and biochemical characters in mahua flowers has been presented in Table 2. Weight of fresh mahua flowers ranged from 2.00 gm-2.32 gm with highest in MH 23 followed by MH 22, MH 32, MH 24 and MH 27. The flower juice was

Table 1. Variability in tree age, flowering, fruiting and fruit yield attributes

Genotypes	Age (Year)	Flowering time	Flowers/ fascicle	Fruits/ fascicle	Bearing habit	Leaf area (cm^2)	Harvesting time	Dry-flower yield (kg/ plant)	Fruit yield (kg/ plant)
MH 21	35.00	2nd week March	22.50	6.50	Regular	90.20	4th week May	35.00	73.00
MH 22	40.00	4th week March	24.50	6.80	Regular	105.00	4th week May	37.00	78.00
MH 23	45.00	3rd week March	26.50	7.20	Regular	106.00	3rd week June	39.00	80.00
MH 24	46.00	3rd week March	28.00	7.50	Regular	111.20	2nd week June	41.50	80.50
MH 25	42.00	Ist week March	27.20	7.00	Regular	115.00	1st week June	40.50	78.50
MH 26	38.00	1st week April	30.00	8.00	Regular	120.00	2nd week June	42.00	86.00
MH 27	36.00	2nd week March	31.50	8.50	Regular	111.80	4th week May	43.00	87.00
MH 28	36.00	3rd week March	25.50	7.00	Regular	105.80	3rd week June	38.50	77.00
MH 29	40.00	1st week April	22.00	5.00	Regular	103.00	2nd week June	28.00	72.00
MH 30	38.00	2nd week March	20.20	4.80	Regular	122.00	1st week June	27.50	70.00
MH 31	42.00	1st week April	18.00	4.20	Regular	115.20	4th week May	27.00	68.00
MH 32	39.00	1st week April	33.50	12.50	Regular	112.45	4th week May	48.00	98.00
MH 33	42.00	3rd week March	22.80	5.50	Regular	113.80	4th week May	28.50	70.00
MH 34	44.00	2nd week March	24.00	6.00	Regular	108.00	3rd week June	30.20	75.00
MH 35	48.00	2nd week March	28.50	8.60	Regular	114.50	3rd week June	41.00	85.00
CD (*P=0.05*)	-	-	4.41	0.70	-	5.16	-	-	-

found to be highest (67.00%) in MH 32 followed by MH 31, MH 30 and MH 29, while pomace per cent was noted to be highest in MH 26 (38.10). Total soluble solids, total sugar, reducing sugar and vitamin C content of flowers was the highest in MH 32 ie 26.20 %, 23.78%, 20.13% and 62.60 mg/ 100g respectively, it was closely followed by MH 26, MH 33, MH 22 and MH 34. Titratable acidity of fresh mahua flowers ranged from 0.09-0.27% being highest in MH-28.Weight of mahua fruit was found to be maximum in MH 34 followed by MH 25, MH 35, MH 24 and MH 33, while least fruit weight was recorded in MH 21 and MH 29. The fruits of MH 22 recorded maximum husk per cent (62.71) and that of MH 35 the lowest (57.08). The seed per cent was found to be maximum in MH 35 (42.91) followed by MH 24, MH 25, MH 26 and MH 34. The total soluble solids, total sugar and vitamin C contents of the fruits were maximum in MH 32 i.e., 13.80%, 11.75%, 8.73%, 60.00 mg/100g respectively followed by MH 25, MH 27, MH 26 and MH 28. Singh *et al.* (1999) and Anonymous (2002) have also recorded the variation in fruit quality attributes in different mahua genotypes. They also emphasized that early maturing genotypes had more juice content than late ones. It might be due to low temperature prevailing during early flowering period.

The kernel percent varied from 74.13-82.68 with highest in MH 24, it was closely followed by MH 35, MH 34, MH 25, and MH 26, while least kernel content was recorded in MH 23. Similarly shell per cent varied from 17.57-25.50 being at the top in MH 23. The chemical composition of kernel also showed variation in terms of protein and minerals (Table 3). The highest protein and mineral contents were recorded in MH 32 *i.e.*, 23.34 and 4.48 % respectively, it was closely followed by MH 32, MH 28, MH 29, MH 23 and MH 33. The oil content of the kernel ranged from 40.29-46.68% and it was noted highest in MH 32 (46.68 %) followed MH 23, MH 34, MH 28 and MH 35. Mahua can play an important role in vegetable oil production, as it is one of the highest yielding trees per unit area. Singh *et al.* (1999) observed similar results in different mahua genotypes. Genetic diversity in kernel characters among different genotypes of pecan nut and Persian walnut was also recorded under cold arid conditions (Thompson and Baker, 1993; Sharma and Sharma, 2001 and Kaushal and Sharma, 2002). Correlation studies provide reliable information on nature and extent of relationship for bringing out improvement in yield and other traits. There was significant positive association of flowers and fruit per fascicle, flower weight and flower yield with fruit yield per plant. These traits may be observed for their positive behaviour while selecting superior genotypes. Machewade *et al.* (2003) surveyed the chironji (*Buchanania lanzan*) growing area of Maharastra and studied correlation and path analysis and concluded that there was highest significant positive association of number of panicles and total number of fruit per tree with weight of fruit. Singh and Mishra (2004) reported that fruit weight showed significant positive correlation with flower length and breadth, petal length and breadth, filament and anther length, stigma and ovary diameter and bud length at flower opening.With respect to all traits studied in these genotypes, MH 32, MH 34, MH

Table 2. Variability in physico-chemical attributes of mahua flowers

Genotypes	Flower weight (g)	Juice (%)	Pomace (%)	Stamen (%)	TSS (%)	Acidity (%)	Total sugar (%)	Reducing sugar (%)	Vitamin-C (mg/100g)
MH 21	2.20	63.50	35.69	0.81	24.50	0.12	21.89	17.54	56.13
MH 22	2.30	62.10	37.20	0.70	26.00	0.13	23.13	19.34	52.14
MH 23	2.32	64.00	35.22	0.78	25.80	0.19	22.70	18.13	61.20
MH 24	2.28	63.50	35.60	0.90	24.10	0.17	21.13	17.34	56.23
MH 25	2.26	62.80	36.27	0.93	24.50	0.23	21.15	17.32	54.45
MH 26	2.29	61.00	38.10	0.90	26.10	0.21	23.47	19.56	53.14
MH 27	2.28	64.80	34.36	0.84	25.10	0.25	22.12	18.00	55.45
MH 28	2.16	63.70	35.47	0.83	23.80	0.27	20.70	17.13	57.45
MH 29	2.22	64.00	35.11	0.81	24.50	0.23	21.49	17.45	58.46
MH 30	2.00	65.00	33.97	0.83	24.89	0.21	21.79	17.89	53.93
MH 31	2.12	66.00	33.14	0.86	25.13	0.18	22.43	18.46	54.00
MH 32	2.30	67.00	32.09	0.91	26.20	0.11	23.78	20.13	62.60
MH 33	2.23	62.00	37.07	0.93	26.00	0.09	23.00	19.52	61.13
MH 34	2.14	63.00	36.08	0.92	25.80	0.10	22.87	18.91	60.59
MH 35	2.13	64.12	34.98	0.90	24.90	0.16	21.89	17.93	58.36
CD (*P=0.05*)	**0.09**	**1.34**	**1.93**	**NS**	**0.62**	**0.02**	**0.53**	**0.52**	**1.54**

Table 3. Variability in physico- chemical attributes of mahua fruits and kernels

Genotypes	Mahua fruits										Mahua kernels						
	Fruit weight (g)	Husk weight (g)	Husk (%)	Seed weight (g)	Seed (%)	TSS (%)	Acidity (%)	Total sugar (%)	Reducing sugar	VitaminC (mg/100g)	Kernel weight (g)	Kernel (%)	Shell weight (g)	Shell (%)	Protein (%)	Minerals (%)	Oil (%)
MH 21	21.50	13.45	62.55	8.05	37.44	12.45	0.12	10.14	7.03	45.00	6.32	78.50	1.73	21.49	20.50	4.13	42.00
MH 22	22.50	14.11	62.71	8.39	37.28	11.45	0.19	9.19	6.14	52.34	6.39	76.16	2.00	23.83	21.39	4.11	43.50
MH 23	26.15	15.17	58.01	10.98	41.98	11.89	0.21	9.45	6.24	56.47	8.14	74.13	2.80	25.50	22.36	3.39	45.60
MH 24	28.30	16.17	57.14	12.13	42.86	12.90	0.19	10.30	7.14	50.49	10.03	82.68	2.10	17.31	20.87	4.19	42.68
MH 25	29.50	16.87	57.19	12.63	42.81	13.50	0.16	11.45	8.30	53.14	10.19	80.68	2.44	19.32	21.39	4.28	43.29
MH 26	24.50	14.11	57.59	10.39	42.40	13.11	0.18	11.13	8.12	45.13	8.34	80.26	2.05	19.73	20.45	4.35	42.28
MH 27	23.10	13.78	59.65	9.32	40.34	13.45	0.11	11.41	8.24	48.00	7.13	76.50	2.19	23.49	22.37	4.19	43.00
MH 28	22.50	13.34	59.28	9.16	40.71	13.10	0.12	11.10	8.10	47.14	7.03	76.74	2.13	23.25	22.89	3.18	45.24
MH 29	21.50	12.87	59.86	8.63	40.13	12.14	0.09	10.08	7.02	18.31	6.83	79.14	1.80	20.85	22.48	4.10	40.29
MH 30	23.80	13.88	58.31	9.95	41.80	12.40	0.09	10.11	7.08	49.45	7.78	78.19	2.17	21.80	21.50	3.15	41.50
MH 31	25.11	14.90	59.33	10.21	40.66	11.80	0.10	9.40	6.45	53.61	8.13	79.62	2.08	20.37	21.00	3.14	43.50
MH 32	24.00	14.14	58.91	9.86	41.08	13.80	0.09	11.75	8.73	60.00	7.73	78.39	2.13	21.60	23.34	4.48	46.68
MH 33	27.58	16.13	58.48	11.45	41.50	12.46	0.13	10.14	7.13	52.49	9.13	79.73	2.32	20.26	22.11	3.92	42.57
MH 34	29.70	17.19	57.87	12.51	42.12	11.50	0.15	9.53	6.56	53.11	10.10	80.73	2.41	19.26	23.10	3.83	45.00
MH 35	28.50	16.27	57.08	12.23	42.91	12.80	0.16	9.26	7.27	55.60	10.08	82.42	2.15	17.57	21.50	3.73	44.67
CD	2.14	1.32	1.74	1.37	1.12	0.51	NS	0.62	0.63	2.12	1.10	0.59	0.30	1.34	0.61	0.39	1.19
(P=0.05)																	

Table 4. Correlation studies in mahua genotypes

Characters	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	1															
2	**0.92	1														
3	0.16	0.06	1													
4	*0.62	0.52	-0.22	1												
5	0.03	0.26	0.06	-0.26	1											
6	-0.02	-0.25	-0.09	0.28	**-0.99	1										
7	0.21	0.27	0.24	0.32	-0.12	0.12	1									
8	0.07	-0.12	0.20	-0.06	-0.06	-0.06	*-0.56	1								
9	0.12	0.02	0.41	-0.03	-0.20	0.18	0.11	-0.28	1							
10	0.06	-0.01	0.30	-0.01	-0.23	0.22	0.15	-0.39	**0.98	1						
11	0.17	0.05	0.49	-0.05	-0.16	0.14	0.07	-0.17	**0.99	**0.94	1					
12	0.16	0.04	0.49	-0.08	-0.17	0.15	0.02	-0.19	**0.97	**0.93	**0.99	1				
13	0.23	0.29	-0.06	0.04	0.37	-0.37	0.17	-0.02	0.01	-0.01	0.03	-0.04	1			
14	*0.61	*0.55	-0.13	0.07	-0.26	0.26	0.25	-0.25	0.03	0.05	0.00	0.06	-0.08	1		
15	**0.93	**0.90	0.47	*0.62	0.07	-0.06	0.07	0.13	0.06	0.01	0.09	0.08	0.06	*0.53	1	
16	**0.96	**0.97	0.16	*0.55	0.22	-0.21	0.30	0.00	0.03	-0.02	0.08	0.07	0.25	*0.56	**0.92	1

1: Flowers per fascicle, 2: Fruits per fascicle, 3: Leaf area (cm^2),), 4: Flower weight (g), 5: Flower juice (%), 6: Flower pomace (%), 7: Flower TSS (%), 8: Flower acidity (%), 9: Fruit weight (g), 10: Husk weight (g), 11: Seed weight (g), 12: Kernel weight (g), 13: Kernel Protein (%), 14: Kernel minerals (%)15: Dry-flower yield (kg/ plant), 16: Fruit yield (kg/ plant)

r: 0.514 and 0.641 at 5 and 1 per cent respectively

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

35, MH 26, MH 27, MH 23, and MH 33 were found to be promising on the basis of desired horticultural characters. Vegetatively propagated promising genotypes have been planted in the field for their further evaluation.

References

AOAC (1980) Official methods of Analysis, Association of official Agricultural chemists. Washington USA.

Anonymous (2002) Annual Report, Central Institute for Arid Horticlture, Bikaner, p 31.

Devi P S, Thangam M, Desai A R and Adsule PG (2002) Studies on variavility in physico-chemical characters of different jamun (*Syzygium cumini* Skeels) accessions from Goa. *Indian J Hort* **59**: 153-156.

Kaushal R and Sharma SD (2002) Genetic divergence in seedling trees of pecan (*Carya illioensis* (Wang) K Koch) for various metric nut and kernel characters in Himachal Pradesh. *Theoret Hort J* **15**: 11-17.

Karale A R, Wagh A P, Pawar BG and More TA. (1999) Association of fruit characters in tamarind. *J Maharastra Agril Univ* **24(3)**: 319-320.

Keskar BG, Karale AR, Dhawale BC and Chaudhary KG (1989a) Improvement of jamun by selection. *Maharashtra J Hort* **4**: 117-20.

Keskar BG, Karale AR, Dhawale BC and Chaudhary KG (1989 b) Improvement of tamarind by selection. *Maharashtra J Hort* **4**: 121-24.

Kundu S, Ghosh DK and Maity SC (2001) Evaluation of some local types of Jamun (*Syzygium cumini* Skeels) of West Bengal. *Environment and Ecology* **19**: 872-874.

Maiti CS and Mitra, SK (2002) Studies on genetic resources of jackfruit (*Artocarpus heterophylus* Lamk) in West Bengal. *The Hort J* **15**: 33-43.

Machewad PM, Shinde GS and Munde VM (2003) Correlation and path analysis studies in *charoli* (*Buchanania lanzan Spreng*). *The Hort J* **16**: 29-34.

Mitra SK (1998) Genetic diversity of jackfruit (*Artocarpus heterophylus* Lamk) *Indian Hort* **43**: 1.

Pareek OP and Awasthi OP (2002) Genetic resources of tamarind. *Indian J Plant Genet Resour* **15**: 197-202.

Rangana S (1986) Hand Book of Analysis and Quality Control for fruit and Vegetable Products, 2nd Edn. Tata Mc Graw Hill Publishing Co. Ltd. New York.

Rai Deepti and Mishra KK (2005) Studies on genetic divergence in Bael (*Aegle marmelos* Correa) *Indian J Hort* **62**: 152-154.

Sakhyan HP, Sehgal RN and Bhrot NP (2004) Morphological characters variation in different species of sea buckthorn in cold deserts of Himachal Pradesh. *Indian J Forestry* **27**: 129-32.

Sharma OC and Sharma SD (2001) Genetic divergence in seedling trees of Persian walnut (*Juglans regia* L.) for various metric nut and kernel characters in Himachal Pradesh. *Scientia Hort* **88**: 163-71.

Singh IS (1998) Mahua–An oil-bearing tree. Technical Bulletin, PP 3-11, ND University of Agriculture and Technology, Kumarganj, Faizabad, UP, India.

Singh IS, Srivastava AK and Singh B (1999) Improvement of some under-utilized fruits through selection *J Applied Hort* **1**: 34-37.

Singh VP and Mishra KK (2004) Estimation of variability parameters for floral traits and yield in Bael (*Aegle marmelos* Correa) *Progressive Hort* **36**: 253-258.

Singh Sanjay and Singh AK (2005) Genetic variability in jamun (*Syzygium cumini* Skeels) in Gujarat *Progressive Hort* **37**: 144-148.

Singh Sanjay and Singh AK (2005) Genetic diversity in *mahua* (*Bassia latifolia*) under semi arid ecosystem of Gujarat. *Indian J Agril Sci* **75**: 519-23.

Thompson TE and Baker JF (1993). Heritability and phenotypic correlation of six pecan nut characteristics. *J American Soc Hort Sci* **118**: 415-418.

Direct Organogenesis in *Dioscorea* Species

KI Asha* and GM Nair[1]
NBPGR Regional Station, Vellanikkara, Thrissur 680 654 (Kerala)
[1]Tropical Botanical Garden and Research Institute, Palode, Thiruvananthapuram (Kerala)

Protocol was developed for direct adventitious shoot regeneration from leaf and petiole explants of six species of *Dioscorea* in MS medium augmented with varying concentrations and combinations of cytokinins and auxins. Leaf explants responded well in cultures of *Dioscorea pentaphylla, D. hamiltonii, D. wightii* and *D. intermedia* followed by petiole in *D. bulbifera* and *D. hispida*. Cytokinins are effective in promoting direct shoot initiation. Amongst different cytokinins, BA was effective in producing maximum bud sprouting from leaf explants of *D. pentaphylla*, where 3 bulbils and 8 shoot buds got regenerated in 2 mg/l while *D. wightii* in BA at 4 mg/l induced 3 shoots. Kinetin (2 mg/l) in the medium also induced 16 shoots from leaf explants of *D. hamiltonii*. Synergistic effect of BA (3 mg/l), Kin (1 mg/l) and NAA (1 mg/l) initiated the development of 12 shoots in *D. pentaphylla* from leaf explants.

Key words: *Dioscorea*, Diosgenin, Bulbil, Micropropagation, Direct Organogenesis

Yams, members of the genus *Dioscorea* L. producing edible tubers and bulbils are of immense economic importance (Ammirato, 1984). They constitute the staple carbohydrate food, which contains high protein and mineral contents for millions in many tropical and subtropical countries. Moreover, wild species are of medicinal and pharmacological importance as they are sources of steroidal sapogenins especially diosgenin, which is the precursor in the commercial synthesis of sex hormone and corticosteroids (Coursey, 1967). They being vegetatively propagated and producing highly heterozygous seeds and having problems of shy flowering, non-synchronization in flowering and even non-flowering needs biotechnological approaches for clonal multiplication. The present study was aimed to standardize protocols for the rapid clonal multiplication of the twelve species available in Southern Western Ghats through direct organogenesis. In the method of direct organogenesis, adventitious shoots arise directly from the tissues of the explant without a callus phase. In *Dioscorea floribunda*, from the excised leaves, cultures were initiated by Sinha and Chaturvedi (1979). The regenerative proliferation and development of multiple shoots occurred from the pulvinus tissue of the leaf explants devoid of axillary buds and were successfully transplanted into soil. Direct organogenesis has also been recorded in *D. opposita*, where immature leaves were used as the explant (Kohmura *et al.*, 1995). Similarly, cultivated forms also behaved in culture with direct organogenesis as in *D. rotundata* (Nwachukwu *et al.*, 1996) and *D. batatus* (Matsubara *et al.*, 1992).

In the present experiment, direct organogenesis was obtained from leaf or petiole explants of six species of *Dioscorea* in MS medium augmented with varying concentrations and combinations of cytokinins and auxins. Leaf explants responded well in cultures of *D. pentaphylla, D. hamiltonii, D. intermedia* and *D. wightii* followed by petiole in *D. bulbifera* and *D. hispida*. The other explants tried namely stem, root and bulbil did not give any positive response.

Materials and Methods

One accession each from the 12 species of *Dioscorea* (Table 1) having distribution in Southern Western Ghats, procured from NBPGR Regional Station, Thrissur and grown in the green house of the Department of Botany, University of Kerala, Thiruvananthapuram served as the explant source for the present experiments. Leaf, stem, petiole, root and bulbil segments from vines of healthy and disease free mother plants of 4-months-old were used. The explants were initially washed in running tap water for 30-60 minutes, then in aqueous 10% Labolene for 15-20 minutes and again in tap water and in sterile distilled water to remove the adhering surface contaminants. They were then sterilized inside the laminar airflow chamber using aqueous 0.1% $HgCl_2$ for 5-20 minutes and then rinsed in sterile double distilled water 4-5 times in order to remove the adhering sterilants.

**Author for correspondence, e-mail: ashakarthy@rediffmail.com)*

Table 1. Materials used and locality of collection

Species Name	IC Number	Locality of collection
Dioscorea bulbifera L.	202349	Peechi, Thrissur, Kerala
Dioscorea pentaphylla L.	202367	Peechi, Thrissur, Kerala
Dioscorea hispida Dennst	202370	Nilambur, Malappuram, Kerala
Dioscorea tomentosa Heyne	202379	South Canara, Karnataka
Dioscorea pubera Bl.	202382	Begur, Wynad, Kerala
Dioscorea intermedia Thw.	202384	Santhanpara, Idukki, Kerala
Dioscorea spicata Roth.	202383	Thirthahally, Coorg, Karnataka
Dioscorea oppositifolia L.	202386	Valpara, Palghat, Kerala
Dioscorea wightii Hook. f.	214855	Mundanthurai, Tamil Nadu
Dioscorea belophylla Voight	248181	Devakolly, Coorg, Karnataka
Dioscorea wallichii Hk. f.	202312	Courtallum, Tirunelveli, Tamil Nadu
Dioscorea hamiltonii Hk.	202328	Vadakkancherry, Thrissur, Kerala

The explants were then trimmed to approximate sizes by removing off the cut ends after blotting in sterile filter paper before inoculation.

For the induction of direct adventitious buds, leaf, stem, petiole, bulbil and root segments (0.5-1 cm) were inoculated onto sterile culture tubes containing 15 ml of MS basal medium (Murashige and Skoog, 1962) augmented with varying concentrations and combinations of cytokinins *viz.*, BA, Kin, TDZ and 2-iP (0.5-10 mg/l) or auxins *viz.*, NAA, IAA, IBA (0.5-5 mg/l) alone or combinations of the two (0.5-3 mg/l). The cultures were then kept in the culture room maintained under 12 h photoperiod at a light intensity of 3000 lux at a temperature of 25±1°C and at 70-80% RH. The responding explants were transferred to fresh media either of the same composition or to lower concentrations for further proliferation and elongation. The shoots developed were separated from the growing clusters and transferred to rooting medium.

Micro-shoots obtained through direct organogenesis were rooted within 15 days either in MS basal medium or medium containing auxins *viz.*, IAA, IBA or NAA (0.5–2 mg/l). The rooted plantlets were transferred to tubes containing basal liquid medium with reduced levels of sucrose (1-2%) for hardening. The hardened plantlets were transferred to plastic cups containing soilrite and covered with moistened plastic bags to maintain maximum humidity and were kept in culture room for 2-3 weeks. The plantlets were nourished with 1/10 dilute Hogland's solution (Epstein, 1972) on every 3rd day for 2 weeks. The plantlets with newly sprouted leaves were then transplanted to pots containing garden soil and sand mixture in 1:1 ratio under green house conditions. The survival rate of plants was recorded as 5 replicates per treatment, each repeated 3 times.

Results

Dioscorea species were successfully micropropagated through direct organogenesis. Response of the various explants to different hormones, *viz.* cytokinins and auxins, either alone or in combination was studied.

Micropropagation was achieved in six species namely *Dioscorea bulbifera, D. pentaphylla, D. hispida, D. intermedia, D. hamiltonii* and *D. wightii* through adventitious *de novo* organogenesis from leaf and petiole explants when inoculated on to MS medium supplemented with cytokinins *viz.* BA/Kin/TDZ/2-ip alone or in conjunction with auxins *viz.* NAA/IAA/IBA/2,4-D. Surface sterilization of different explants in aqueous mercuric chloride at 0.1% and 0.2% for various time exposures (5-20 min.) showed that 0.1% $HgCl_2$ in an exposure time of 5-10 min. in case of leaf and petiole and 12-15 min. in case of stem and bulbil and 20 min. for root explants was found to be the best to obtain 85-90% contaminant free cultures for all the 12 species.

In *Dioscorea bulbifera*, young petiole alone showed organogenetic response in 2,4-D (3 mg/l) in the medium developing a bulbil from one of the cut ends (Plate-1. 1) which on subculture to basal MS developed a shoot. In *D. pentaphylla*, leaf explants developed 3 bulbils and 8 shoot buds directly from the explant on BA (2 mg/l) (Table 2). Synergistic effect of BA (3 mg/l), Kin (1 mg/l) and NAA (1 mg/l) after 25 days of culture resulted in the development of 12 shoot buds in this species from leaf explants (Table 2; Plate-1, 2), while in 60 days, the number of shoots increased to 43 (Plate-1, 3). These shoot buds on transfer to MS basal medium resulted in elongation and were subsequently transferred to rooting medium.

In *D. hispida*, from the cut end of young petiole, a single shoot bud was developed in 2,4-D (1 mg/l) after 30 days of culture (Plate 1, 4), which on subculture to TDZ (3 mg/l) produced 2 more shoot buds from the base.

Leaf segments of *D. hamiltonii* inoculated on medium containing TDZ (1mg/l), on subculture to Kin (2 mg/l), developed 16 shoots (Table 2; Plate-1, 5). In *D. wightii*, BA (4 mg/l) initiated the development of 3 shoots from leaf explants, which, on subculture to MS

Table 2. Effect of hormones on direct organogenesis in six species of *Dioscorea*

Species Name	Conc. of hormones (mg/l)								No. of shoots /
(Explant)	BA	Kin	TDZ	2-ip	IAA	IBA	NAA	2,4-D	bulbils (30 days)
D. bulbifera									
(Petiole)	-	-	-	-	-	-	-	**3.0**	1 (bulbil)
D. pentaphylla	**2.0**	-	-	-	-	-	-	-	8 / 3 (bulbils)
(Leaf)	3.0	1.0	-	-			1.0	-	12 shoots
D. hispida									
(Petiole)	-	-	-	-	-	-	-	1.0	1 shoot
D. hamiltonii									
(Leaf)	-	-	1.0	-	-	-	-	-	16 shoots
D. wightii									
(Leaf)	4.0	-	-	-	-	-	-	-	3 shoots
D. intermedia									
(Leaf induced root)	-	2.0	-	-	-	0.5	-	-	1 shoot

produced 3 more shoots with the elongation of the existing shoots in 45 days of culture (Plate-1, 6). In *D. intermedia*, leaf explants on culture media failed to show shoot organogenesis but resulted in the development of feathery white roots in IBA (0.5 mg/l). However, in this species, leaf disc cultured in IAA, IBA and NAA (3-5 mg/l) initiated roots in 12 days. The IAA/IBA raised roots after 40 days developed shoot directly. IBA raised roots shooted in a combination of Kin (2 mg/l) and IBA (0.5 mg/l) and produced branches (Plate-1, 7).

D. bulbifera responded very slowly in culture with regard to rooting. In presence of NAA (0.5 mg/l) in the medium it produced healthy roots in 30 days (Plate-2, 1). The other species *viz.*, *D. hispida*, *D. hamiltonii* and *D. wightii* took only 10-15 days for healthy rooting in presence of NAA (0.5 mg/l) (Plate-2, 3, 4, 5). *D. pentaphylla* and *D. intermedia* produced roots without a separate rooting medium (Plate-2, 2, 6).

The rooted shoots were transferred to liquid MS medium supplemented with 2% sucrose over filter paper bridges and were transferred to plastic cups containing soilrite covered with plastic bags for hardening and acclimatization. Sprinkling them with Hogland's solution at intervals of 3 days for 2 weeks provided nourishment to the plantlets. After 15 days, the hardened plantlets were planted in pots containing garden soil and sand in the ratio 1:1 and were then shifted to green house conditions for establishment. Survival rate of the regenerants was from 85% in *D. hispida* and *D. wightii*, 88% in *D. hamiltonii* and *D. bulbifera* to 94% in *D. pentaphylla* and *D. intermdia*, which grew luxuriantly as the green house grown mother plants (Plate-3, 16).

Discussion

Members of the genus *Dioscorea* being vegetatively propagated possess unique problems in genetic conservation as well as improvement. Hence there is a need to employ non-conventional propagation method like tissue culture to propagate the different species of *Diosorea*. With the aim to standardize protocols for rapid clonal multiplication, twelve different species of *Dioscorea* of the southern Western Ghats, were selected, of which six of them yielded positive results in terms of *de novo* adventitious shoot organogenesis.

By several trials appropriate explant sterilization procedure was standardized for each species with minimal rate of microbial contamination and without damage to the tissues. 0.1% mercuric chloride and exposure to 8-10 minutes in case of leaf and petiole explants and 12-15 minutes for stem, bulbil and root explants was adequate to get 85-90% contaminant free cultures in all the experiments.

Selection of appropriate nutrient medium forms the initial and essential step in plant tissue culture. Earlier reports by Acedo, *et al.* (1994) and Nair, *et al.* (1994) also affirmed the potentiality of MS basal medium on micropropagation of edible yams.

In the present study, direct organogenesis was achieved from leaf and petiole explants of six species of *Dioscorea* in MS medium augmented with varying concentrations and combinations of cytokinins and auxins. Direct organogenesis in *Dioscorea* species varied according to the species, type of the explant and treatment with plant growth regulators.

Adventitious shoot formation directly from excised

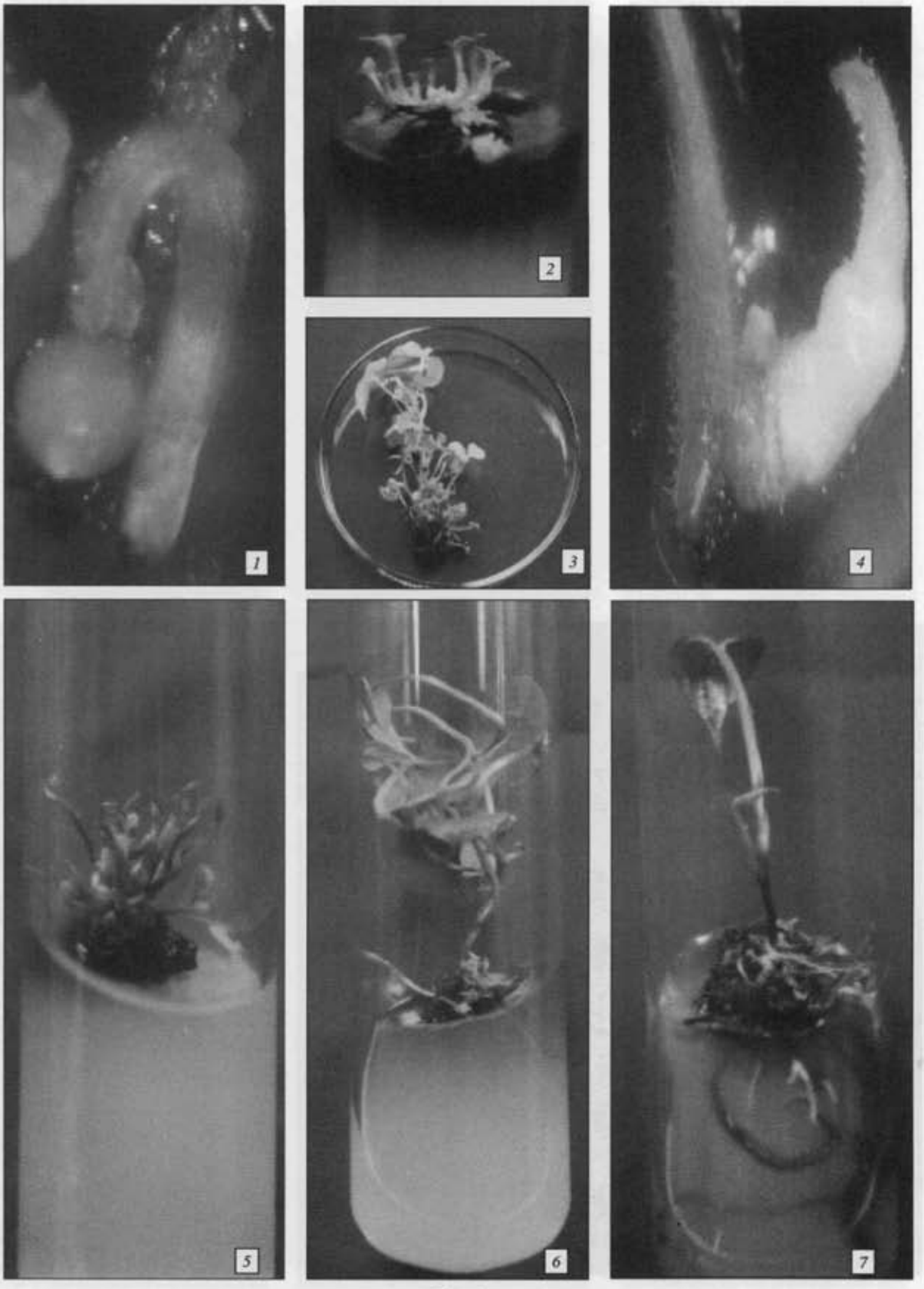


Plate 1

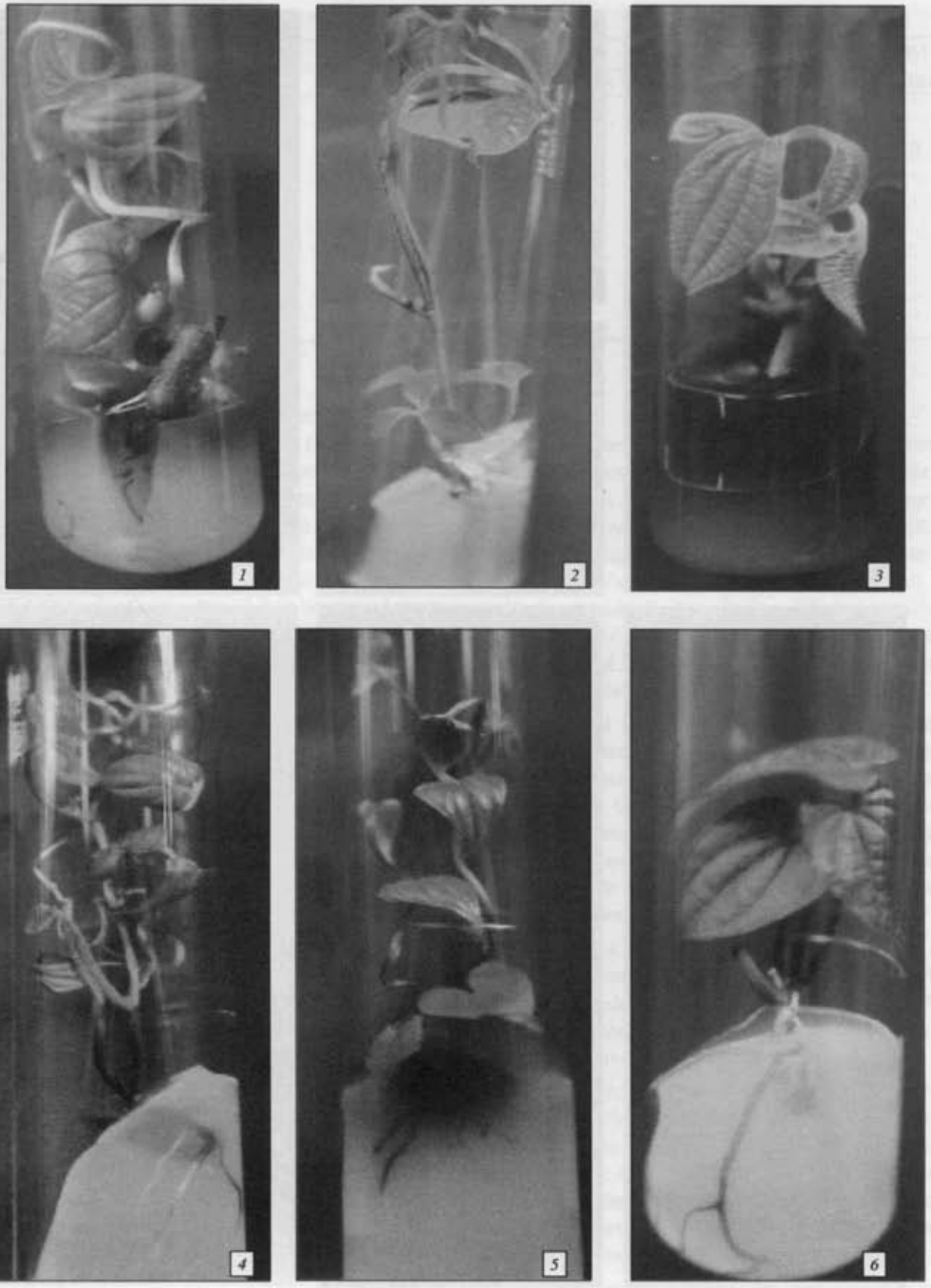


Plate 2

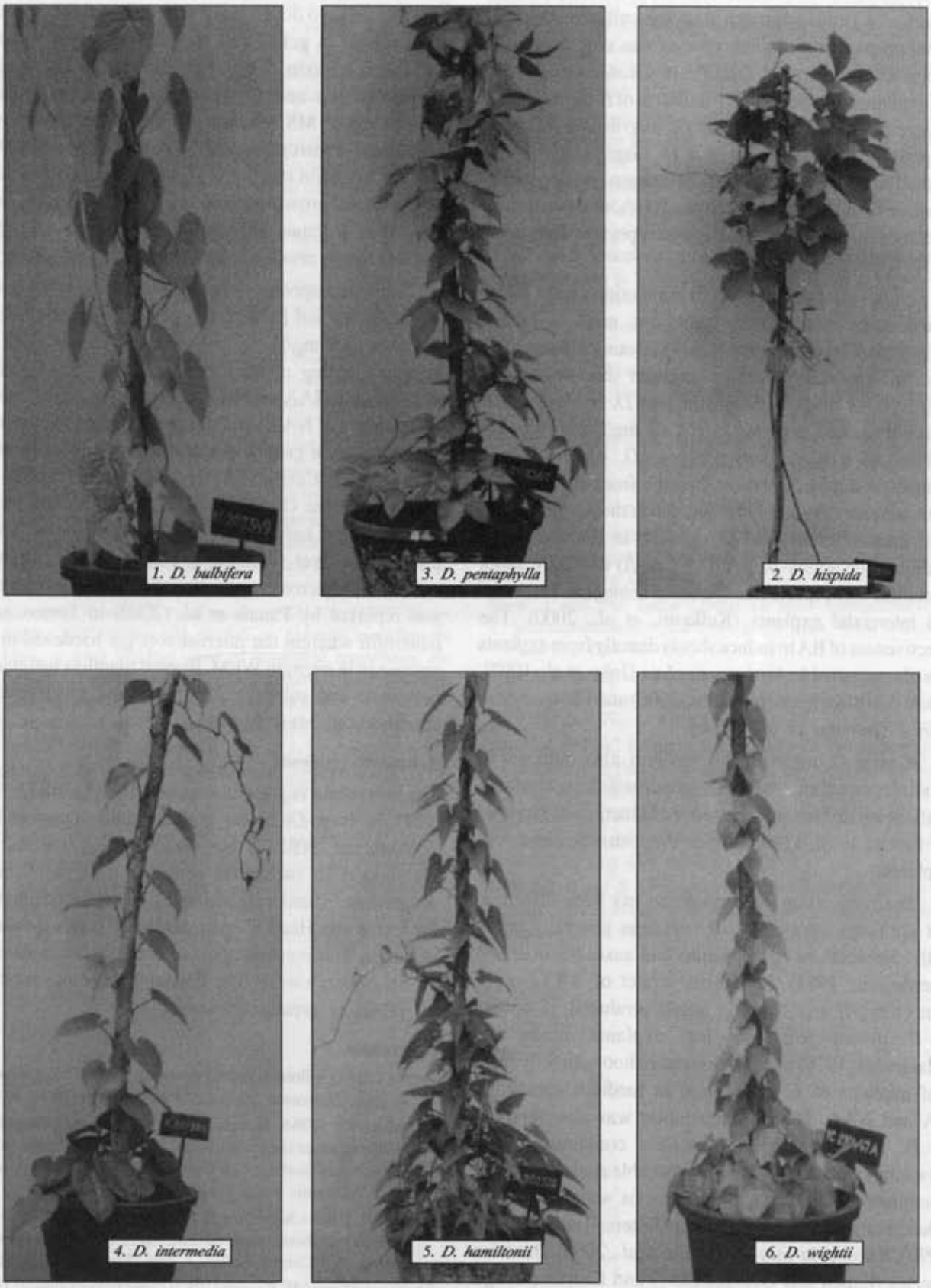

1. D. bulbifera
3. D. pentaphylla
2. D. hispida
4. D. intermedia
5. D. hamiltonii
6. D. wightii

Plate 3

organs as a better approach than the callus method for clonal propagation of plant species was emphasized by Bhojwani and Razdan (1983). In *Dioscorea* species, leaf explants responded well in cultures of *D. pentaphylla, D. hamiltonii, D. wightii* and *D. intermedia* followed by petiole in *D. bulbifera* and *D. hispida*. The stem, root and bulbil explants did not give *de novo* organogenesis. Superiority of leaf explants for greater shoot regeneration potential is in accordance with earlier reports by Kohmura, *et al.* (1995) in *D. opposita*.

Cytokinins are effective in promoting direct shoot initiation. Of the various cytokinins used to induce adventitious bud sprouting from various explants, BA was effective in producing maximum shoots from the leaf explants of *D. pentaphylla* and *D. wightii*. In *D. pentaphylla*, leaf explants in BA (2 mg/l) developed 3 bulbils and 8 shoot buds while in *D. wightii*, BA at 4 mg/l produced 3 shoots directly from the explant. Kohmura *et al.* (1995) could induce direct shoot regeneration from immature leaves of *D. opposita* in BA containing medium. The ability of BA (0.5-5 mg/l) to induce shoot formation was reported in *Withania somnifera* from leaf and internodal explants (Kulkarni, *et al.*, 2000). The effectiveness of BA to induce shoots directly from explants was also reported in *Naragamia alata* (John *et al.*, 1997), *Vanda coerulea* (Seeni and Latha, 2000) and *Clerodendron inerme* (Baburaj *et al.*, 2000).

Kinetin (2 mg/l) in the medium also induced 16 shoots from leaf explants of *D. hamiltonii*. Similar pattern of shoot bud initiation in presence of kinetin was reported by Pereira *et al.* (1995) from *Maytenus ilicifolia* root explants.

The application of a cytokinin has been effective, but optimum rates of shoot initiation generally occur with combinations of cytokinins and auxin (George and Sherrington, 1984). Synergistic effect of BA (3 mgl), Kin (1 mg/l) and NAA (1 mg/l) produced 12 shoots in *D. pentaphylla* from leaf explants. Sinha and Chaturvedi (1979) could also induce shoots directly from leaf explants of *D. floribunda* in medium containing BA and NAA. Direct regeneration was also reported in *D. rotundata* in MS medium containing NAA (Nwachukwu, *et al.*, 1996). A favourable auxin-cytokinin combination for direct organogenesis was reported in other plants like *Camelina sativa* (Tattersall and Milliam, 1999), *Kaemferia galanga* (Shirin *et al.*, 2000), *Brassica* species (Eapen and George, 1997) and *Curcuma longa* (Salvi *et al.*, 2000).

The *de novo* developed microshoots of the 5 species were rooted in gelled full strength basal MS medium or with the auxin NAA. Microshoots of the species *D. pentaphylla* and *D. intermedia* developed healthy roots in basal MS medium itself without any growth regulators. In *Jatropha curcas*, Sujatha and Mukta (1996) could also obtain rooting in regenerated shoots in basal MS without growth regulators. Similar results were noticed in *Solanum viarum* (Chand and Chand, 1995) and *Maranta arundinacea* (Manjula *et al.*, 1999).

The other species such as *D. bulbifera, D. hispida, D. hamiltonii* and *D. wightii* produced roots in presence of NAA (0.5 mg/l). Of the different auxins used for inducing rooting of micro shoots, NAA was found to be superior to IAA and IBA in producing healthy roots. The efficacy of NAA in inducing roots from microshoots was reported in genera like *Manihot esculenta* (Mussio *et al.*, 1998), *Curcuma longa* (Salvi *et al.*, 2000) and *Vanda coerulea* (Seeni and Latha, 2000). The rooted plantlets were hardened in liquid MS medium having 2% sucrose over filter paper bridges. Such results of reduction in sucrose concentration enhancing hardening was reported by Panaia *et al.* (2000) in *Symonanthus bancroftii* wherein the microshoots got hardened in 2% sucrose in ½ strength WPM. Rooted plantlets maintained in soilrite and subsequently transferred to greenhouse conditions showed 85-94% survival.

Acknowledgements

The first author is grateful to the Director Dr BS Dhillon, NBPGR, New Delhi for granting study leave and Dr Z. Abraham, NBPGR Regional Station, Thrissur for his support in successful completion of the research programme. Thanks are also due to Dr N Omanakumari, Professor and Head, Department of Botany, University of Kerala, Thiruvananthapuram for the facilities provided for the research work. The financial assistance provided by ICAR is greatly acknowledged.

References

Acedo VZ, AQ Villordon and ES Quevedo (1994) Callus induction in yam (*Dioscorea alata* L.) *J Root Crops* **20(1)**: 64-66.

Ammirato PV (1984) Induction, maintenance and manipulation of development in embryonic cell suspension cultures. In: *Cell Culture and Somatic Cell Genetics of Plants* Vol.1. Vasil IK (ed.), Academic Press, New York. 139-151.

Baburaj S, P Ravichandran and M Selvapandian (2000) *In vitro* adventitious shoot formation from leaf cultures of *Clerodendron inerme* (L.) Gaertn. *Indian J. Exp. Biol.* **38**: 1274-1276.

Bhojwani SS and MK Razdan (1983) *Plant Tissue Culture: Theory and Practice*. First Edition. Elsevier Sci. Publ. Amsterdam.

Chand PK and S Chand (1995) High frequency plant regeneration from *Solanum viarum* protoplasts. *J. Herbs Spices Medic. Plants* **3(4):** 21-34.

Coursey DG (1967) *Yams An Account of the Nature, Origins, Cultivation and Utilization of the Useful Members of the Dioscoreaceae*. Longmans, Green & Co. Ltd., London.

Eapen S and L George (1997) Plant regeneration from peduncle segments of oil seed *Brassica* species: Influence of silver nitrate and silver thiosulfate. *Plant Cell Tiss. Org. Cult.* **51:** 229-232.

Epstein E (1972) *Mineral Nutrition of Plants. Principles and Perspectives*. John Wiley, New York 29.

George EF and PD Sherrington (1984) *Plant Propagation by Tissue Culture. Handbook and Directory of Commercial Laboratories*. Exegetics Ltd., Eversely, UK.

John S, EV Soniya, K Valsala and GM Nair (1997) *In vitro* adventitious shoot formation from leaves and leaf derived calli of *Naragamia alata* W & A. *Indian. J. Exp. Biol.* **35(11):** 1249-1251.

Kohmura H, H Araki and M Imoto (1995) Micropropagation of 'yamatoimo' Chinese yam (*Dioscorea opposita*) from immature leaves. *Plant Cell Tiss. Org. Cult.* **40(3):** 271-276.

Kulkarni AA, SR Thengane and KV Krishnamurthy (2000) Direct shoot regeneration from node, internode, hypocotyls and embryo explants of *Withania somnifera*. *Plant Cell Tiss. Org. Cult.* **62:** 203-209.

Manjula S, PS Kavitha, B RaniDaniel and GM Nair (1999) Tissue culture and biochemical studies in *Maranta arundinacea* Linn., a tuber yielding plant of medicinal importance. In: *Tropical Tuber Crops in Food Security and Nutrition*. Balagopalan C, Nayar TVR, Sundaresan S, Premkumar T and Lakshmi KR (eds.), Oxford Publishing Co., New Delhi. 256-264.

Matsubara S, Y Chmori, T Komasadomi and H Takada (1992) Multiplication of Chineseyam 'Ichouimo' (*Dioscorea batatus* Decne.) by multiple buds culture. *Scientific Reports of the Faculty of Agriculture*. Okayama University **79:** 37-44.

Murashige T and F Skoog (1962) A revised medium for rapid growth and bioasssays with tobacco tissue culture. *Physiologia Plantarum*. **15:** 473-497.

Mussio I, MH Chaput, I Serraf, G Ducreux and D Sihachakr (1998) Adventitious shoot regeneration from leaf explants of an African clone of cassava (*Manihot esculenta* Crantz) and analysis of the conformity of regenerated plants. *Plant Cell Tiss. Org. Cult.* **53(3):** 205-211.

Nair NG, M Unnikrishnan and A Mukherjee (1994) Use of *in vitro* culture in the improvement of tuber crops. In: *Advances in Horticulture, Tuber Crops*. Vol.8. Chadha, KL and Nayar, GG (eds.), Malhotra Publishing House, New Delhi, India. p. 211-232.

Nwachukwu EC, A Sonnino and ENA Mbanaso (1996) Influence of NAA concentration and of explant source on plantlet regeneration in white guinea yam *Dioscorea rotundata* Poir. *Journal of Genetics and Breeding* **50(2):** 181-183.

Panaia M, T Senaratna T, E Bunn, KW Dixon and K Sivasithamparam (2000) Micropropagation of the critically endangered Western Australian species, *Symonanthus bancroftii* (F Muell.) L Haegi (Solanaceae). *Plant Cell Tiss. Org. Cult.* **63:** 23-29.

Pereira AMS, JR Moro, RHM Cerdeira and SC Franca (1995) Effect of phytoregulators and physiological characteristics of the explant on micropropagation of *Maytenus ilicifolia*. *Plant Cell Tiss Org Cult* **42:** 295-297.

Salvi ND, L George and S Eapen (2000) Direct regeneration of shoots from immature inflorescence cultures of turmeric. *Plant Cell Tiss Org Cult.* **62:** 235-238.

Seeni S and PG Latha (2000) *In vitro* multiplication and ecorehabilitation of the endangered Blue Vanda. *Plant Cell Tiss Org Cult* **61:** 1-8.

Shirin F, S Kumar, and Y Mishra (2000) *In vitro* plantlet production system for *Kaempferia galanga*, a rare Indian medicinal herb. *Plant Cell Tiss Org Cult* **63:** 193-197.

Sinha M and HC Chaturvedi (1979) Rapid clonal propagation of *Dioscorea floribunda* by *in vitro* culture of excised leaves. *Curr Sci* **48(4):** 176-178.

Sujatha M and N Muktha (1996). Morphogenesis and plant regeneration from tissue cultures of *Jatropha curcas*. *Plant Cell Tiss Org Cult* **44:** 135-141.

Tattersall A and S Milliam (1999) Establishment and *in vitro* regeneration studies of the potential oil crop species *Camelina sativa*. *Plant Cell Tiss Org Cult.* **55:** 147-149.

SHORT COMMUNICATION

Collection and Conservation of Some Gourd Landraces of Tribal Areas of Rajasthan

DK Samadia
Central Institute for Arid Horticulture, Bikaner-334 006 (Rajasthan)

Key words: Cucurbitaceous gourds, Exploration, Landraces, Tribal and Arid Region

The farmers in the northwestern parts of India, particularly in the arid region of western Rajasthan, grow some semi-domesticated forms belonging to *Citrullus* and *Cucumis* groups. The *Arawalli* hill ranges separate this region from the eastern semi arid and sub-humid areas of Rajasthan, Gujarat and Central India, where *Cucumis*, *Luffa*, *Lagenaria*, *Momordica* and *Coccinia* are widely adapted and enormous diversity is available (Umesh Chandra, 1995; Pareek *et al.*, 1999). The native genetic resources of these species which possesses genes for adaptation, quality, yield, abiotic and biotic stresses, is under severe threat of erosion due to manifold reasons of socio-economic nature. Realizing this, an exploration was undertaken for survey, collection and conservation of genetic diversity of some important gourds.

This mission-oriented work was conducted during 2002 to 2004 under National Agricultural Technology Project on Sustainable Management of Plant Biodiversity. For the survey and collection of gourd germplasm from tribal areas, an intensive exploration was made in November 2002. A total of 55 accessions in the form of landraces and local cultivars comprising of bottlegourd (18), ridged gourd (19), sponge gourd (15) and bitter gourd (3) were collected. The collections were made from 85 diverse sites in Rajasthan and Gujarat, lying between 22° and 29° N latitude and 72° and 76° E longitude. Biased, random and bulk sampling procedures were followed for collecting fruits of gourds (2 to 15) for formulation of accessions in the targeted crops.

During the exploration, in depth discussions were held with the growers and tribal people to collect passport information on the germplasm sites, methods of crop production, plant growth and fruit yielding characters, uses and seed conservation, etc. and the data were recorded. The collected accessions were evaluated crop wise under RBD with three replications during kharif season of 2003-04 at CIAH, Bikaner. Seed enhancement of all the accessions was done and deposited for the long-term conservation in National Gene Bank at NBPGR, New Delhi.

As the Indian subcontinent is primary and secondary centre of regional diversity for large number of cucurbitaceous crops, the arid and semi arid regions of Rajasthan and areas of adjoining states also possess rich genetic diversity in melons, gourds and cucumber. Gourds include *Benincasa hispida* (Thunb) Cogn., ashgourd; *Lagenaria siceraria* (Molina) Standl, calabash or bottle gourd; *Coccinia grandis* (L.) Voigt, Ivy or scarlet gourd; *Momordica charantia* (L.), bittergourd; *Momordica dioica*, spine gourd; *Luffa acutangula*, ridge gourd and *Luffa cylindrica*, sponge gourd. Among these, bottle gourd, ridge gourd, sponge gourd, bitter gourd, spine gourd and ivy gourd are adapted and grow well in the arid and semi-arid areas, areas near to the foothills of *Arawalli* and in tribal dominated parts of Rajasthan, and also in the adjoining areas of northern Gujarat and western Madhya Pradesh.

Farmer's fields and homestead gardens (*Bari*) were surveyed in the majority of growing areas and hot spots of variability pockets where cucurbitaceous vegetables particularly gourds have been grown over the period. In non-traditional areas, these crops are grown for domestic purposes. Therefore, farmer's fields where assured irrigation facilities for commercial vegetable crops were surveyed. Samples were collected directly from the available gourd plants or seeds as stored to raise future crops. During the surveys it was observed that the rate of adoption of high yielding varieties was high particularly in bottle gourd and bitter gourd, under remunerative vegetable farming systems. However, some traditional vegetable growers were maintaining the local cultivars as an open pollinated mixed seeds of desired population. In tribal dominating areas, gourds were in cultivation as a need based crops. Here enormous

variability existed owing to preservation of landraces or primitive selections for own requirements and also socio-economic needs and farming systems. Both biased and random population sampling strategies was followed to collect the maximum genetic variability from the tribal houses and villages.

In general, the rainy season gourd crops were ready to harvest as tender fruits in September whereas the mature fruits were available from October–December. In Rajasthan, the northwestern arid areas of Bikaner, Pali and Nagour, central semi-arid areas of Ajmer and Bhilwara and sub-humid to humid areas of Chittorgarh, Udaipur, Rajsamand, Banswara, Dungarpur and Sirohi and Dahod and Panchmahal areas of northeastern Gujarat were surveyed. In these areas, agro-climatic conditions, rainfall, farming systems and socio-economic needs predominantly supports the types of crop cultivation. Gourd cultivation was more concentrated in semi-arid to humid parts of central and south-east-western Rajasthan and northern Gujarat. The tribal dominating areas of Ajmer, Bhilwara, Chittorgarh, Nimbherha, Pratapgarh, Ghatol, Banswara, Kushalgarh, Sagwara, Dungarpur, Salumber, Jaisamand, Udaipur, Rajsamand, Pindwara and Sirohi in Rajasthan and Jalod, Piplod, Dahod, Baria, Godhara Lunawara and Modasa in Gujarat have rich genetic diversity. In this area, the average rainfall is from 500-750 mm but the distribution is variable and uncertain. The crop productivity is low. Most of the fields were with undulating topography and hilly, or few plain. In tribal villages, peasant farmers used to grow number of vegetable crops for their domestic consumption and also to fulfills some family income by selling them in to local markets (weekly *hatt*). Among cucurbits, bottle gourd, sponge gourd, ridged gourd, bitter gourd, cucumber, snapmelon and pumpkin were major and ivygourd, spinegourd and *kachri* were minor rainy season crops either in fields as mixed crops or in vegetable *bari* or trailed on trees, shrubs, live hedges, fenced material or on the roof of hut.

A rich genetic diversity of bottlegourd was observed in tribal dominating parts of Rajasthan and Gujarat. The maximum variability exhibiting areas were in the districts of Chittorgarh, Banswara, Dungarpur, Udaipur, Dahod and Panchmahal. A total of 18 population samples were made which includes landraces, primitive selections and local cultivars. A wide range of variation was recorded for plant growth and fruit shape, size, colour and tenderness. Variation in mature fruit and seed characters was also recorded (Table 1). Farmers of tribal and *mali* community were very conscious for the preservation of desirable types of landraces by timely seed storage, regeneration and continuity in production. The accession DKS/AHLS 23 which produced only bitter fruits, was being maintained by a tribal family for over more than 70 years (to measure and serve the *Tadi* liquor). On evaluation, AHLS 23, AHLS 24, AHLS 27 and AHLS 28 were found to be potential germplasm material for multiple characters.

During the surveys, it was noticed that the tribal dominating adjoining areas of south Rajasthan, north Gujarat and western Madhya Pradesh are important regions for *Luffa* gourds where wide range of variability existing in the form of wild species, primitive landraces and domesticated local cultivars. In these areas, several

Table 1. Characters observed in the landraces of gourds from tribal areas

CROP/CHARACTERS	Range value
Bottlegourd [*Lagenaria siceraria* (Molina) Standely]	
Fruit shape	Long, round, oblong, pyrifom, club shaped
Fruit colour	Light green, green, dark green, mottled green
Seed colour	White brown, brown, dark brown
Mature fruit length	16 – 85 cm
Seed length	1.15 – 1.92 cm
Seed width	0.445 – 0.815 cm
Test weight (100 seeds)	11.54 – 22.85 g
Number of seeds per fruit	165 – 683
Spongegourd [*Luffa cylindrica* Roem]	
Fruit shape	Straight long, necked long, elliptical, oblong
Fruit colour	Dark green, light green, whitish green
Seed colour	Black, white/dull or glossy
Mature fruit length	10.5 – 39.8 cm
Seed length	0.85 – 1.25 cm
Seed width	0.551 – 0.732 cm
Test weight (100 seeds)	7.754 – 12.124 g
Number of seeds per fruit	65 – 523
Ridged gourd [*Luffa acutangula* and *L. hermaphrodita*]	
Fruit shape	Long cylindrical, spindle, elliptical, club
Fruit colour	Light green, green, dark green
Seed colour	Black, brown black, dark black/glossy or dull
Mature fruit length	6.0 – 95 cm
Seed length	0.75 – 1.25 cm
Seed width	0.41 – 0.85 cm
Test weight (100 seeds)	7.412 – 16.624 g
Number of seeds per fruit	29 – 299
Bitter gourd [*Momordica charantia* L.]	
Fruit shape	Spindle, elliptical, long
Fruit colour	Dark green, green, whitish green,
Mature fruit length	11.45 – 28.54 cm
Seed length	1.02 – 1.35 cm
Seed width	0.51 – 0.92 cm
Test weight (100 seeds)	8.542 – 20.812 g
Number of seeds per fruit	8 – 42

landraces and natural selections were in cultivation and preserved by the tribal families. The maximum variability exhibiting areas were in the districts of Ajmer, Bhilwara, Chittorgarh, Banswara, Dungarpur, Udaipur, Dahod and Panchmahal. In ridge gourd (*kali tori, aara tori*) the tender fruits were of 9 to 90 cm in length. The wild forms were extremely bitter but the domesticated types were less or rarely bitter. The hermaphrodite type "*Satputia*" bears perfect flowers in clusters. The fruits were small in size (5-7 cm) and in clusters (4-7). Tender fruits of spongegourd (smooth gourd, *chikni tori, ghiya tori, gulki*) were much variable in sizes. In *Luffa* gourds, maximum variability was recorded for fruit characters in respect of size, shape, and tenderness and seed characters (Table 1). Nineteen population samples of ridged gourd and 15 of sponge gourd were collected. On evaluation, a wide spectrum of variation were observed and recorded for plant phenological characters, flowering and fruiting behaviour, fruit characters and biotic and abiotic stresses. The genotypes AHRG 1, AHRG 4, AHRG 8 and AHRG 15 in ridgegourd and AHSG 4, AHSG 5 and AHSG 13 of sponge gourd were found to be particularly under arid conditions.

In tribal dominated areas of South Rajasthan and north Gujarat, *M. dioica* (spine gourd, *kakoda*) occurs in semi wild form. It is perennial and dioecious. *M. charantia* (bittergourd, *karela)* is annual and monoecious Tender fruits of both the species have been used as curries and pickled. In bittergourd, the availability of local cultivars and landraces was very low where as a high range in adoption of cultivars was observed. Four bittergourd land races were evaluated for growth, flowering, fruiting, maturity, fruit yield and quality and seed and reaction to biotic and abiotic stresses under hot arid environment.

References

Pareek OP, BB Vashishtha and DK Samadia (1998) Genetic diversity in drought hardy cucurbits from hot arid zone of India. *IPGRI APO Regional Newsletter for Asia, the Pacific and Oceania*. **28:** 22-23.

Umesh Chandra (1995) Diversity in cucumber and melons from Rajasthan. *Indian J Pl Genet Resour* **8(1):** 11-15.

SHORT COMMUNICATION

Isoenzyme Polymorphism in *Citrus* spp. and *Poncirus trifoliata* (L.) Raf.

T Dhurjati*, GM Poornima and Awtar Singh
National Research Centre for Citrus, Nagpur 440 010 (Maharashtra)

Key words: Isozymes, Genetic relationships, *Citrus* Species

The genus *Citrus*, belonging to the family Rutaceae, subfamily Aurantioideae, tribe Citreae and subtribe Citrinae having its origin in North-eastern India and Southeast Asia is one of the most widely produced fruit species in the world. Several species used as scion cultivars, such as sweet oranges, mandarins, lemons and grapefruits are cultivated commercially. Many other *Citrus* species and hybrids with related genera are used as rootstocks on which the commercially important scion is grafted. Basically the "true *Citrus*" group of fruit trees consists of six closely related genera namely *Citrus, Fortunella, Poncirus, Microcitrus, Eremocitrus* and *Clymenia,* which are highly inter-fertile, with the possible exception of *Clymenia.*

The taxonomic relationships among *Citrus* species have been a source of debate for a long time with respect to the species status and relationships. The well-known taxonomies, of Swingle (1943) and Tanaka (1969) differ widely in the number of species, the former recognizing 16 and the latter 159 in the citrus group. Another classification by Barrett and Rhodes (1976) recognized three basic species for subgenus *Citrus,* namely pummelo (*Citrus grandis* (L.) Osbeck), citron (*Citrus medica* L.) and mandarin (*Citrus reticulata* Blanco) (Torres *et al.*, 1978). *Citrus* species have been identified for taxonomy and systematic purposes using both morphological and non-morphological descriptors (biochemical and molecular markers). Recently a more comprehensive study of the genetic diversity of orange subfamily Aurantioideae using a diverse set of descriptors including molecular markers revealed the existence of two basic affinity groups namely the Orange-mandarin group and Lime-lemon-citron-pummelo group (Herrero *et al.*, 1996).

Biochemical marker studies involving isozyme polymorphism have been very useful in cultivar identification (Barret and Rhodes, 1976), classification of *Citrus* species (Herrero *et al.*, 1996), differentiation of nucellar and zygotic seedlings (Torres *et al.*, 1982) and genetic mapping (Jarrell *et al.*, 1992). Isoenzymatic polymorphism is expected in citrus due to the fact that most of the present day cultivars arose from natural hybridization. The present study was undertaken as a precursor to the ongoing molecular marker based analysis of citrus genetic diversity to specifically gain a preliminary insight into the allelic diversity of four isozyme systems in nine modal citrus species as defined by Torres *et al.* (1978). Therefore, the aims of this current survey were: 1) to conduct a preliminary investigation of levels of genetic diversity within and between species and to assess the suitability of the technique for further studies within the genus using four isozyme systems, and 2) to use the data to construct a dendrogram describing similarities between taxa and to compare the results with the accepted taxonomy for the genus *Citrus*. Owing to limited intraspecific sampling and the low number of isozyme loci used, values for genotype and allele frequencies and observed heterozygosity need to be treated with caution. Further sampling and analysis is required, before accurate estimates of these indicators of genetic diversity are obtained.

Leaf samples for this study were sampled from the National Citrus Germplasm Repository of National Research Centre for Citrus, Nagpur (Table 1). Young leaves (minimum of 5 samples) from nine different citrus species [*Citrus aurantifolia* (Christm) Swingle, *C. aurantium* (L); *C. grandis,* (L) Osbeck; *C. jambhiri* (Lush); *C. medica,* L; *C. paradisi,* Macf; *C. reticulata* Blanco; *C. sinensis* (L) Osbeck; *C. limon* (L) Burm. f] and one citrus relative [*Poncirus trifoliata* (L).Raf] were collected in polyethylene bags and subjected to a survey of isozyme variation. In case of mandarin, rough lemon and trifoliate orange, 16, 24 and 15 cultivars, respectively, were assayed (Table 1). Fresh leaf tissue from each sample was extracted by grinding in cold (4°C) 0.1 M Tris buffer containing 10mM KCl, 0.10 mM $MgCl_2$, 1mM EDTA, 14 mM beta-mercaptoethanol, 0.10 M ascorbic acid and 0.20 g/ml PVP for AAT, PGM

Corresponding author E-mail: tarakdhurjati@yahoo.com

Table 1. Citrus species and cultivars

Species	Cultivar/Local name/ Cultivar name/No. of samples
Citrus aurantifolia (Christm.) Swingle	Acid lime (Kagzi lime)
Citrus aurantium L.	Sour Orange (Tirupati)
Citrus grandis (L.) Osbeck	Pummelo (Local)
Citrus jambheri Lush	Rough lemon (Jamberi)
	(14-9-13, Limonaria, Assam, Sohsarkar, Mithitulia, Telankhedi, Sohmyndong, 58-8-III 4,8780, katajamir, Sohjhalia, S. Africa, Jullandahari khatti, Chethali, Tharsa, MP, Jattikhatti, Citrunelle, Tirupati, Rahuri, Chase, Florida, Local, Schaub
Citrus medica L.	Citron (Etrog Citron)
Citrus paradisi Macf.	Grapefruit (Flame, Ray Ruby)
Citrus reticulata Blanco	Mandarins (Corsica no. 2(21), Page Mandarin, Citrus Clementine, Caffin Clementine, Corsica No.1, Clementine Montreal, Dhakula Local, Corsica No. 1 (4CN11), Marisol, Nagpur Seedless, Nagpur Mandarin, Mudkhed Seedless, Yonezawa, Frost Owari, Dobashibeni, Sunchusha)
Citrus sinensis (L.) Osbeck	Sweet Orange (Mosambi, Washington Navel, Shamouti)
Citrus limon (L.) Burm.f.	Lemon (NRCC repository)
Poncirus trifoliata (L.) Raf.	Trifoliate Orange (Yamaguchi Roubidoux, Argentina, Williams, Florida, Srirampur, Gotharoad, Large-flowered, USA, English Large, Flying Dragon, Rich 16-6, Local, Gonicoppal, Chethali).

and PGI and 0.1M cold (4°C) potassium phosphate buffer, pH7.2 for the isozyme Peroxidase. The ground tissue was centrifuged at 27000Xg for 20 min. (2 to 4°C). The samples were assayed for four isozyme systems namely Aspartate amino transferase (EC2.6.1.1; AAT), Phospho gluco isomerase (EC5.3.1.9; PGI), Phospho gluco mutase (EC2.7.5.1; PGM) and Peroxidase (EC 1.11.1.7; PRX) which were chosen based on their robustness and stability.

Polyacrylamide gel electrophoresis was performed in a vertical slab gel apparatus. The gel slab consisted of a stacking portion of 5% acrylamide in 1M, tris-HCl, pH 6.8 and a resolving part of 12% acrylamide in 1.5M, tris-HCl, pH 8.8. The electrode buffer was 25mM Tris, 250mM glycine pH 8.3 for all the isozymes studied. Electrophoresis was carried out at 4°C for 3-4 hours. Gels were stained according to Shields *et al.* (1983). Allele scoring and notation was according to Torres *et al.* 1978. Allele designation by alphabet letters in increasing order of speed of migration is as follows, S specifying a slowly migrating enzyme or subunit, M for medium, I for intermediate; F for fast and T for faster. Alleles were scored by numbering from '1' to 'n' from the fastest to slowest to migrate from the origin. To exemplify a specific allele (FS) with fast and slow migrating bands, three bands would be considered as a heterozygote and a single band (FF/SS) as a homozygote for dimeric enzymes and two bands (FS) would be considered as a heterozygote and a single band (FF/SS) is considered a homozygote for monomeric enzyme. Allele frequencies for seven isozyme loci were calculated and analyzed to develop a matrix of genetic distances calculated as per the Nei's (1972) genetic distance measure, to describe the variation between different citrus species.

The standard Nei's genetic distance is $D_{xy} = -\ln (I_{xy})$, where I_{xy} (Genetic Identity) is the average interpopulation heterozygosity (J_{xy}) divided by the square root of the product of J_x and J_y, where J_x & J_y are average homozygosity values of population x and population y, respectively. The values of D vary from zero (identical allele frequencies) to infinity (do not share alleles). Genetic distances were calculated based on allele frequencies, according to Nei (1972), and then used to generate a UPGMA dendrogram with the software package TFPGA (Miller Mark, 1997).

The results showed distinct isozymic polymorphism between different citrus species. All the cultivars within a species showed monomorphic isozyme profiles with similar alleles in all the four isozyme systems used in the study. The number of alleles and loci varied according to the isozyme system used. Two loci each were scored for AAT (Aat-1 and 2), PGM (Pgm-1 and Pgm-2), PGI (Pgi-1and 2) and one locus was scored for PRX (Prx-1) profile. PGI and AAT isozymes having a dimeric quartenary structure gave three bands in a heterozygote, while PRX and PGM which are monomers, resolved two bands in a heterozygote. The number of alleles varied with a minimum of two (F or T and S) for Pgm-1and Prx locus to a maximum of five alleles (F or T, S, M and I) in Pgi-1 locus (Fig 1).

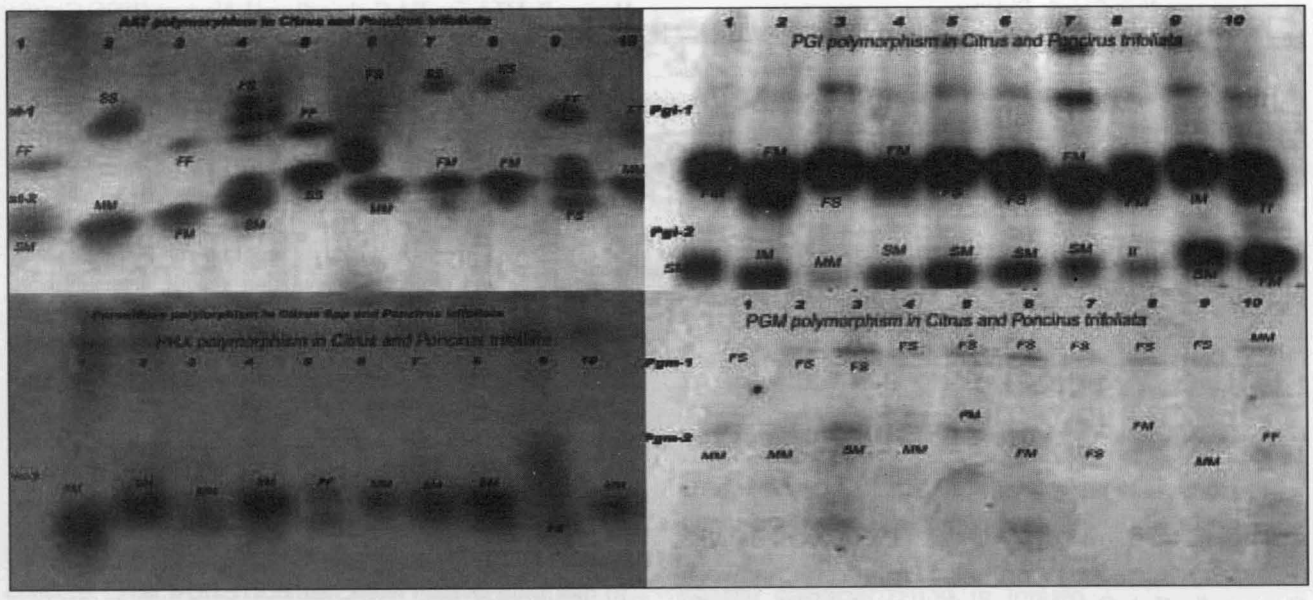


Fig 1. Representative Zymograms (Clockwise, AAT, PGI, PGM and PRX) of different Citrus species and Poncirus trifoliata Lanes 1-10: 1) Acid lime, 2) Sour orange, 3) Pummelo, 4) Rough lemon, 5) Citron, 6) Grapefruit, 7) Nagpur mandarin, 8) Sweet orange, 9) Lemon and 10) Trifoliate orange

A total of seven polymorphic loci were resolved and 24 alleles were scored with an average of 3.4 alleles per locus. All the samples analyzed within the species showed similar banding patterns. The average expected heterozygosity of or Nei's genetic diversity of 0.59 was obtained between species considered. The results of Nei's original measures of genetic identities/distances revealed highest genetic identity (GI) of 0.8839 between rough lemon and acid lime and the least GI of 0.15 between lemon and trifoliate orange (Table 2). The genetic relationships between different *Citrus* species were expressed based on UPGMA (Unweighted pair group method using arithmetic averages) cluster constructed from the genetic distance matrix with resampling of 1000 replicates bootstrapping for validation.

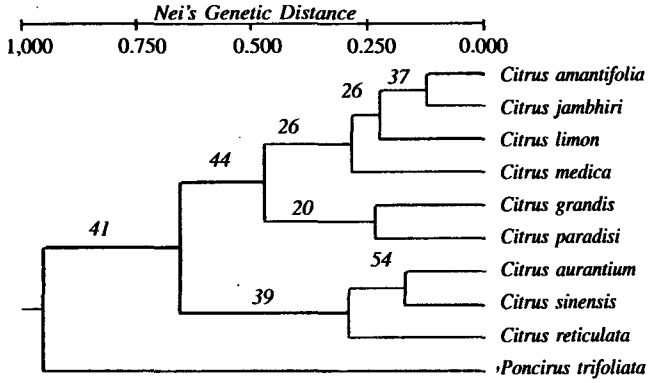
Mandarin clustered with sweet orange and sour orange, which belong to the mandarin-orange group, while pummelo clustered with grapefruit (Fig. 2). This conforms with the fact that grapefruit has originated in the new world as a natural hybrid of pummelo with sweet orange. Further, it is known that limes have evolved from citrons and the clustering of limes, lemons in the citron affinity group confirms the results according to the established citrus taxonomy (Swingle, 1943; Tanaka, 1967; Herrero *et al.*, 1996) although rough lemon and lemon are known to have a more complicated origin.

Table 2. Distance matrix based on Nei's (1972) distance measure

Pop ID	1	2	3	4	5	6	7	8	9	10
1	****	0.63	0.7	0.88	0.79	0.72	0.47	0.44	0.83	0.40
2	0.45	****	0.55	0.83	0.30	0.73	0.72	0.84	0.47	0.38
3	0.30	0.59	****	0.67	0.55	0.79	0.55	0.42	0.57	0.52
4	0.12	0.17	0.39	****	0.61	0.76	0.68	0.64	0.76	0.37
5	0.23	1.20	0.59	0.48	****	0.52	0.33	0.26	0.73	0.28
6	0.32	0.30	0.23	0.26	0.64	****	0.70	0.61	0.44	0.65
7	0.75	0.31	0.58	0.37	1.09	0.34	****	0.76	0.41	0.42
8	0.81	0.17	0.86	0.43	1.33	0.49	0.26	****	0.38	0.35
9	0.18	0.74	0.54	0.26	0.30	0.81	0.88	0.94	****	0.15
10	0.91	0.96	0.64	0.98	1.25	0.42	0.85	1.04	1.89	****

Nei's genetic identity (above diagonal) and genetic distance (below diagonal)

1) *Citrus aurantifolia* 2) *Citrus aurantium* 3) *Citrus grandis* 4) *Citrus jambheri* 5) *Citrus medica* 6) *Citrus paradisi* 7) *Citrus reticulata* 8) *Citrus sinensis* 9) *Citrus limon* 10) *Poncirus trifoliata*



Numbers at nodes indicate bootstrap values

Fig 2. UPGMA dendrogram depicting relationships among Citrus spp. and Poncirus trifoliata

According to Barret and Rhodes (1976), sour orange (*C. aurantium*), probably originated from a cross between *C. grandis* (L.) Osbeck and *C. reticulata* Blanco. In conclusion, *Citrus* species clustered largely into two basic affinity groups of lime-lemon-citron-pummelo and orange-mandarin clusters and the isoenzyme phenotypes could differentiate the inter-specific relationships between nine modal citrus species and *Poncirus trifoliata.*

References

Barrett HC and AM Rhodes (1976) A numerical taxonomic study of affinity relationships in cultivated *Citrus* and its close relatives. *Syst Bot* **1:** 105-136.

Herrero R, MJ Asins, EA Carbonell and L Navarro (1996) Genetic diversity in the orange subfamily Aurantioideae, intraspecies andintragenus genetic variability. *Theor Appl Genet* **92:** 599-609.

Jarrell DC, ML Roose, SN Traugh and RS Kupper (1992) A genetic map of *Citrus* based on the segregation of isozymes and RFLPs in an intergeneric cross. *Theor Appl Genet* **84:** 49-56.

Miller Mark P (1997) Tools for population genetic analysis, (TFPGA, 1.3ver): A windows program for the analysis of allozyme and molecular population genetic data. Software distributed by author at www.marksgeneticsoftware.net/tfpga.htm

Nei M (1972) Genetic distances between populations. *American Naturalist* **106:** 283-392

Swingle WT (1943) The botany of *Citrus* and its wild relatives of the orange subfamily (family Rutaceae, subfamily Aurantioideae) *In* HJ Webber and LD Batchelor (Eds.), *The citrus industry*, Vol. I, p.129-474. Univ Calif Press Berkeley.

Tanaka T (1969) Taxonomic problems of citrus fruits in the *Orient Bull* Univ Osaka Prefect, Ser B **21:** 133-138

Torres AM, RK Soost and U Diedenhofen (1978) Leaf isozymes as genetic markers in *Citrus*. *Am J Bot* **65:** 869-881.

Torres AM, RK Soost and TM Lastovicka (1982) *Citrus* isozymes: Genetics and distinguishing nucellar from zygotic seedlings. *Heredity* **73:** 335-339.

Shields, CR, Orton TJ and Stuber CW (1983) An outline of general resource needs and procedures for the electrophoretic separation of active enzymes from plant tissue. *In* Tanksley SD and TJ Orton (Eds.) Isozymes in Plant Genetics and Breeding, Part A Elsevier Science Publishers, Amsterdam.

SHORT COMMUNICATION

Morphological Characterization of Tomato Varieties

Chitra Devi L, Sushil Pandey[1], NC Singhal[1] and AK Singh[2]
Conservation Division, National Bureau of Plant Genetic Resources, New Delhi 110 012
[1]Professor, Division of Seed Science and Technology, IARI, New Delhi 110 012
[2]Assistant Professor, Regional Station, GBPUA&T, Tanakpur (Uttarakhand)

Characterization provides information about genetic diversity between two varieties at morphological as well as molecular level. The varying qualities and characters of different varieties created an interest to identify them. With the proliferation of newly developed varieties in tomato, the task of establishing identity of these varieties and of maintaining the seed purity has become a major concern. The visual identification and separation of varieties on the basis of seed morphology is the simplest and quickest method. However, in crop like tomato, the seed morphological polymorphism is too narrow to classify. Therefore, growing the crop for morphological observations on seedling, plant and fruit characters become obvious. The International Union for the Protection of New Varieties (UPOV) has prepared guidelines for varietal characterization in crops including tomato. Morphological characters such as growth habit (Tewari and Chaudhary, 1990), number of locules (Singh *et al.*, 1974) and fruit shape (Tay and Chen, 1993) in tomato have been used for varietal characterization. The present study was aimed at elucidating information on the extent of use of morphological characters for varietal characterization in tomato.

Twenty-two commercial varieties and three hybrids of tomato (Table 1) were grown in two replications of 25 plants each under field conditions at IARI during 1999 and 2000. Important morphological characters, classified as essential, as per UPOV guidelines for DUS testing in tomato, were selected for characterization and observations were recorded visually at different growth

Table 1. Seed sources of varieties under study for characterization

Variety	Seed Source	Pedigree
Pusa Sheetal	IARI, New Delhi	699 x Balkan
Pusa 120	IARI, New Delhi	Anahu
Pusa Gaurav	IARI, New Delhi	Glamour x Watch
Pusa Early Dwarf	IARI, New Delhi	Improved Meeruti x Red Cloud
Pusa Ruby	IARI, New Delhi	Sioux x Improved Meeruti
Chikoo	IARI, New Delhi	Selection
Junagarh Ruby	IARI, Regional Station, Karnal	Big Silari x Pusa Ruby
Marglobe	IARI, Regional Station, Karnal	EC 54722 (T-2768)
Roma	IARI, Regional Station, Karnal	EC 54851 and directly released as variety IC 76310
Soiux	IARI, Regional Station, Karnal	American introduction/and directly released as variety IC 76313
Best of All	IARI, Regional Station, Karnal	American introduction/and directly released as variety IC 76311
Arka Abha	IIHR, Bangalore	Pure line Selection (VC-8-1-21AVRDC Taiwan)
Arka Meghali	IIHR, Bangalore	Pedigree selection (F_8), from cross Arka Vikas x IIHR-554
Arka Saurabh	IIHR, Bangalore	Selection from Canadian Breeding line V-685
Arka Vikas	IIHR, Bangalore	Selection from American variety Tip Top
PKM-1	TNAU, Coimbatore	An induced mutant from Annaji tomato
CO-3	TNAU, Coimbatore	EMS induced mutant of CO-1
CO-2	TNAU, Coimbatore	Pure line isolated from USSR type
Hisar Arun	HAU, Hisar	PED x K-1
Hisar Lalit	HAU, Hisar	Resistant Bangalore (RB) x HS -101
Pant Bahar	GBPUAT, Pantnager	Selection from germplasm line AC-238
Pant T-3	GBPUAT, Pantnager	Selection from germplasm line AC 292
Pusa Hybrid-1	IARI, New Delhi	Pusa Sheetal x Chikoo
Pusa Hybrid-2	IARI, New Delhi	Pusa – 120 x Pusa Gaurav
Pusa Hybrid-4	IARI, New Delhi	Pusa – 120 x Chikoo

Email: chitra_nbpgr@rediffmail.com

stages. In addition to the UPOV characters, plant growth habit was also included (Tewari and Chaudhary, 1990).

The result on classification of twenty-two varieties and three hybrids based on plant and fruit characters has been presented in Tables 2 and 3. The twenty-five morphological characters recorded at different growth stages revealed that no single character could classify the cultivars individually except the shape of fruit which were typicall in Pusa Gaurav (plum), Chikoo (heart) and Roma (pear). However, it was possible to identify a cultivar using a set of characters in sequence.

The study revealed that there was no variation for the characters like anthocyanin pigmentation on seedling leaf, leaf division, style pubescence, flower colour and epidermis of fruit in all the varieties and hybrids (Table 2 and 3). Hence, such characters could not be relied upon for classifying the tomato varieties. These results are in conformity with the results of Ilame (1994).

In the present investigation, the characters viz., locules per fruit, fruit shape, plant type, stem flexibility and pericarp thickness were reliable to reproduce. Similar findings were also reported by Singh *et al.* (1974), Kaur *et al.* (1976), Ilame (1994) and Tewari (1996) in tomato respectively.

Further, the stem pubescence was observed to be useful in grouping the varieties. This qualitative trait, less affected by environment can form an important component of tomato varietal identification. Thus, from this study it is evident that characterization helps in realizing the genetic potential of the varieties. In addition classification of growth type will help the breeders while formulating the programme for development of hybrids for specific traits like days to flowering, duration of flowering and synchronization of flowering.

Table 2. Characterization of tomato cultivars based on plant characters (90 days after transplanting)

Cultivars	Plant growth type	Stem pubescence	Stem flexibility	Leaf pose	Leaf colour	No. leaves under Ist inflorescence at 70 DAT
Pusa Sheetal	D	W	F	H	Mg	Fe
Pusa 120	Sd	W	F	Se	Dg	Ma
Pusa Gaurav	D	W	If	Se	Mg	Ma
Pusa Early Dwarf	D	W	If	H	Mg	Ma
Pusa Ruby	I	W	F	H	Dg	Ma
Chikoo	D	W	F	H	Lg	Ma
Junagadh Ruby	I	M	F	Se	Dg	Ma
Marglobe	I	W	F	Se	Mg	Ma
Roma	D	W	F	H	Lg	Fe
Soiux	I	W	F	Se	Mg	Ma
Best of All	I	M	F	H	Mg	Fe
Arka Abha	Sd	W	F	H	Mg	Ma
Arka Meghali	Sd	M	F	H	Dg	Ma
Arka Saurabh	Sd	W	F	H	Lg	Ma
Arka Vikas	Sd	W	If	Se	Dg	Ma
PKM-1	D	W	F	H	Mg	Ma
CO-3	Sd	W	If	Se	Mg	Fe
CO-2	I	W	If	Se	Mg	Ma
Hisar Arun	D	W	F	H	Mg	Fe
Hisar Lalit	Sd	W	F	Se	Dg	Ma
Pant Bahar	I	M	F	H	Mg	Ma
Pant T-3	Sd	W	F	H	Mg	Fe
Pusa Hybrid-1	D	W	If	Se	Mg	Fe
Pusa Hybrid-2	Sd	W	If	Se	Dg	Ma
Pusa Hybrid-4	Sd	W	If	Se	Mg	Ma

D=Determinate, Dg=Dark green, F=Flexible, Fe=Few, H=Horizontal, I=Indeterminate, If=Inflexible, Lg=Light green, M=Medium. Ma=Many, Mg=Medium green, Sd=Semi-determinate, Se=Semi-erect, W=Weak

References

Ilme SS (1994) Varietal identification and F_1 seed production techniques in tomato (*Lycopersicon esculentum* Mill). M Sc Thesis, IARI, New Delhi.

Kaur G, Jaiswal SP and Kanwar JS (1976) Variability in certain physico-chemical characters of tomatoes. *Indian Food Pack*, **30:** 5-9.

Singh RR, Mittal RK and Singh HN (1974) Note on variability studies in some intervarietal crosses in tomato. *Prog Hort*, **5:** 55-60.

Tay DCS and Chen MC (1993) Value of colour slides to record variation in vegetable crops. *Seed Sci & Technol* **21:** 605-610.

Table 3. Characterization of tomato cultivars based on fruit characters (135 days after transplanting)

Cultivar	Fruit Size	Fruit shape	Fruit ribbing At calyx	Length of pedicel	Pedicel area pistil scar	Pedicel scar end	Shape of the	Shape of blossom	Transverse section	No. of locules	Pericarp thickness
Pusa Sheetal	M	Sf	Sl	Sh	Dp	M	D	In	An	3	Tn
Pusa 120	L	R	M	Lo	F	L	D	F	Ir	3	Tc
Pusa Gaurav	M	Pl	A	Lo	F	S	D	F	R	1	Tc
Pusa Earky Dwarf	S	R	A	Sh	F	S	D	F	R	2	Tn
Pusa Ruby	M	R	Sl	Sh	Dp	S	D	In	An	4	Tc
Chikoo	M	H	Sl	Lo	F	S	Ste	P	R	1	Tc
Junagadh Ruby	S	Hr	Sl	Sh	F	S	D	F	R	2	Tn
Marglobe	M	R	Sl	Lo	Dp	L	Ste	F	R	4	Tn
Roma	M	Pe	M	Lo	F	M	D	P	R	1	Tc
Soiux	M	R	M	Lo	Dp	M	Ir	In	An	4	Tn
Best of All	M	R	M	Sh	F	S	D	F	R	3	Tc
Arka Abha	M	R	Sl	Sh	Dp	M	Ste	In	R	4	Tn
Arka Meghali	M	R	Sl	Lo	Dp	S	Li	In	Ir	4	Tc
Arka Saurabh	L	R	Sl	Sh	Dp	S	Ir	F	Ir	4	Tc
Arka Vikas	M	Sf	Sl	Sh	Dp	S	Ir	In	An	4	Tc
PKM-1	M	R	Sl	Sh	Dp	S	Li	In	An	3	Tc
CO-3	M	R	M	Lo	Dp	M	D	F	Ir	4	Tc
CO-2	L	R	M	Lo	Dp	L	Li	F	Ir	4	Tn
Hisar Arun	M	Sf	Sl	Lo	Dp	S	D	In	An	3	Tc
Hisar Lalit	M	Sf	M	Sh	Dp	M	Ir	In	An	4	Tc
Pant Bahar	M	Sf	Sl	Sh	Dp	S	Ir	In	An	3	Tc
Pant T-3	M	R	Sl	Sh	Dp	S	Ste	F	R	3	Tc
Pusa Hybrid-1	M	Hr	Sl	Lo	Dp	M	D	F	R	3	Tc
Pusa Hybrid-2	M	Hr	Sl	Lo	F	S	D	F	R	2	Tc
Pusa Hybrid-4	M	Hr	Sl	Lo	F	M	D	F	R	3	Tc

A: Absent, An: Angular, C: Crimson, D: Dot, Dp: Depressed area, F: Flat, H: Heart, Hr: Highly round, In: Indented, Ir: Irregular, L: Large, Li: Linear, Lo: Long, M: Medium depressed, P: Pointed, Pe: Pear, Pl: Plum, R: Round, S: Small, Sf: Slightly flat, Sh: Short, Sl: Slight, Ste: Stellate, Tn: Thin, Tc: Thick, 1: Generally two; occasionally three, 2: Generally two frequently three, 3: Generally 3 or 4, 4: Generally > 4.

Tewari RN (1996) Heterosis breeding for higher productivity and off season production in tomato In: *Vegetable Hybrids and their Seed Production* Training Course by FAO pp. 79.

Tewari RN and Choudhary H (1990) Solanaceous crops. In: *Vegetable Crops in India* (Ed) Bose T K and Som M G Published by Naya Prokash, Calcutta (India).

SHORT COMMUNICATION

Genetic Variability, Correlation and Path Coefficient Analysis for Fruit Yield and its Component Traits in Crambe (*Crambe abyssinica* Hochst. ex RE Fries)

Vandana Joshi, Ranbir Singh, S Mandal and SK Mishra
National Bureau of Plant Genetic Resources, New Delhi 110 012

Key words: ***Crambe abyssinica*, Correlation, Morphotypes, Path analysis, Variability**

Crambe abyssinica Hochst. ex RE Fries belongs to family Cruciferae and is a new industrial oilseed plant species, having oil high in erucic acid content (upto 60%) for industrial purposes (Anthony *et al.*, 1993). Crambe is an erect, herbaceous annual plant with stiff stem, covered with fine short hairs. The main stem branches close to the ground from secondary branches. Leaves are glabrous and basically ovate/lyrate. The inflorescence is a cyme, which with progressive growth become long and indeterminate flowering panicle with racemes of white flowers. Fruit is a capsule (siliqua), initially pale green but turns yellowish on maturity. Each capsule contains a single spherical brown seed. The single seeded fruits are spherical. The pod or hull remains on the seed at harvest and is considered a part of the harvested product (Papathanasiou *et al.*, 1966). Derivatives of erucic acid from seed oil can be used for various chemical applications such as slip agents, plasticizers, lubricants, softeners, anti foamers, fixatives in perfumes etc. (Weiss, 2000). Polymers made from this serve as insulation for high voltage electric lines. It can be used for manufacture of nylons, paint and coating that do not shrink or swell with changes in moisture. Crambe oil due to good stability at high temperature, is also very well suited as lubricant for steel casting.

C. abyssinica is primarily a self pollinated plant but some natural outcrossing has been reported (Beck *et al.*, 1975). Lessman and Meier (1972) reported a lack of adequate genetic variability among initial introductions of crambe for important agronomic traits. Scanty information is available about the existence of genetic variability for fruit yield in *Crambe abyssinica* (Papathanasiou *et al.*, 1966 and Lessman, 1975). But *Crambe abyssinica* germplasm has not been screened in India both for fruit as well as oil yield. The present investigation was undertaken for evaluating some exotic lines with respect to extent of variability and nature of association among oil yield and related characters.

A total of 56 exotic germplasm lines of *Crambe abyssinica* obtained from United States Department of Agriculture (USDA), ARS, Beltsville, Maryland, USA were grown during rabi 2002-03 and 2003-04 at NBPGR, Pusa campus, New Delhi in an augmented block design. Each entry was grown in three rows plot of 3 m length each with row spacing of 45 cm distance and plant spacing of 15 cm. The two checks viz. EC400058 and EC400059 were randomized in each block. The crop was raised adopting standard package and practice under rainfed condition. Data was recorded on five randomly selected plants on various agro-morphological characteristics viz. plant height, number of branches per plant, number of fruits per primary branch, length of primary branch, length of main fruiting branch, number of fruits per main fruiting branch, days to 50% flowering and days to maturity. For determination of total oil content, seeds were dried to 4-5% moisture level in oven at 108°C for 16-18 hrs. The total oil content of the seed samples was determined by a non-destructive method using a Newport NHR analyzer {model-4000} from Oxford Analytical Instruments Ltd UK after calibrating with pure seed oil. Fatty acid analysis was done by Gas Liquid Chromatography (GLC). GLC method developed by Mandal *et al.*, 2002 was followed for establishing erucic acid level of the crambe accessions.

The data after computing for each character was subjected to statistical analysis. Phenotypic coefficient of variation was estimated by the formula suggested by Burton (1952). Phenotypic 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 number of fruits per primary

Table 1. Phenotypic (P) correlation coefficients among eight characters in *Crambe abyssinica*

Characters	Plant height (cm)	Number of primary branches	Days to 50% flowering	Days to mean maturity	Length of primary branch	Number of fruits/ primary branch	Length of main fruiting branch	Number of fruits/main fruiting branch
Plant height (cm)	1.00							
Number of primary branches	0.230							
Days to 50% flowering	-0.367**	0.216						
Days to mean maturity	-0.389**	0.109	0.782**					
Length of primary branch	0.458	-0.025	-0.418**	-0.476**				
Number of fruits/primary branch	0.092	0.287*	0.326*	0.234	-0.003			
Length of main fruiting branch	0.117	-0.398**	-0.499**	-0.316*	0.126	0.052		
Number of fruits/main fruiting branch	0.243	-0.230	-0.324*	-0.183	0.147	0.392*	0.841**	1.00

*: P £ 0.05, **: P £ 0.01

branches were estimated by the method of Dewey and Lu (1959). The data recorded on these checks was averaged individually and then compared with different genotypes. Significant variability was observed in *Crambe abyssinica* germplasm. The variability ranged from 73.00-128.80 cm for plant height, 4.40-52.00 for number of primary branches, 24.00-117.20 cm for length of primary branch, 95.50-568.00 for number of fruits per primary branch, 7.20-44.30 cm for length of main fruiting branch and 8.20-57.20 for number of fruits per main fruiting branch. Seed size varied from 0.8-2.6 mm in diameter and 1000 seed weight varied from 1.83-3.66 g (Mandal *et al.*, 2002). The range of oil content and erucic acid varied from 27.91-44.95 and 45.16-62.20% respectively. The highest phenotypic coefficient of variation was observed for length of main fruiting branch (58.00%) followed by number of fruits per main fruiting branch (45.30%) and number of fruits per primary branches (41.40%). Moderate phenotypic coefficient of variation was observed for number of primary branches (28.90%), length of primary branch (21.10%) and plant height (19.10%). However, days to 50% flowering and days to mean maturity showed low estimates of phenotypic coefficient of variation.

Phenotypic correlation coefficients among eight characters are shown in Table 1. Number of fruits per main fruiting branch showed highly significant and positive association with length of main fruiting branch and number of fruits per primary branch and a negative significant association with days to 50% flowering. Number of fruits per primary branches showed significant and positive association with number of primary branches as well as to days to 50% flowering. Length of main fruiting branch showed significant negative association with number of primary branches, days to 50% flowering and days to mean maturity. Length of primary branch showed highly significant positive association with plant height.

Path coefficient analysis (Table 2) revealed that length of main fruiting branch had the maximum direct effect on number of fruits per main fruiting branch followed by number of fruits per primary branches and plant height. Among these length of main fruiting branch and number of fruits per primary branch had a significant positive correlation with number of fruits per main fruiting branch. No other character had significant direct effect. Number of fruits per primary branch though had a high direct effect as well as significant positive association with number of fruits per main fruiting branch but had maximum indirect effect through length of main fruiting branch. Plant height with a good positive effect had no association with number of fruits per main fruiting branch and showed the maximum positive effect with length of main fruiting branch thus plant height does not fit into a criteria for increasing number of fruits per main fruiting branch in *crambe*.

Length of main fruiting branch might be a good selection criterion for improving the number of fruits per main fruiting branch, since it had highest positive significant association with this characteristic and also showed the high positive direct effect on number of fruits per main fruiting branch. So, selection for length of main fruiting branch might result in significant improvement in number of fruits per main fruiting branch in *Crambe abyssinica*. Number of fruits per primary branches also had highly significant and positive association with number of fruits per main fruiting branch. In the light of the above findings, it may be concluded that improvement in characters like length of main fruiting branch and number of fruits per primary

Table 2. Path coefficient analysis of phenotypic correlation coefficients to determine the direct and indirect effects of different traits on number of fruits per main fruiting branch in *Crambe abyssinica*

Characters	Plant height (cm)	Number of primary branches	Days to 50% flowering	Days to mean maturity	Length of primary branch (cm)	Number of fruits/ primary branch	Length of main fruiting branch (cm)	Correlation coefficient with no. of fruits main fruiting branch @
Plant height (cm)	0.156	-0.004	-0.005	-0.032	0.007	0.023	0.097	0.243
Number of primary branches	0.036	-0.019	0.003	0.009	-0.014	0.073	-0.331	-0.23
Days to 50% flowering	-0.057	-0.004	0.012	0.064	-0.007	0.083	-0.416	-0.324*
Days to mean maturity	-0.061	-0.002	0.010	0.082	-0.008	0.059	-0.264	-0.183
Length of primary branch (cm)	0.072	0.001	-0.005	-0.039	0.016	-0.001	0.105	0.147
Number of fruits/primary branch	0.014	-0.006	0.004	0.019	-0.001	0.254	0.043	0.392*
Length of main fruiting branch	0.018	0.008	-0.006	-0.026	0.002	0.013	0.833	0.841**

@ Correlation coefficient with no. of fruits per main fruiting branch; **significant at 0.01 level; *significant at 0.05 level

branch will help in improving the fruit yield of main fruiting branch in *Crambe*.

References

Al-Jibouri HA, PA Miller and HF Robinson (1958) Genotypic and environmental variances and covariances in an upland cotton cross of inter-specific origin. *Agron J* **50**: 633-636.

Anthony KRM, J Meadley and G Robbelen (1993) *New Crops for temperate regions*. Chapman and Hall, London. 247p.

Beck LC, KJ Lessman and RJ Buker (1975) Inheritance of pubescence and its use in outcrossing measurements between a *Crambe hispanica* type and *C. abyssinica Hochst.* ex. R.E. fries. *Crop Sci* **15**: 221-224.

Burton GW (1952) Quantitative inheritance in grasses. *Proc 6th Int. Grassland Congs.* **1**: 277-283.

Dewey DR and KH, Lu (1959) A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron J* **51**: 515-518.

Lessman KJ and VD Meier (1972) Agronomic evaluation of Crambe as a source of oil. *Crop Sci* **12**: 224-227.

Lessman KJ (1975) Variation in crambe, *Crambe abyssinica* Hochst. *J Amer Oil Chem Soc* **52**: 386-389.

Mandal S, R Singh, S Yadav, G Begum, P Suneja and M Singh (2002). Correlation studies on oil content and fatty acid profile of some Cruciferous species. *Genetic Resources and Crop Evolution* **49**: 551-556.

Meier VD and KJ Lessman (1973 a) Breeding behaviour for crosses of *Crambe abyssinica* and a plant introduction designated for *C. hispanica Crop Sci* **13**: 49-51.

Papathanasiou GA, KJ Lessmen and WE Nyquist (1966) Evaluation of eleven introductions of Crambe, *Crambe abyssinica* Hochst. *Agron J* **58**: 587-589.

Weiss EA (2000) Crambe, niger and jojoba. In: *Oilseed Crops* (eds. EA Weiss) Blackwell Science Ltd. Oxford, London. p 287-326.

SHORT COMMUNICATION

Performance and Genetic Diversity Pattern in the Landraces of *Allium cepa* L.

VSR Krishna Prasad, KE Lawande and V Mahajan
National Research Centre for Onion and Garlic, Rajgurunagar, Pune 410 505 (Maharashtra)

Key words: *Allium cepa* L., Diversity Pattern, Landraces

Performance and diversity pattern are very much important to applied crop breeding, because diversity may reduce vulnerability to pests and at the same time accelerate breeding progress for agronomic trait such as yield. The continuing use of diverse landraces and exotic modern cultivars as parental stock in recent decades has been associated with improved yield and pest resistance in many vegetable crops. A study was undertaken to understand the potentiality of the landraces in terms of yield and the diversity pattern existing in the population. The results of this experiment are presented here.

A total of 114 germplasm accessions collected from various parts of country along with check variety B-780 have been evaluated for their performance and their diversity pattern at Rajgurunagar farm in *kharif* season of the year 2004. All the genotypes were grown in randomized block design with 3 replications in $1m^2$ plots. The data was generated from five competitive plants for various characters *viz.* plant height (PH), no. of leaves (NL), collar thickness (CT), 5 bulb weight (5BW), neck thickness (NT), polar diameter (PD), Equatorial diameter (ED), weight of 'A' grade bulbs (Wt. 'A') weight of 'B'grade bulbs (Wt. 'B') weight of 'C' grade bulbs (Wt. 'C'), total soluble solids (TSS), total yield (TY), marketable yield (MY). Analysis of variance (Table 1) was calculated and non-hierarchical Euclidian Cluster Analysis was performed on the original data of thirteen characters to assess the distinctness of the gene pool through multivariate analysis. The components were utilized for grouping of the genotypes as described by Beale (1969) and elaborated by Spark (1973).

The results indicated that all the characters showed significant differences among the genotypes tested. Variation displayed by thirteen characters in terms of range, mean, SEm, CV and number of superior genotypes in each attribute were presented in Table 2.

The results indicated that the range was maximum in total yield (0.79-4.49 kg), marketable yield (0.75-4.40 kg), TSS (9.33-13.96%) and plant height (31.67-60.82 cm). Further, the variation displayed in 5 bulb weight (0.17-0.36 kg), weight of 'C' grade bulbs (0.14-0.83 kg) is minimal. On perusal of results presented in the table, the study helped to identify 47 genotypes for total yield, 50 for marketable yield, 53 for TSS, 43 for 'A' grade bulbs, 56 for neck thickness, 60 for 5 bulb weight, 56 for number of leaves and 54 for plant height as superior genotypes among 114 lines tested in kharif season.

On perusal of mean data, the top 15 germplasm lines (in descending order) performing superior in marketable yield, total yield, 5 bulb weight, TSS, equatorial diameter, polar diameter, neck thickness and earliness are presented in Table 3. The results indicated that the germplasm lines NRCOG-1012, B-780, NRCOG-85, 975, 1000, 938, 893, 1009, N-53, 985, K-519-R and K-923 were promising both in the marketable and total yield. The accession NRCOG-925, 1033, 985, 998, and 1032 were found superior for 5-bulb weight, whereas NRCOG-966, 879, 924, 923, 953 recorded minimum

Table 1. Analysis of variance for 13 attributes in 115 landraces of onion

Source	df	Mean sum of squares												
		PH	NL	CT	5 BW	NT	PD	ED	Wt. 'A'	Wt. 'B'	Wt. 'C'	TSS	TY	My
Replication	2	1421.09	7.84	0.29	0.004	0.003	1.38	0.08	1.39	0.48	0.11	0.88	4.13	3.04
Treatment	113	91.94**	2.99**	0.04**	0.004**	0.02**	0.28**	0.32**	0.50**	0.30**	0.05**	2.26**	1.43**	1.42**
Error	226	42.79	1.53	0.02	0.002	0.01	0.15	0.13	0.20	0.09	0.03	0.91	0.40	0.41

*and ** indicates significant at 5% and 1% level of probability

Table 2. Phenotypic variations in 13 characters

Characters	Range	Mean	SE (±)	CV (%)	No. of superior genotypes
Plant height (cm)	31.67–60.82	45.15	0.44	14.48	54
No.of leaves	5.60–10.40	8.10	0.07	15.29	56
Collar thickness (cm)	0.62–1.28	0.91	0.009	16.55	–
5 bulb weight (kg)	0.17–0.36	0.27	0.003	16.48	60
Neck thickness (cm)	0.26–0.70	0.42	0.007	25.71	56
Polar diameter (cm)	2.38–4.55	3.73	0.02	10.51	–
Equatorial diameter (cm)	2.32–5.40	4.70	0.02	7.77	–
Weight of 'A' grade bulbs (kg)	0.15–2.20	0.75	0.03	60.29	43
Weight of 'B' grade bulbs (kg)	0.29–2.20	0.92	0.02	32.48	–
Weight of 'C' grade bulbs (kg)	0.14–0.83	0.38	0.01	50.38	–
TSS (%)	9.33–13.96	11.24	0.06	8.51	53
Marketable yield (kg)	0.75–4.40	2.83	0.04	22.47	50
Total yield (kg)	**0.79–4.49**	**2.93**	**0.04**	**21.99**	**47**

thickness. The variety B-780 continued to prove superior in terms of yield and growth attributes. However, NRCOG-1012 (44.9 t/ha) showed supremacy in yield with moderate resistant reaction against thrips followed by B-780, NRCOG-85, NRCOG-1009 and NRCOG-975.

Diversity Pattern

A wide genetic base with acceptable level of productivity and high general combining ability to yield superior segregants are essential in the parental selection. Selection of parents in onion has been on the basis of per se performance. The majority of the breeders have restricted their selection to known material and made intensive effort for local adaptation, as a result of which certain gene blocks were rapidly fixed along with correlated response, which in many cases has been in the adverse direction. Keeping in view, the data collected from the experiment of entire 115 landraces of onion were subjected to multivariate analysis. The classificatory procedures for earmarking distant genotypes have been emphasized by several workers (Griffing and Lindstorm, 1954; Moll *et al.*, 1962; Arunachalam, 1981).

Table 3. Performance of top 15 genotypes in terms of yield and its related characters

Acc no.	MY (t/ha)	Acc No.	TY (t/ha)	Acc. No.	5BW (g)	Acc. No.	TSS (%)	Acc. No.	ED (cm)	Acc. No.	PD (cm)	Acc. No.	NT (cm)	Acc. No.	Earliness
1012	44.00	1012	44.90	925	0.36	AK	14	914	5.40	1004	4.55	966	0.24	933	96
B-780 (c)	43.40	B-780 (c)	44.20	1033	0.36	MH-20 LR	13.1	991	5.24	914	4.28	879	0.26	930	96
85	42.50	85	42.50	998	0.35	905	12.93	72-1-R	5.22	925	4.27	924	0.28	923	98
975	39.80	1009	41.00	1032	0.34	991	12.86	1033	5.21	1009	4.26	923	0.29	948	98
1000	39.10	975	39.90	985	0.34	915	12.82	915	5.20	954	4.26	958	0.30	927	98
938	38.90	1000	39.50	ADR (c)	0.34	1003	12.73	85	5.20	1001	4.22	1036	0.30	914	98
893	38.90	72-1-R	39.20	918	0.33	998	12.66	1009	5.19	991	4.21	904	0.30	910	98
1009	38.50	893	38.90	973	0.33	914	12.47	ADR (c)	5.16	1033	4.17	696	0.31	971	98
N-53 (c)	38.20	938	38.90	AK	0.32	B-780 (c)	12.46	K-513-5C	5.12	986	4.16	N-53 (c)	0.31	917	99.33
939	37.30	K-519-R	39.60	940	0.32	999	12.46	AK	5.05	988	4.14	888	0.32	955	99.33
1001	36.80	N-53 (c)	38.50	B-780 (c)	0.32	918	12.34	918	5.03	976	4.13	976	0.33	952	99.33
985	36.40	985	38.20	K-513-5C	0.31	995	12.33	B-780 (c)	5.02	1000	4.12	1000	0.33	954	99.33
980	36.40	950	37.80	975	0.31	121 DR	12.33	940	5.00	999	4.12	964	0.33	998	99.33
AK	36.30	1001	37.40	1015	0.31	888	12.29	925	4.98	1006	4.08	925	0.34	919	99.33
K-519-R	36.10	939	37.20	952	0.31	889	12.28	917	4.97	K-519-R	4.06	927	0.34	944	99.33
911	35.60	973	37.10	N-53 (c)	0.31	1012	12.26	973	4.96	N-53 (c)	3.82	52	0.34	N-53 (c)	102
923	35.20	923	36.70	991	0.31	N-53 (c)	10.26	N-53 (c)	4.93	B-780 (c)	3.98	B-780 (c)	0.66	B-780 (c)	106
ADR (c)	35.10	ADR (c)	35.10	–	0.20	ADR (c)	10.13	–	5.10	ADR (c)	4.00	ADR (c)	0.36	ADR (c)	100.66
GM		28.23		29.38		0.27		11.24		4.70		3.73		0.42	99.10

Table 4. Distribution of 115 landraces of onion in different clusters

Cluster Number	No. of landraces in each cluster	Landraces in each cluster
I	22	NRCOG-048, 993, K-513-5C, 910, 889, 905, 940, 1016, 953, 1033, 918, 995, 915, 988, 999, 991, 998, 1003, Arka Kalyan, 121-DR, MH-20-LR, 981
II	2	NRCOG-696, 879
III	18	NRCOG-064, 966, 946, 956, 954, 924, 1020, 958, 972, 949, 934, 1008, 960, 941, 970, 919, 996, 1021.
IV	15	NRCOG-922, 974, 930, 971, 943, 931, 942, 964, 932, 944, 1010, 1022, 961, 975, 1036
V	1	NRCOG-1037
VI	12	NRCOG-891, 907, 1035, 955, 1019, 906, 950, 893, 945, 938, 939, 1025
VII	8	NRCOG-904, 948, 888, 911, 917,903, 914, 72-1-R
VIII	8	NRCOG-987, 990, 986, Behary Red, 1009, 1012, 085, B-780
IX	28	NRCOG-901, 976, 983, 992, 1015, 1032, 925, 1001, 1004, 1006, 994, 1005, 72-1-DR, 26-OP-DR, 900, K-519-R, 909, 937, 933, 921, 952, 973, 985, 923, N-53, 927, 1000, 980
X	1	Agri Found Dark Red

A total of 6555 D^2 values corresponding to all the 115 possible pairs of entries were computed as per the method suggested by Rao (1952). A total of 10 clusters were formed with number of landraces in each cluster from 1(cluster X) to 22 (cluster I). The distribution of 115 landraces of onion in different clusters was presented in Table 4.

The results indicated that cluster IX (28) had maximum number of genotypes followed by cluster I (22), cluster III (18) and cluster IV (15). The variety Agri Found Dark Red and NRCOG-1037 fell in separate clusters. A combination of 8 entries of high yielding lines along with B-780 and Behary red fell in cluster VIII. Further, these results revealed that, there was no specific relationship between the clustering pattern of the genotypes and their geographic sources. The tendency of the cultivars occurring in clusters was cutting across geographic diversity revealed that the pattern or distribution of genotypes from different geographical locations into different clusters was at random, demonstrating the geographical isolation may not be the only factor for causing genetic diversity. These results are in conformity with the findings of Krishna Prasad (1995) in bush bean and Krishna Prasad *et al.* (1993) in cucumber. Further, the results suggested that geographic isolation is not the only factor causing genetic diversity and this point should be considered while selecting parents for hybridization programme.

Table 5. Contribution of characters towards genetic divergence of the onion germplasm analyzed in the study

Character	Times ranked 1st	Contribution (%)
Plant height	553	8.44
No. of leaves	360	5.49
Collar thickness	540	8.24
5 bulb weight	422	6.44
Neck thickness	542	8.27
Polar diameter	427	6.51
Equatorial diameter	343	5.23
Weight of 'A' grade bulbs	447	6.82
Weight of 'B' grade bulbs	853	13.01
Weight of 'C' grade bulbs	372	5.68
TSS	860	13.12
Marketable yield	637	9.72
Total yield	199	3.04

The selection of parents on large phenotypic differences may be useful but there are several instances where a single gene can provide large-scale differences in plant height, maturity and disease resistance. Therefore measures of quantifying diversity have become important in classifying the material commonly used by the breeders.

On perusal of results (Table 5) weight of 'B' grade bulbs and TSS appeared to contribute maximum towards divergence followed by marketable yield, plant height, and neck thickness.

The cluster mean per plot yield was maximum in cluster IX, followed by cluster VIII, VII and VI. Minimum yield was observed in cluster II. Only five clusters recorded above mean values both in marketable yield and total yield (Table 6). The divergent lines with high yield potential and some degree of resistance to disease will be identified for formulating the breeding programme.

Hundred and fourteen accessions of onion were

Table 6. Cluster means for 13 attributes of 115 landraces of short day onion

Clusters	PH (cm)	NL (cm)	CT	5 B Wt (kg)	NT (cm)	PD (cm)	ED (cm)	Wt 'A' (kg)	Wt 'B' (kg)	Wt 'C' (kg)	TSS %	MY (kg)	TY
I	45.27	8.11	0.89	0.29	0.48	3.69	4.83	0.73	0.89	0.40	12.25	2.67	2.79
II	38.83	6.46	0.71	0.27	0.28	3.57	4.27	0.86	0.22	0.18	11.93	0.78	0.83
III	41.54	7.92	0.85	0.25	0.39	3.55	4.57	0.43	0.56	0.30	10.74	2.11	2.27
IV	41.08	7.28	0.84	0.24	0.37	3.66	4.59	0.54	0.86	0.53	10.53	2.61	2.72
V	49.80	8.60	1.00	0.17	0.35	3.60	2.32	0.17	0.47	0.54	9.73	2.53	2.73
VI	48.34	8.93	1.00	0.27	0.41	3.54	4.67	0.59	0.91	0.28	11.15	3.16	3.25
VII	50.58	8.55	0.89	0.25	0.40	3.80	4.93	0.85	0.93	0.31	11.83	3.19	3.32
VIII	52.21	9.20	1.10	0.27	0.65	3.97	4.85	1.08	1.14	0.35	11.43	3.28	3.37
IX	44.83	7.93	0.93	0.29	0.40	3.92	4.76	1.05	1.22	0.39	11.00	3.29	3.40
X	47.50	8.06	0.82	0.34	0.36	4.00	5.16	0.90	1.07	0.41	10.13	3.51	2.51
Mean	45.99	8.10	0.90	0.26	0.40	3.73	4.49	0.72	0.82	0.36	11.07	2.71	2.71

evaluated for genetic diversity. The accessions were grouped in ten clusters. Cluster IX had maximum of 28 accessions followed by cluster I (22) and cluster II (18). The tendency of the cultivars occurring in clusters was cutting across geographic diversity revealed that geographic isolation may not be the only factor for causing genetic diversity. Therefore selection of parents possessing large phenotypic variability and from divergent clusters will be useful in onion improvement.

References

Arunachalam V (1981) Genetic distance in plant breeding. *Indian J. Genet.* **41(2):** 226-236.

Beale EMI (1969) Euclidian Cluster Analysis. Paper to the 37th session of the International Statistical Institute, UK.

Griffing B and EW Lindstrom (1954) A study of the combining ability of corn hybrids having varying proportion of corn belt and non corn belt germplasm. *Agron J* **46:** 454-552.

Krishna Prasad VSR, DP Singh and RP Singh (1993) Biological divergence in the landraces of Indian cucumber (*Cucumis sativus* L). *Indian J Hort* **50(1):** 46-50

Krishna Prasad VSR (1995) Genetic diversity of yield and its components in bush bean (*Phaseolus vulgaris* L.). Genotypes under sub-humid affisol of Eastern India. *Indian J.Hort.* **52(1):** 46-50

Moll RN, WS Salhauna and HF Robinsan (1962) Heterosis and genetic diversity in varieties crosses of maize. *Crop Sci* **2:** 197-198

Rao CR (1952) Advances Statistical Methods in Biochemical Research, John Wiley and Sons Inc. New York.

Spark DN (1973) Euclidian Cluster Analysis Algorithm. *Appl. Stat.* **22:** 126-130

SHORT COMMUNICATION

Walnut Selections from Chamba District of Himachal Pradesh

Dinesh Singh and K Kumar[1]
Dr YS Parmar University of Horticulture & Forestry, Farm Science Centre (KVK), Saru, Chamba 176 310 (Himachal Pradesh)
[1]Department of Fruit Breeding & Genetic Resources, Dr YS Parmar University of Horticulture & Forestry, Nauni, Solan 173 230 (Himachal Pradesh)

Key words: *Juglans regia* L., Seedling tree selections, Yield, Nut, Kernel

Walnut (*Juglans regia* L.), a nut par excellence grown in India since antiquity especially in North-Western Himalaya, which is considered to be one of the secondary centre of diversity of cultivated walnut as maximum variability for primitive types is present in this region (Sharma and Kumar, 1994). Seedlings are found growing as scattered trees in the dry and wet temperate regions of India. The major walnut comes from these seedling trees of unknown origin, from natural forests and plants raised in farmers backyards (Pandey *et al.* 2001). Many of these local plantings have evolved through natural and human selection and represent distinct ecotypes and landraces. Meagre efforts have been made for selection of superior walnut genotypes with desirable traits from these seedling trees. In order to make use of this variability, efforts must be made to survey different seedling walnut growing areas to select the promising types.

Keeping in view the existing variability of seedling walnut trees, the present investigations were undertaken with the objective to select superior walnut genotypes from naturally occurring population of seedling tree stands.

A field survey was undertaken during the year 2003 and 2004 in remote and wet temperate areas of Chamba district in Himachal Pradesh. As a result of sustained exploration with the co-operation of local inhabitants a total of 450 walnut trees of seedling origin of varying age (ranging between 9 and 87 years) growing scattered in three locations namely Pangi, Bharmour and Tissa were surveyed. The location and geographical features of the study area are represented in Figure 1.

On the basis of growth, yield, nut and kernel characters, 20 trees were pre-selected for further studies. A random sample of 30 nuts from each tree was taken and observations on various tree growth, nut and kernel characters were recorded as per UPOV guidelines (UPOV, 1988). Nut and kernel weight was weighed on digital balance whereas kernel percentage was calculated as under:

$$\text{Kernel (\%)} = \frac{\text{Kernel weight}}{\text{Nut weight}} \times 100$$

Shell thickness was measured at near centre of half shell with the help of digital Vernier's Caliper (Mitutoyo, Japan–CD–6" CS). For the estimation of kernel protein, the nitrogen content was estimated following the Kjeldahl method as described by McKenzie and Wallace (1954). Protein content was worked out by multiplying N content with a factor of 5. 3 suggested for tree nuts (Khanizadeh *et al.*, 1995). Kernel oil was determined by following the method of Folch *et al.* (1957).

Observations on growth habit (Table 1) of selected walnut trees indicate spreading type of growth habit

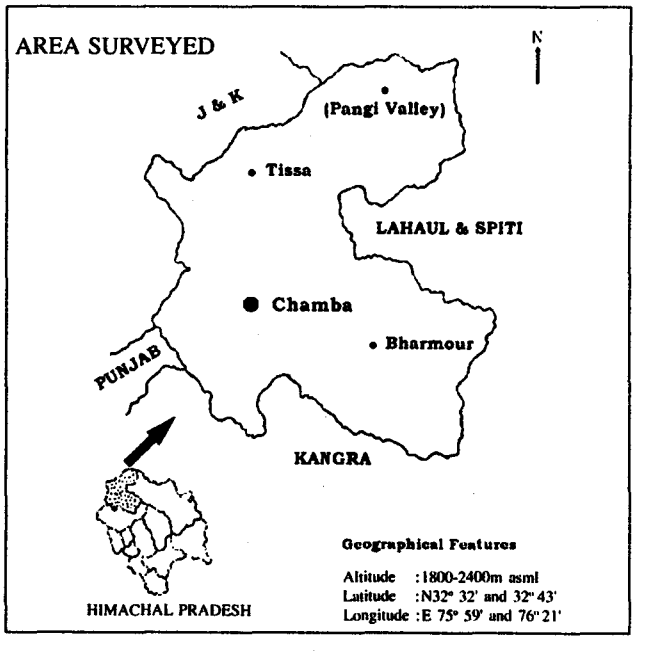


Fig. 1. Geographical features of the area surveyed

Table 1. Tree characters of walnut selections

	Tree characters				
Selection No.	Growth habit	Nut yield (kg/tree)	Age (years)	Flowering season	Date of maturity
Tree No.1P	Spreading	450	80	First week of May	Last week of September
Tree No.2P	Spreading	400	65	First week of May	Last week of September
Tree No.3P	Spreading	150	20	First week of May	Last week of September
Tree No.4P	Spreading	500	75	First week of May	Last week of September
Tree No.5P	Spreading	400	60	First week of May	Last week of September
Tree No.6P	Spreading	375	50	First week of May	Last week of September
Tree No.7P	Spreading	350	46	First week of May	Last week of September
Tree No.8P	Spreading	200	38	First week of May	Last week of September
Tree No.9P	Spreading	400	65	First week of May	Last week of September
Tree No.10P	Spreading	500	70	First week of May	Last week of September
Tree No.1B	Spreading	500	87	First week of April	Last week of August
Tree No.2B	Erect	180	36	First week of April	Last week of August
Tree No.3B	Spreading	150	18	First week of April	Last week of August
Tree No.1T	Spreading	25	9	First week of May	First week of October
Tree No.2T	Spreading	45	15	First week of May	Last week of October
Tree No.3T	Spreading	90	18	First week of May	Last week of October
Tree No.4T	Spreading	250	25	First week of April	First week of October
Tree No.5T	Spreading	175	20	First week of April	Last week of September
Tree No.6T	Erect	150	22	First week of April	Last week of September
Tree No.7T	Spreading	250	45	Last week of April	Last week of September

in most selections except erect habit in Tree No. 2B and Tree No. 6T. As regards, season of flowering it varied from as early as first week of April (Tree No.1B, Tree No.2B, Tree No.3B, Tree No. 4T, Tree No.5T, Tree No. 6T) to first week of May (Tree No. 1P, Tree No.2P, Tree No. 3P, Tree No.4P, Tree No. 5P, Tree No. 6P, Tree No. 7P, Tree No. 8P, Tree No.9P, Tree No. 10P, Tree No. 1T, Tree No. 2T, Tree No.3T) with Tree No. 7T recording peak flowering in last week of April. Similarly nut maturation time extended from last week of August (Tree No.1B, Tree No. 2B, Tree No. 3B) to last week of October in Tree No. 2T and Tree No. 3T with two selections namely Tree No. 1T and Tree No. 4T exhibiting nut maturity in first week of October. Data from Table 1 show that out of these 20 seedling trees selected, Tree No.4P, Tree No. 10P and Tree No. 1B gave highest yield (500kg/ tree) whereas lowest nut yield was recorded in Tree No. 1T (25 kg/ tree).

Data from Table 2 reveals that nut weight (g), shell thickness (mm), kernel weight (g), shelling (%), kernel oil (%), and kernel protein (%) vary from 7.1g (Tree No. 1P) to 22.3 g (Tree No. 4P), 0.71mm (Tree No. 2P) to 2.54 mm (Tree No. 6T), 3.91g (Tree No. 7P) to 9.58g (Tree No. 4P), 30.13 % (Tree No. 6P) to 72.95 % (Tree No. 1P), 47% (Tree No. 2T) to 63.2 % (Tree No. 8P) and 15.2 % (Tree No. 2P) to 22.3 (Tree No. 2T), respectively.

The perusal of data presented above revealed a considerable variation in tree nut, kernel and yield characters of seedling trees at the three locations under present study. Variations in nut, kernel and yield characters have also been reported from the various walnut growing areas of Himachal Pradesh by Chauhan and Sharma (1979), Sharma and Sharma (1998, 2001), Sharma and Kumar (2005). It is clear from present and past studies that there are differences between variation among different nut and kernel characters of different locations in seedling trees where these studies were carried out. These differences may be attributed to genetic constitution of the particular seedling and environmental conditions at a particular locality, and thus represent valuable gene sources. In the present study, some of the selections bear heavily up to 500 kg/ tree, some bear exceptionally large nuts (up to 22.30 g), and still some of the selections are extremely thin shelled (0.71 mm) and record up to 72 % of kernel recovery.

All the twenty seedling tree selections initially marked and studied here have extreme variation for individual character and can be utilized in walnut improvement work for incorporating such traits in existing commercial cultivars. But all these marked seedling trees do not fulfill commercial requirement and only six genotypes (Tree No. 4P, Tree No. 1B, Tree No. 2P, Tree No. 1P, Tree No. 8P and Tree No. 2T) produce moderate to high nuts and kernels of

Table 2a. Nut characters of walnut selections

Selection No.	Nut shape longitudinal section to suture	Nut shape through suture	Shell colour	Shell texture	Nut diameter to suture	Nut length (mm)	Shell seal	Nut wt. (g)	Shell thickness (mm)	Shell strength
Tree No.1P	Ovate	Ovate	Light	Medium	25.20	33.26	Strong	7.10	1.63	Intermediate
Tree No.2P	Elliptic	Elliptic	Light	Medium	26.31	41.13	Intermediate	8.50	0.71	Weak
Tree No.3P	Trapezoid	Triangular	Medium	Medium	35.24	36.65	Strong	15.50	2.10	Intermediate
Tree No.4P	Trapezoid	Ovate	Brown	Rough	40.47	48.94	Intermediate	22.30	2.06	Strong
Tree No.5P	Trapezoid	Ovate	Dark brown	Very rough	36.97	36.76	Strong	12.50	1.80	Intermediate
Tree No.6P	Trapezoid	Triangular	Light	Intermediate	36.99	32.88	Strong	14.80	2.39	Strong
Tree No.7P	Circular	Ovate	Intermediate	Intermediate	25.62	29.18	Strong	9.00	2.35	Strong
Tree No.8P	Trapezoid	Triangular	Intermediate	Intermediate	35.32	33.76	Strong	14.10	1.97	Intermediate
Tree No.9P	Trapezoid	Ovate	Dark	Intermediate	31.14	36.76	Strong	11.00	1.52	Intermediate
Tree No.10P	Trapezoid	Ovate	Brown	Rough	34.34	33.69	Strong	14.30	1.54	Weak
Tree No.1B	Circular	Ovate	Light	Smooth	32.48	34.12	Intermediate	12.13	1.44	Intermediate
Tree No.2B	Trapezoid	Ovate	Medium	Rough	38.28	38.24	Strong	14.86	2.47	Strong
Tree No.3B	Elliptic	Elliptic	Medium	Medium	27.85	34.60	Strong	12.95	1.71	Intermediate
Tree No.1T	Trapezoid	Ovate	Dark	Medium	31.46	32.93	Strong	16.50	2.48	Strong
Tree No.2T	Circular	Elliptic	Dark	Medium	27.50	28.84	Strong	11.70	1.58	Intermediate
Tree No.3T	Trapezoid	Ovate	Dark	Rough	36.60	38.24	Strong	12.60	2.23	Intermediate
Tree No.4T	Elliptic	Ovate	Medium	Rough	34.00	38.29	Intermediate	12.10	1.74	Intermediate
Tree No.5T	Elliptic	Elliptic	Medium	Smooth	30.50	37.16	Intermediate	16.90	2.30	Intermediate
Tree No.6T	Trapezoid	Circular	Dark	Medium	33.90	35.21	Strong	18.40	2.54	Strong
Tree No.7T	Ovate	Ovate	Dark	Medium	39.00	41.70	Strong	15.40	2.17	Strong

Table 2b. Kernel characters of walnut selections

Selection No.	Kernel colour	Kernel weight (g)	Shelling (%)	Kernel oil (%)	Kernel protein (%)
Tree No.1P	Light	5.18	72.95	58.20	15.60
Tree No.2P	Very light	4.12	48.47	52.30	15.20
Tree No.3P	Medium	8.54	55.09	61.00	16.40
Tree No.4P	Dark	9.58	42.95	49.50	16.00
Tree No.5P	Medium brown	4.30	34.40	60.00	18.70
Tree No.6P	Light	4.46	30.13	60.10	19.00
Tree No.7P	Medium	3.91	43.44	56.80	18.00
Tree No.8P	Medium	6.80	48.22	63.20	18.65
Tree No.9P	Dark	4.85	40.72	51.50	18.40
Tree No.10P	Brown	8.50	59.44	50.90	19.50
Tree No.1B	Medium	6.10	50.28	50.00	20.70
Tree No.2B	Medium	6.80	45.76	49.70	20.00
Tree No.3B	Dark	7.25	55.98	52.00	19.60
Tree No.1T	Medium	8.10	49.09	54.20	19.80
Tree No.2T	Dark	6.09	52.05	47.00	22.30
Tree No.3T	Dark	5.25	41.66	47.50	21.80
Tree No.4T	Medium	5.10	42.14	57.50	17.50
Tree No.5T	Light	7.80	46.15	53.40	18.00
Tree No.6T	Medium	8.80	47.82	50.30	20.90
Tree No.7T	Light	6.85	44.48	49.55	21.10

desirable quality. They have been selected and recommended for field conservation, mass multiplication and testing under standard field conditions in diverse agro-climatic zones.

References

Chauhan JS and Sharma SD (1979) Phenotypic variability in walnuts of Kinnaur district of HP. *Indian Journal of Agricultural Sciences* **49**: 420-423.

Folch J, Lees M and Stanley S (1957) A simple method for isolation and purification of total lipids from animal tissues. *Journal of Biological Chemistry* **226**: 497-506.

Khanizadeh S, Buszard D, Zarkadas CG (1995) Misuse of the kjeldahl method for estimating protein content in plant tissues. *Hort Science* **30 (7)**: 1341-1342.

McKenzie HA and Wallace, HS (1954) Kjeldahl determination of nitrogen, a critical study of digestion conditions of temperature, catalyst and oxidizing agent. *Australian Journal of Chemistry* **7**: 55.

Pandey G, Joshi BD and Mandal S (2001) Collection and characterization of Walnut (*Juglans regia* L.) from Himachal Pradesh. *Indian J Plant Genet Resour* **14(3):** 368-370.

Sharma SD and Sharma OC (1998) Studies on variability in nuts of seedling walnut (*J. regia* L.) in relation to tree age. *Fruit Varieties Journal* **52(1):** 20-23.

Sharma OC and Sharma SD (2001) Correlations between nut and kernal characters of Persian walnut seedling trees of Garsa valley in Kullu District of Himachal Pradesh. *Acta Horticultura* **544:** 129-131.

Sharma Ritu and Kumar K (2005) Selecting walnuts from seedling tree populations in some villages of District of Sirmour (HP). India. *Acta Horticultura* **696:** 85-90.

Sharma RL and Kumar K (1994) Genetic diversity and scope of walnut improvement in India. In: *Progress in Temperate Fruit Breeding* (Eds. H Schmidt and M Kellerhals) pp.447-449. Kluwer Academic Publishers, Dordrecht, The Netherlands.

UPOV (1988) General Information: International Union for the Protection of New Varieties of Plants/TG/125/1 (PROG.) Geneva, Switzerland.

SHORT COMMUNICATION

Dormancy Breaking Treatments to Improve Seed Germination in *Delonix regia* Ref.

Sandeep Kumar[1], Kalyani Srinivasan, Sanjeev Saxena and Manju Uprety
National Bureau of Plant Genetic Resources, New Delhi 110 012
[1]National Institute of Science Communication and Information Resources, New Delhi 110 012

Key words: *Delonix regia*, Dormancy, Seed germination, Mechanical scarification, Sulphuric acid treatment, Boiling water treatment

Delonix regia (Bojer ex Hook.) Ref. of family Leguminosae commonly known as flame tree or gulmohar is a popular ornamental medium-sized tree planted in avenues and gardens. The tree is usually grown from seed during rainy season and can also be raised from cuttings. The seed germination is generally poor. The major reasons of poor germination include empty seeds, agro-ecological conditions, time of seed collection and age of mother tree, etc. Further, high degree of dormancy exhibited by seeds is a problem for undertaking plantation work in this species. The primary reason for dormancy is the presence of hard seed coat which makes the seed impermeable to water and hinders the exchange of gases causing mechanical impediment to the growth of embryos. The success of any plantation work, therefore, requires maximum germination thereby necessitating treatments for breaking dormancy.

Removal of hard seed coat or its softening results in enchanced germination. Several physical and chemical treatments have been suggested for breaking the seed dormancy for leguminous species (Rolston, 1978). The present study was undertaken to investigate the response of various physical and chemical seed scarification treatments for improving the germination.

Fresh seeds of *Delonix regia* were procured from forestry college, Sirsi, Karnataka (IC 424910). Seeds were checked for health, insect damage and other physical purity parameters. The seeds were given dormancy breaking treatments. One set of untreated seeds served as control.

Sulphuric Acid (SA): Seeds were immersed in 98 per cent sulphuric acid for 10, 20, 30, 40 and 60 min.(referred as SA_1, SA_2, SA_3, SA_4, SA_5 respectively). The treated seeds were thoroughly washed in running water before the germination test.

Hot Water (HW): Seeds were immersed in a hot water bath at 60°C for one hour, 70°C for 45min, 75°C for 30 min, 80°C for 15min and 100°C for 5min (referred as HW_1, HW_2, HW_3, HW_4, HW_5 respectively) and allowed to cool for 30 min at room temperature.

Boiling Water (BW): Boiling water (at 100°C) was poured over the seeds and allowed to cool down at room temperature for 24 hrs.

Direct Burning (DB): The chalazal end of the seed was carefully charred for one minute directly on flame of Bunsen burner and allowed to cool at room temperature.

Dry Heat (DH): The seeds were subjected to dry heat in an air circulated oven at 65 $\pm$1°C for 16$\pm$1hr

Mechanical Scarification (MS): Seeds were uniformly rubbed for five minutes by a coarse sand paper (No.100).

Mechanical Abrasion (MA): Inner surface and the lid of the petri plates were lined with sand papers (No.100). These petri plates containing seeds were placed over a mechanical shaker set at 240 rpm.

Germination Test: Three replications of 25 seeds each were tested for germination by rolled towel method. Seeds were kept in the dark in a germinator maintained at 30°C and evaluated for germination on the seventh day.

Speed of Germination: The speed of germination as a vigour test was measured by counting the number of seeds that germinated every day and expressed as Mean Germination Time (MGT) in days using the formula $MGT = \sum nd / n$ where n denotes the number of seeds germinating on day d. The reciprocal of MGT (1/MGT) was calculated as germination per day (GPD).

The data was subjected to statistical analyses and means were compared using critical difference values.

Table 1. Effect of various dormancy breaking treatments on germination and mean germination time of *Delonix regia* seeds

Treatment*	Germination (%)	Hard Seeds (%)	Dead Seeds (%)	Mean Germination Time (days)
Control	10	90	0	8.7
Sulphuric acid treatment for 10 min	54	44	2	8.4
Sulphuric acid treatment for 20 min	62	30	8	7.2
Sulphuric acid treatment for 30 min	64	24	12	7.0
Sulphuric acid treatment for 40 min	76	10	14	5.9
Sulphuric acid treatment for 60 min	84	4	12	5.5
Hot water treatment 60°C for one hr	70	26	4	8.0
Hot water treatment 70°C for 45 min	76	14	10	7.1
Hot water treatment 75°C for 30 min	80	20	0	6.2
Hot water treatment 80°C for 15 min	82	14	4	5.8
Hot water treatment 100°C for 5 min	28	12	60	4.6
Boiling water treatment	86	0	14	2.08
Direct burning treatment	70	10	20	1.33
Dry heat treatment	30	60	10	6.83
Mechanical scarification	24	76	0	7.41
Mechanical abrasion	90	10	0	2.36
CD	**6.26**	**4.7**	**2.1**	**0.72**

All the treatments tried in the experiment resulted in decreasing hard seeds and an increase in germination percentage as compared to the control (Table 1). Sulphuric acid treatment resulted in softening of the seed coats thus decreasing hard seeds and consequently increasing the germination percentage. This may be due to the activation of the hydrolytic enzymes present in the seed due to accelerated imbibition resulting in enhanced germination. These observations confirmed the finding of Zodap (1991) and Sudarsan Rao *et al.* (1999). A progressive increase in the germination percentage of the seed with the duration of acid treatment was observed in the present study and treatment for 60 minutes was found to be the best. The Mean Germination Time (MGT) showed a gradual decrease with duration of acid treatment, thus indicating a faster rate of germination in seeds treated for longer duration. Duarte (1974) reported improved germination in *Delonix* seeds after a concentrated sulfuric acid soak for 0.5 to 5 hours.

Hot water treatments break in seed coat dormancy in several legumes has been reported by Rehman *et al.* (1999). Immersing the seeds in hot water at higher temperature for less duration was more effective in increasing germination percentage as compared to longer duration at lower temperature. However, treatment with hot water at 100°C for 5 minutes decreased the germination percentage as the number of dead seeds increased. The optimum germination test result among hot water treatments was obtained for the seed lot treated at 80°C for 15 minutes where the percentage of germination was significantly high (82%), as well as the MGT lower than the other combination of treatments reflecting a higher speed of germination. In another study Millat-E-Mustafa (1989) recommended 90°C water for 10 seconds followed by 24 hour imbibition as a dormancy breaking treatment in *Delonix*.

The treatment with boiling water and mechanical scarification also resulted in increased germination percentage. Maximum germination improvement was achieved with manual scarification with sand paper. These treatments had the lower MGT indicating faster germination. These observations support the finding of Padma *et al.* (1993) in some hard coated acacias. Hot-wire scarification was reported to improve seed germination. Direct burning improved the seed germination rate as well as germination percentage significantly as compared to other treatments in the present study (Sandiford, 1988). The dry heat treatment at a constant temperature of 60°C for 16 hrs and mechanical abrasion treatments also significantly increased germination as compared to the control but were not as effective as other treatments.

Thus, of the several treatments applied to break the seedcoat imposed dormancy in the seeds of *Delonix regia* (Fig. 1) mechanical scarification using sand paper was found to be the best followed by boiling water treatment, sulphuric acid treatment for 60 minutes and hot water treatment at 80°C for 15 minutes. The germination per day was better in direct burning, followed by boiling water and mechanical scarification treatments.

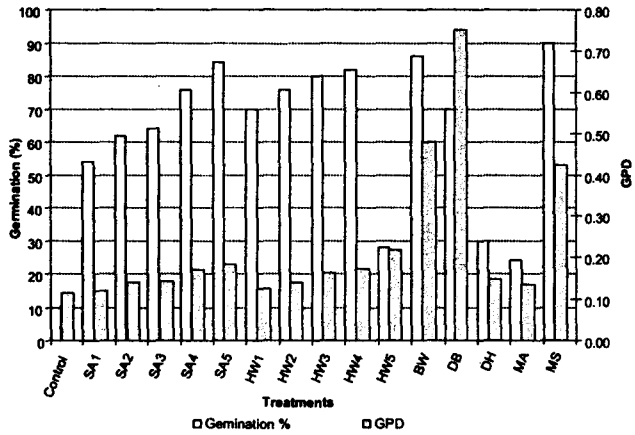


Fig1. Effect of various treatments on germination percentage and germination per day in Delonix regia *seeds (SA_1, SA_2, SA_3, SA_4, SA_5: Sulphuric acid treatment for 10, 20, 30, 40 and 60 min respectively; HW_1, HW_2, HW_3, HW_4, HW_5: Hot water treatment 60°C for one hour, 70°C for 45min, 75°C for 30 min, 80°C for 15min and 100°C for 5min respectively; BW: Boiling water treatment; DB: Direct burning treatment; DH: Dry heat treatment; MS: Mechanical scarification; MA: Mechanical abrasion)*

Of these however, boiling water treatment is simple and requires no special skills and can be easily adopted by nursery men for bulk treatment of seeds for seedling production. Sulphuric acid treatment on the other hand requires special skills and involves risk. Mechanical scarification although is safe is most time consuming treatment especially when large quantities of seeds are to be treated.

References

Rolston MP (1978) Water impermeable seed dormancy. *Botanical Review* **44:** 365-396.

Zodape (1991) The improvement of germination of some forest species by acid scarification. *Indian Forester* **117:** 61-66.

Rao S, SRK Murthy, GV Humantha Rao and A Narayan (1999) Effect of different treatments on germination and early seedling growth of four avenue tree species. In: *Seed and Nursery Technology of Forest Trees* (Eds. DGW Edwards and SC Naithani) pp 279-284

Duarte O (1974) Improving Royal Poinciana seed germination. *Plant Propagator* **20:** *15-16.*

Rehman SR, NJ Losescher and PJC Harris (1999) Dormancy breaking and germination of *Acacia salicina* Lindl. seeds. *Seed Science and Tech* **27:** 553-557.

Millat-E-Mustafa M (1989) Effect of hot water treatment on the germination of seed of *Albizzia lebbeck* and *Delonix regia*. *Bano-Biggyan-Patrika* **18:** 63-64.

Padma V, BM Reddy and G Satyanarayan (1993) Breaking dormancy in certain *Acacia* spp. by presowing seed treatment. *Seed Research* **21:** 26-30.

Sandiford M (1988) Burnt offerings: an evaluation of the hot-wire seed scarifier. *Commonwealth Forestry Review* **67:** 285-292.

Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of **ICAR in its XIII[th] meeting held on 23[rd] December, 2004** at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 42 germplasm lines out of 116 proposals considered.

Pusa T 3336 (INGR No. 04080; IC427824), Wheat (*Triticum aestivum* L.) germplasm with resistance to leaf blight

SMS Tomar[1], Bhanwar Singh[1], Vinod[1], MK Menon[2], M Sivasamy[2] and DV Singh[1]
[1] *Indian Agricultural Research Institute, New Delhi 110 012*
[2] *IARI Regional Station Wellington 643 231 (Tamil Nadu)*

Spot blotch or leaf blight caused by *Drechslera sorokiniana* (Sacc.) Subram. & Jain (= *Helminthosporium sativum* = *Bipolaris sorokiniana*) has recently become a serious disease of wheat particularly in northeastern region of Indo-Gangetic plains. Resistance to leaf blight is low in commercial wheat cultivars (Singh *et al.*, 1995). Therefore, concerted efforts were made to generate genetic diversity for leaf blight resistance. Segregating generations of Lok Bharti x DARF (Derivative *Agropyron* Resistance Falcon, an exotic line carrying alien segment from *Lophopyrum elongatum*) were screened for leaf blight resistance at hot spot locations, such as Wellington (South India) and Pusa (Bihar). A selection Pusa T 3336 was identified and further screened at many locations. It exhibited high degree of resistance. The leaf surface of Pusa T 3336 is waxy, which was confirmed by scanning electron microscopy that revealed, leaf surface for the presence of platelet like wax particles distributed all over the leaf epidermis, but more condensed in the guard cells.

Qualitative and quantitative analysis through gas liquid chromatography (GLC) revealed the presence of eight C-atom homologues in Pusa T 3336, while three C-atom homologues were quantified in moderately resistant genotypes and two and one C-atom homologues in most susceptible genotypes (e.g. Agra Local). The germination of leaf blight fungus conidia on the leaf surface of Pusa T 3336 was very low and germ tube showed papillate structures compared to the susceptible check showing hyphal penetration through stomata (Das et al., 1999), confirming its resistant reaction. Pusa T 3336 produces bold grain with high thousand-kernel weight of 50 g. This genotype also showed resistance to all the three wheat rusts and powdery mildew.

References

Das Soma, R Agarwal, P Dureja and DV Singh (1999) Leaf surface waxes in relation to resistance against spot blotch (*Drechslera sorokiniana*) of wheat. *Acta Phytopathologica et Hungarica* **34:** 75-84.

Singh RV, AK Singh and SP Singh (1995) Progress of work under national centre on foliar diseases during 1994-95. Paper presented in 34[th] All India Wheat Research Workers' workshop, AICWIP, ICAR, UAS Dharwad, August 1995.

DW-1001 (INGR No. 04081; IC445070), Wheat (*Triticum durum* Desf.) Germplasm with Gamma Gliadin-45 Band

Bhudeva Singh Tyagi, Jag Shoran and RK Gupta
Directorate of Wheat Research, Karnal 132 001 (Haryana)

Durum wheat in India occupies more than 2 million ha area with the total production of 3.5 mt. However the end product quality of the varieties grown in India needs to be improved immediately. It is known that the presence or absence of low molecular weight glutenins (LMW-1 and LMW-2) are closely linked to Gamma-45 and Gamma-42 gliadins. To develop varieties with Gamma-45 gliadins, which have superior pasta quality,

* *Communicated by Dr. Anurudh Kumar Singh, Member Secretary, Plant Germplasm Registration Committee, National Bureau of Plant Genetic Resources, Indian Council of Agricultural Research, Pusa Campus, New Delhi*

Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of **ICAR in its XIII[th] meeting held on 23[rd] December, 2004** at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 42 germplasm lines out of 116 proposals considered.

Pusa T 3336 (INGR No. 04080; IC427824), Wheat (*Triticum aestivum* L.) germplasm with resistance to leaf blight

SMS Tomar[1], Bhanwar Singh[1], Vinod[1], MK Menon[2], M Sivasamy[2] and DV Singh[1]
[1] *Indian Agricultural Research Institute, New Delhi 110 012*
[2] *IARI Regional Station Wellington 643 231 (Tamil Nadu)*

Spot blotch or leaf blight caused by *Drechslera sorokiniana* (Sacc.) Subram. & Jain (= *Helminthosporium sativum* = *Bipolaris sorokiniana*) has recently become a serious disease of wheat particularly in northeastern region of Indo-Gangetic plains. Resistance to leaf blight is low in commercial wheat cultivars (Singh *et al.*, 1995). Therefore, concerted efforts were made to generate genetic diversity for leaf blight resistance. Segregating generations of Lok Bharti x DARF (Derivative *Agropyron* Resistance Falcon, an exotic line carrying alien segment from *Lophopyrum elongatum*) were screened for leaf blight resistance at hot spot locations, such as Wellington (South India) and Pusa (Bihar). A selection Pusa T 3336 was identified and further screened at many locations. It exhibited high degree of resistance. The leaf surface of Pusa T 3336 is waxy, which was confirmed by scanning electron microscopy that revealed, leaf surface for the presence of platelet like wax particles distributed all over the leaf epidermis, but more condensed in the guard cells.

Qualitative and quantitative analysis through gas liquid chromatography (GLC) revealed the presence of eight C-atom homologues in Pusa T 3336, while three C-atom homologues were quantified in moderately resistant genotypes and two and one C-atom homologues in most susceptible genotypes (e.g. Agra Local). The germination of leaf blight fungus conidia on the leaf surface of Pusa T 3336 was very low and germ tube showed papillate structures compared to the susceptible check showing hyphal penetration through stomata (Das et al., 1999), confirming its resistant reaction. Pusa T 3336 produces bold grain with high thousand-kernel weight of 50 g. This genotype also showed resistance to all the three wheat rusts and powdery mildew.

References

Das Soma, R Agarwal, P Dureja and DV Singh (1999) Leaf surface waxes in relation to resistance against spot blotch (*Drechslera sorokiniana*) of wheat. *Acta Phytopathologica et Hungarica* **34:** 75-84.

Singh RV, AK Singh and SP Singh (1995) Progress of work under national centre on foliar diseases during 1994-95. Paper presented in 34[th] All India Wheat Research Workers' workshop, AICWIP, ICAR, UAS Dharwad, August 1995.

DW-1001 (INGR No. 04081; IC445070), Wheat (*Triticum durum* Desf.) Germplasm with Gamma Gliadin-45 Band

Bhudeva Singh Tyagi, Jag Shoran and RK Gupta
Directorate of Wheat Research, Karnal 132 001 (Haryana)

Durum wheat in India occupies more than 2 million ha area with the total production of 3.5 mt. However the end product quality of the varieties grown in India needs to be improved immediately. It is known that the presence or absence of low molecular weight glutenins (LMW-1 and LMW-2) are closely linked to Gamma-45 and Gamma-42 gliadins. To develop varieties with Gamma-45 gliadins, which have superior pasta quality,

* *Communicated by Dr. Anurudh Kumar Singh, Member Secretary, Plant Germplasm Registration Committee, National Bureau of Plant Genetic Resources, Indian Council of Agricultural Research, Pusa Campus, New Delhi*

Table 1. Mean yield of DW 1001

Year of Testing		DW 1001	*Checks*			C.D.
			PBW 34	WH 896	PDW 233	
Mean Yield (q/ha) National /Zonal	1st Year	48.9	–	–	43.0	2.8
	2nd Year	48.8	46.6	45.2	46.5	1.1
	3rd Year	53.3	52.3	50.9	51.9	1.0
	Mean	50.2	49.4	47.6	47.1	–

a program was initiated at the Directorate of Wheat Research, Karnal and DW 1001 with Gamma-45 gliadin, disease resistance and high yield was developed.

DW 1001 appeared 11/33 times in the first non-significant group of genotypes as compared to the checks PBW 34 (4/26 times) and PDW 233 (4/33 times). It showed better potential of producing more ears per unit area and ranked first in agronomic trials. It is also resistant to Karnal bunt. Some other salient features of DW 1001 are- presence of Gamma Gliadin-45 band, giving yield advantage of 2.3 q/ha over check (ranked first) at all levels of fertilizer doses, resistance to the most prevalent brown rust races 77-5 and 77-2 at adult plant stage, resistant to Karnal bunt, powdery mildew and foot rot diseases and high Beta-carotene (6.8 ppm), above international standards.

Morphologically, it has semi-erect growth habit with a height of 98 cm, dark green foliage, flowering in about 100 days and maturing in 144 days; ear are straw white coloured, tapering, dense, and amber grain with 47 g 1000-grain weight. It is also moderately resistant to leaf blight disease.

DBP-01-16 (INGR No. 04082; IC445071), Wheat (*Triticum durum* Desf.) Germplasm with High Beta-Carotene

Bhudeva Singh Tyagi, Jag Shoran and RK Gupta
Directorate of Wheat Research, Karnal 132 001 (Haryana)

India grows about 60 varieties of three species of wheat, namely *T. aestivum*, *T. durum* and *T. dicoccum* under different ecological conditions. For a good pasta product from durum wheat, high beta-carotene is a basic requirement. But in most Indian varieties the beta-carotene is very low (around 5-6 ppm). The Directorate of Wheat Research (DWR) has developed the genotype, DBP 01-16 with very high beta-carotene (9-10 ppm). This is a selection from cross, PBW 34 x DCB 25 produced at DWR, Karnal. The genotype is also better in protein content, grain size, height, heading days and yield than the best available varieties.

DBP 01-16 has plant height is 95 cm and leaves are green, waxy with medium width. It flowers in about 90 days, and matures in 140 days; ear are tapering and dense; grain amber, hard, angular with 1000-grain weight of 44g. It is resistant to all three rusts of wheat and leaf blight. The waxy nature of flag leaves and ears helps in performing better in hot and rain-fed conditions.

Table 1. Comparison of DBP 01-16 for beta-carotene and other traits with best checks

Characteristic	DBP01-16 (PBW34/DCB 25)	PBW 34 Check	PDW 233 Best check	Raj 1555 Check
Beta-carotene** (ppm)	9-10	4-4.6	6-6.7	4.3-4.8
Protein content*(%)	13.5	12.0	11.2	11.8
Thousand grain wt* (g)	44	45	44	45
Heading days*	90	92	95	89
Plant height*(cm)	95	95	97	95

* Mean values of the trait during last four years.
** Range values of the trait during last four years.

TL 2877 (INGR No. 04083; IC427816), Triticale (*Triticosecale*) Germplasm with Multiple Resistances to Pest and Diseases

GS Dhindsa, Indu Sharma, AS Grewal, SK Mann and GS Deol
Punjab Agricultural University, Ludhiana 141 005 (Punjab)

TL 2877 has amber grain and has shown multiple resistance to diseases, such as Karnal bunt, stem rust, yellow rust, brown rust, leaf blight, powdery mildew, flag smut and several pests, such as foliar aphid, wheat

Table 1. Mean yield of DW 1001

Year of Testing		DW 1001	*Checks*			C.D.
			PBW 34	WH 896	PDW 233	
Mean Yield (q/ha) National /Zonal	1st Year	48.9	–	–	43.0	2.8
	2nd Year	48.8	46.6	45.2	46.5	1.1
	3rd Year	53.3	52.3	50.9	51.9	1.0
	Mean	50.2	49.4	47.6	47.1	–

a program was initiated at the Directorate of Wheat Research, Karnal and DW 1001 with Gamma-45 gliadin, disease resistance and high yield was developed.

DW 1001 appeared 11/33 times in the first non-significant group of genotypes as compared to the checks PBW 34 (4/26 times) and PDW 233 (4/33 times). It showed better potential of producing more ears per unit area and ranked first in agronomic trials. It is also resistant to Karnal bunt. Some other salient features of DW 1001 are- presence of Gamma Gliadin-45 band, giving yield advantage of 2.3 q/ha over check (ranked first) at all levels of fertilizer doses, resistance to the most prevalent brown rust races 77-5 and 77-2 at adult plant stage, resistant to Karnal bunt, powdery mildew and foot rot diseases and high Beta-carotene (6.8 ppm), above international standards.

Morphologically, it has semi-erect growth habit with a height of 98 cm, dark green foliage, flowering in about 100 days and maturing in 144 days; ear are straw white coloured, tapering, dense, and amber grain with 47 g 1000-grain weight. It is also moderately resistant to leaf blight disease.

DBP-01-16 (INGR No. 04082; IC445071), Wheat (*Triticum durum* Desf.) Germplasm with High Beta-Carotene

Bhudeva Singh Tyagi, Jag Shoran and RK Gupta
Directorate of Wheat Research, Karnal 132 001 (Haryana)

India grows about 60 varieties of three species of wheat, namely *T. aestivum*, *T. durum* and *T. dicoccum* under different ecological conditions. For a good pasta product from durum wheat, high beta-carotene is a basic requirement. But in most Indian varieties the beta-carotene is very low (around 5-6 ppm). The Directorate of Wheat Research (DWR) has developed the genotype, DBP 01-16 with very high beta-carotene (9-10 ppm). This is a selection from cross, PBW 34 x DCB 25 produced at DWR, Karnal. The genotype is also better in protein content, grain size, height, heading days and yield than the best available varieties.

DBP 01-16 has plant height is 95 cm and leaves are green, waxy with medium width. It flowers in about 90 days, and matures in 140 days; ear are tapering and dense; grain amber, hard, angular with 1000-grain weight of 44g. It is resistant to all three rusts of wheat and leaf blight. The waxy nature of flag leaves and ears helps in performing better in hot and rain-fed conditions.

Table 1. Comparison of DBP 01-16 for beta-carotene and other traits with best checks

Characteristic	DBP01-16 (PBW34/DCB 25)	PBW 34 Check	PDW 233 Best check	Raj 1555 Check
Beta-carotene** (ppm)	9-10	4-4.6	6-6.7	4.3-4.8
Protein content*(%)	13.5	12.0	11.2	11.8
Thousand grain wt* (g)	44	45	44	45
Heading days*	90	92	95	89
Plant height*(cm)	95	95	97	95

* Mean values of the trait during last four years.
** Range values of the trait during last four years.

TL 2877 (INGR No. 04083; IC427816), Triticale (*Triticosecale*) Germplasm with Multiple Resistances to Pest and Diseases

GS Dhindsa, Indu Sharma, AS Grewal, SK Mann and GS Deol
Punjab Agricultural University, Ludhiana 141 005 (Punjab)

TL 2877 has amber grain and has shown multiple resistance to diseases, such as Karnal bunt, stem rust, yellow rust, brown rust, leaf blight, powdery mildew, flag smut and several pests, such as foliar aphid, wheat

Table 1. Mean yield of DW 1001

Year of Testing		DW 1001	*Checks*			C.D.
			PBW 34	WH 896	PDW 233	
Mean Yield (q/ha) National /Zonal	1st Year	48.9	–	–	43.0	2.8
	2nd Year	48.8	46.6	45.2	46.5	1.1
	3rd Year	53.3	52.3	50.9	51.9	1.0
	Mean	50.2	49.4	47.6	47.1	–

a program was initiated at the Directorate of Wheat Research, Karnal and DW 1001 with Gamma-45 gliadin, disease resistance and high yield was developed.

DW 1001 appeared 11/33 times in the first non-significant group of genotypes as compared to the checks PBW 34 (4/26 times) and PDW 233 (4/33 times). It showed better potential of producing more ears per unit area and ranked first in agronomic trials. It is also resistant to Karnal bunt. Some other salient features of DW 1001 are- presence of Gamma Gliadin-45 band, giving yield advantage of 2.3 q/ha over check (ranked first) at all levels of fertilizer doses, resistance to the most prevalent brown rust races 77-5 and 77-2 at adult plant stage, resistant to Karnal bunt, powdery mildew and foot rot diseases and high Beta-carotene (6.8 ppm), above international standards.

Morphologically, it has semi-erect growth habit with a height of 98 cm, dark green foliage, flowering in about 100 days and maturing in 144 days; ear are straw white coloured, tapering, dense, and amber grain with 47 g 1000-grain weight. It is also moderately resistant to leaf blight disease.

DBP-01-16 (INGR No. 04082; IC445071), Wheat (*Triticum durum* Desf.) Germplasm with High Beta-Carotene

Bhudeva Singh Tyagi, Jag Shoran and RK Gupta
Directorate of Wheat Research, Karnal 132 001 (Haryana)

India grows about 60 varieties of three species of wheat, namely *T. aestivum*, *T. durum* and *T. dicoccum* under different ecological conditions. For a good pasta product from durum wheat, high beta-carotene is a basic requirement. But in most Indian varieties the beta-carotene is very low (around 5-6 ppm). The Directorate of Wheat Research (DWR) has developed the genotype, DBP 01-16 with very high beta-carotene (9-10 ppm). This is a selection from cross, PBW 34 x DCB 25 produced at DWR, Karnal. The genotype is also better in protein content, grain size, height, heading days and yield than the best available varieties.

DBP 01-16 has plant height is 95 cm and leaves are green, waxy with medium width. It flowers in about 90 days, and matures in 140 days; ear are tapering and dense; grain amber, hard, angular with 1000-grain weight of 44g. It is resistant to all three rusts of wheat and leaf blight. The waxy nature of flag leaves and ears helps in performing better in hot and rain-fed conditions.

Table 1. Comparison of DBP 01-16 for beta-carotene and other traits with best checks

Characteristic	DBP01-16 (PBW34/DCB 25)	PBW 34 Check	PDW 233 Best check	Raj 1555 Check
Beta-carotene** (ppm)	9-10	4-4.6	6-6.7	4.3-4.8
Protein content*(%)	13.5	12.0	11.2	11.8
Thousand grain wt* (g)	44	45	44	45
Heading days*	90	92	95	89
Plant height*(cm)	95	95	97	95

* Mean values of the trait during last four years.
** Range values of the trait during last four years.

TL 2877 (INGR No. 04083; IC427816), Triticale (*Triticosecale*) Germplasm with Multiple Resistances to Pest and Diseases

GS Dhindsa, Indu Sharma, AS Grewal, SK Mann and GS Deol
Punjab Agricultural University, Ludhiana 141 005 (Punjab)

TL 2877 has amber grain and has shown multiple resistance to diseases, such as Karnal bunt, stem rust, yellow rust, brown rust, leaf blight, powdery mildew, flag smut and several pests, such as foliar aphid, wheat

Table 1. Reaction of TL 2877 to disease under AICW & BIP (1996-2003)

Year	Karnal bunt	Stem rust *South*	Leaf rust HS/ACI South	Leaf rust HS/ACI North	Stripe rust North	Leaf blight	Powdery mildew	Flag smut	AICW& BIP reports page number
1996-97	0	10R/0.3	20MR/1.4TMS	TMS/0.1	0	33-55	R (cultures 4,5,6,7)	–	15,50,58,89-90,123, 128,129
1999-00	1.2	0	0	0	0	23	2	0	118
2000-01	2.8	0	0	10S/1.5	0	36	5	0	104
2001-02	Moderately resistant to leaf blight; resistant to Karnal bunt, powdery mildew, flag smut								95
2002-03	0	0	TR	0	0	46	0	0	120

brown mite, shoot fly and root aphid in multi-location trials conducted under the All India Coordinated Wheat and Barley Improvement Programme (AICW & BP). These results have been summarised in Table 1 and 2.

Table 2. Reaction of TL2877 to pests under AICW & BIP (2001-2003)

Year	Foliar aphid (1-5 scale)	Brown wheat mite (Mite population/10 cm^2)	Shoot fly (%)	Root aphid (No.)
2000-01	5	4	11	1
2001-02	5 (2 at Pant Nagar)	15.60	6.71	2
2002-03	5	4.45	3.71	3

DT-18 (INGR No. 04084; IC427825), Triticale (*Triticosecale*) Germplasm with Multiple Tolerances to Wheat Pest and Diseases

Bhanwar Singh, SMS Tomar, Vinod and Rajendra Singh
Indian Agricultural Research Institute, New Delhi 110 012

Triticale line DT 18, with multiple tolerances to wheat pest and diseases, derived from the cross, TL 68 x DT 940 was developed through pedigree method in the Division of Genetics, Indian Agricultural Research Institute, New Delhi. It was identified mainly for resistance /tolerance to wheat brown mite.

In all India co-ordinated wheat trials the average yield of DT 18 under rain-fed conditions of northern hill zone was 24.8 q/ha, which was significantly higher over three control varieties, namely, CPAN 1796, Sonalika and TL 2656 (Triticale). In addition, it is resistant to foliar diseases like rusts, and powdery mildew, ideally suited for cultivation in northern hill zone, which has cooler climate and light soils. Breeding for genetic resistance to wheat brown mite, to mitigate yield losses is the best approach. DT 18 consistently exhibited lower mite incidence for ten successive years under natural infestation conditions in multi-location trials under the entomological nurseries (Anon.1989-1994). This genotype has potential for better grain yield over controls in the northern hilly zone. Therefore, it can serve, as a useful germplasm in triticale and wheat breeding programme for development of wheat mite resistant genotypes. It is likely that the resistance is imparted to mite by the full complement of R genome from *Secale cereale* in triticale.

Reference

Anonymous (1989-1994) DWR Progress Report from 1989 to 1994. Entomological and Pathological Nurseries.

Table 1. Reaction of TL 2877 to disease under AICW & BIP (1996-2003)

Year	Karnal bunt	Stem rust *South*	Leaf rust HS/ACI South	Leaf rust HS/ACI North	Stripe rust North	Leaf blight	Powdery mildew	Flag smut	AICW& BIP reports page number
1996-97	0	10R/0.3	20MR/1.4TMS	TMS/0.1	0	33-55	R (cultures 4,5,6,7)	–	15,50,58,89-90,123, 128,129
1999-00	1.2	0	0	0	0	23	2	0	118
2000-01	2.8	0	0	10S/1.5	0	36	5	0	104
2001-02	Moderately resistant to leaf blight; resistant to Karnal bunt, powdery mildew, flag smut								95
2002-03	0	0	TR	0	0	46	0	0	120

brown mite, shoot fly and root aphid in multi-location trials conducted under the All India Coordinated Wheat and Barley Improvement Programme (AICW & BP). These results have been summarised in Table 1 and 2.

Table 2. Reaction of TL2877 to pests under AICW & BIP (2001-2003)

Year	Foliar aphid (1-5 scale)	Brown wheat mite (Mite population/10 cm^2)	Shoot fly (%)	Root aphid (No.)
2000-01	5	4	11	1
2001-02	5 (2 at Pant Nagar)	15.60	6.71	2
2002-03	5	4.45	3.71	3

DT-18 (INGR No. 04084; IC427825), Triticale (*Triticosecale*) Germplasm with Multiple Tolerances to Wheat Pest and Diseases

Bhanwar Singh, SMS Tomar, Vinod and Rajendra Singh
Indian Agricultural Research Institute, New Delhi 110 012

Triticale line DT 18, with multiple tolerances to wheat pest and diseases, derived from the cross, TL 68 x DT 940 was developed through pedigree method in the Division of Genetics, Indian Agricultural Research Institute, New Delhi. It was identified mainly for resistance /tolerance to wheat brown mite.

In all India co-ordinated wheat trials the average yield of DT 18 under rain-fed conditions of northern hill zone was 24.8 q/ha, which was significantly higher over three control varieties, namely, CPAN 1796, Sonalika and TL 2656 (Triticale). In addition, it is resistant to foliar diseases like rusts, and powdery mildew, ideally suited for cultivation in northern hill zone, which has cooler climate and light soils. Breeding for genetic resistance to wheat brown mite, to mitigate yield losses is the best approach. DT 18 consistently exhibited lower mite incidence for ten successive years under natural infestation conditions in multi-location trials under the entomological nurseries (Anon.1989-1994). This genotype has potential for better grain yield over controls in the northern hilly zone. Therefore, it can serve, as a useful germplasm in triticale and wheat breeding programme for development of wheat mite resistant genotypes. It is likely that the resistance is imparted to mite by the full complement of R genome from *Secale cereale* in triticale.

Reference

Anonymous (1989-1994) DWR Progress Report from 1989 to 1994. Entomological and Pathological Nurseries.

Maize (*Zea mays* L.) Inbred Line With Resistance To Post Flowering Stock Rots

S Shankar Lingam and R Vidyasagar
Agricultural Research Station, Acharya NG Ranga Agricultural University, Amberpet, Hyderabad 500 013 (Andhra Pradesh)

BPPTI 32 (INGR No. 04085; IC396385)

Post Flowering Stalk Rot (PFSR) caused by a complex, comprising three fungi, namely, *Cephalosporium acremonium, Macrophomina phaseolina, Fusarium moniliforme* and one bacterium *Erwinia carotovora* var. *zeae* causes severe yield losses in India. BPTTI 32 is a new inbred line resistant to PFSR, derived from the resistant pool synthesized through full-sib recurrent selection method, adopted for improving this pool prior to derivation of the inbred lines by the standard ear-to-row method. Inbreeding was carried out with toothpick screening method in PFSR sick plot, *i.e.* selfing accompanied by toothpick inoculation with the causal organisms. The PFSR resistant pool included resistant hybrids, composite varieties and synthetics evaluated under All India Co-ordinated Maize Improvement Trials. It has better general combining ability compared to other sister inbred lines. Table 1 presents the morpho-agronomic characteristics of inbred lines BPTTI 32.

BPTTI 32 has semi-open tassel with light purple silk and produce orange yellow seed. The PFSR disease rating of 2.1 classifies this inbred line as highly resistant to this disease.

BPPTI 34 (INGR No. 04086; IC396387)

Post Flowering Stalk Rot (PFSR) caused by a complex, comprising three fungi, namely, *Cephalosporium acremonium, Macrophomina phaseolina, Fusarium moniliforme* and one bacterium *Erwinia carotovora* var. *zeae* causes severe yield losses in India. BPTTI 34 is a new inbred line resistant to PFSR, derived from the resistant pool synthesized through full-sib recurrent selection method, adopted for improving this pool prior to derivation of the inbred lines by the standard ear-to-row method. Inbreeding was carried out with toothpick screening in PFSR sick plot, i.e. selfing accompanied by toothpick inoculation with causal organisms. The PFSR resistant pool included resistant hybrids, composite varieties and synthetics evaluated under All India Co-ordinated Maize Improvement Trials. It has bold grains compared to other sister inbred lines. Table 2 presents the morpho-agronomic characteristics of inbred line BPTTI 34.

BPTTI 34 has open tassel with silk colour light purple and orange seeded. The PFSR disease rating of 2.4 classifies this inbred line as highly resistant to this disease.

Table 1. Morpho-agronomic characteristics of inbred line BPTTI 32**

Inbred Genotype	Days to silk	Pl. ht. (cm)	E.H. (cm)	E.L. (cm)	E.G (cm)	Kernel Rows/ear	Kernel/ row	100-kernel wt. (g)	Disease score*(1-9)
BPPTI 32-1-1-2-2-1-1 bulk	70(R)	126	35	9	10	14	14	18.5	2.1

*1=healthy, 9=highly susceptible: Disease rating of 5 and below is resistant
** Payak (1993)

Table 2. Morpho-agronomic characteristics of inbred line BPTTI 34**

Inbred Genotype	Days to silk	Pl. ht. (cm)	E.H. (cm)	E.L. (cm)	E.G (cm)	Kernel (rows/ear)	Kernel/ row	100-kernel wt. (g)	Disease score* (1-9)
BPPTI 34-1-2-1-1-1-2-bulk	70(R)	116	45	8	9	10	16	30	2.4

*1=healthy, 9=highly susceptible: Disease rating of 5 and below is resistant
** Payak (1993)

Reference

Payak, MM (1983) "Premature Drying in Maize" bulletin on "Techniques of Scoring for Resistance to Important Diseases of Maize". All India Co-ordinated Maize Improvement Project, New Delhi, 96-100.

Reference

Payak, MM (1983) "Premature Drying in Maize" bulletin on "Techniques of Scoring for Resistance to Important Diseases of Maize". All India Co-ordinated Maize Improvement Project, New Delhi, 96-100.

BML-6 (INGR No. 04119; IC 411282), Maize (*Zea mays* L.) Inbred Line with Maydis Leaf Blight, Turcicum Leaf Blight and Sorghum Downy Mildew Disease Tolerance and Good Combining Ability

Sai Kumar Ramanujam, E Satyanarayana, P Shanthi, P Mary Rekha, S Ravindra Babu and B Srinivas
Agricultural Research Station, Acharya NG Ranga Agricultural University, Amberpet, Hyderabad 500 013 (Andhra Pradesh)

This maize inbred line was derived through pedigree selection from stalk rot resistant germplasm, screened at the pathology section of the Agricultural Research Station, Acharya NG Ranga Agricultural University, Amberpet, Hyderabad, through modification and improvement method by introgressing a series of elite materials and through the adoption of restricted pollination coupled with pedigree selection. It has anthocyanin pigmentation on leaf sheath, husk cover and culm. It is good both as female and male parent. Presence of specific purple colour dot at the tip of the glumes of the tassel is a typical characteristic. Plants are tall and sturdy with drooping medium side branches, tassel is of medium size, loose and green glumes and silk, husk tip cover is medium green. Cob is cylindrical and rigid, tip filled, straight row, yellow orange flint, slight dent, white. It is tolerant to Maydis leaf blight, Turcicum leaf blight and sorghum downy mildew disease and has good combining ability.

HKI-1332 (INGR No. 04120; IC 408329), Maize (*Zea mays* L.) Inbred Line with Dark Green Erect Leaves and Medium Maturity

Sain Dass, Kulbir Singh Dhanju and Pawan Arora
Regional Station Uchani, Chaudhary Charan Singh Haryana Agricultural University, Karnal 132 001 (Haryana)

HKI-1332 is a medium maturing, productive line developed at the Chaudhary Charan Singh Haryana Agricultural University, Regional Research Station, Uchani, Karnal. The line is derived from Pool-32, CIMMYT, Mexico through selection and continuous selfing.

The important characters of the line are early to medium maturity, medium height (100-115 cm in *Kharif* and 65-70 cm in *Rabi*) sturdy, leaf broad, erect, dark green; stem green; tassel medium, erect with few secondary branches; anther green; glumes green; silk green; husk cover green and tight; ear cylindrical, medium (10.5-12.5 cm in different seasons), white heart, grain up to tip, irregular kernel rows; grain flint, light orange, round and medium bold. It takes 49-51 days and 129-130 days to 50 percent tasselling and 51-54 and 132-133 days to silking in *Kharif* and *Rabi* season, respectively. It yielded 22-25 q/ha in different seasons.

The line is responsive to high doses of fertilizer, productive and has wider adaptability, therefore can be utilized in breeding programme in both the season. It is a good general combiner both as seed parent and pollinator. Three years data revealed that the line is resistant to maydis leaf blight [(*Drechslera maydis* Nisik.) Subram and Jain] with a score of 2.0 to 3.5 (Table 1).

Table 1. Disease reaction of HKI-1332 against maydis leaf light under artificial inoculation conditions

Season-*Kharif*	HKI-1332	CM-600 (check)
2000	2.0	4.5
2001	2.0	4.5
2002	3.5	5.0
2003	2.5	5.0
Mean	2.5	4.7

References

Annual Report (1999-2001) Description of HAU Maize inbred lines, Directorate of Maize Research, Cummings Laboratory, Pusa Campus, New Delhi. pp 102-104

BML-6 (INGR No. 04119; IC 411282), Maize (*Zea mays* L.) Inbred Line with Maydis Leaf Blight, Turcicum Leaf Blight and Sorghum Downy Mildew Disease Tolerance and Good Combining Ability

Sai Kumar Ramanujam, E Satyanarayana, P Shanthi, P Mary Rekha, S Ravindra Babu and B Srinivas
Agricultural Research Station, Acharya NG Ranga Agricultural University, Amberpet, Hyderabad 500 013 (Andhra Pradesh)

This maize inbred line was derived through pedigree selection from stalk rot resistant germplasm, screened at the pathology section of the Agricultural Research Station, Acharya NG Ranga Agricultural University, Amberpet, Hyderabad, through modification and improvement method by introgressing a series of elite materials and through the adoption of restricted pollination coupled with pedigree selection. It has anthocyanin pigmentation on leaf sheath, husk cover and culm. It is good both as female and male parent. Presence of specific purple colour dot at the tip of the glumes of the tassel is a typical characteristic. Plants are tall and sturdy with drooping medium side branches, tassel is of medium size, loose and green glumes and silk, husk tip cover is medium green. Cob is cylindrical and rigid, tip filled, straight row, yellow orange flint, slight dent, white. It is tolerant to Maydis leaf blight, Turcicum leaf blight and sorghum downy mildew disease and has good combining ability.

HKI-1332 (INGR No. 04120; IC 408329), Maize (*Zea mays* L.) Inbred Line with Dark Green Erect Leaves and Medium Maturity

Sain Dass, Kulbir Singh Dhanju and Pawan Arora
Regional Station Uchani, Chaudhary Charan Singh Haryana Agricultural University, Karnal 132 001 (Haryana)

HKI-1332 is a medium maturing, productive line developed at the Chaudhary Charan Singh Haryana Agricultural University, Regional Research Station, Uchani, Karnal. The line is derived from Pool-32, CIMMYT, Mexico through selection and continuous selfing.

The important characters of the line are early to medium maturity, medium height (100-115 cm in *Kharif* and 65-70 cm in *Rabi*) sturdy, leaf broad, erect, dark green; stem green; tassel medium, erect with few secondary branches; anther green; glumes green; silk green; husk cover green and tight; ear cylindrical, medium (10.5-12.5 cm in different seasons), white heart, grain up to tip, irregular kernel rows; grain flint, light orange, round and medium bold. It takes 49-51 days and 129-130 days to 50 percent tasselling and 51-54 and 132-133 days to silking in *Kharif* and *Rabi* season, respectively. It yielded 22-25 q/ha in different seasons.

The line is responsive to high doses of fertilizer, productive and has wider adaptability, therefore can be utilized in breeding programme in both the season. It is a good general combiner both as seed parent and pollinator. Three years data revealed that the line is resistant to maydis leaf blight [(*Drechslera maydis* Nisik.) Subram and Jain] with a score of 2.0 to 3.5 (Table 1).

Table 1. Disease reaction of HKI-1332 against maydis leaf light under artificial inoculation conditions

Season-*Kharif*	HKI-1332	CM-600 (check)
2000	2.0	4.5
2001	2.0	4.5
2002	3.5	5.0
2003	2.5	5.0
Mean	2.5	4.7

References

Annual Report (1999-2001) Description of HAU Maize inbred lines, Directorate of Maize Research, Cummings Laboratory, Pusa Campus, New Delhi. pp 102-104

Barley (*Hordeum Vulgare* Cv. Distichon) Germplasm with Better Malting Quality

RPS Verma, B Sarkar and Sewa Ram
Directorate of Wheat Research, PB No. 158, Agrasain Marg, Karnal 132001

DWR37 (INGR No. 04087; IC443610)

DWR37 is a two-row better malting quality barley line developed through pedigree selection method of breeding at the Directorate of Wheat Research (DWR), Karnal. It was developed through hybridisation between two-row exotic barley varieties "Clipper" and six-row variety PL172, released in Punjab. The new genotype expressed very good malting quality with better individual values for low husk (9.9%) and low beta glucan (4.47%) content in the grain under the All India Coordinated Wheat and Barley Improvement Programme (AICW&BIP) Barley Network trials (Table 1). DWR37 has erect growth habit, medium plant height (93 cm), medium maturity duration, narrow erect green leaves, parallel ear with intermediate spike density, light yellow ear and awn at maturity. It has hard grain with bold size and oval shape, having average 30 grains/spike and is resistant to yellow rust (ACI 4.0) and leaf blight (DD score 12). It can be utilized as a source for improving malting quality.

DWR38 (INGR No. 04088; IC443611)

DWR38 is a new two-row genotype with better malting quality, especially high hectolitre weight (68 Kg/hl) (Table 2). This genotype was developed through hybridisation in a three way cross involving, BCU73, DL88 and Clipper followed by pedigree selection method. It is an erect plant type with medium height (88 cm), green foliage and waxy leaf sheath and ear. It flowers in 85-90 days and has intermediate ear density with 32-34 grains/ ear. The grains are light yellow oval shaped having mean thousand-grain weight of 50 g. This genotype is also resistant to leaf blight (12), and yellow rust (ACI 4.1). DWR38 can be used as a source of better grain quality (hectolitre weight), in breeding programme for development of superior malt quality barley.

DWR39 (INGR No. 04089; IC443612)

DWR39 is a better source for very important malting quality traits with low grain beta glucan content (4.29%) and low wort viscosity (1.454 m pas). This genotype was developed by three way cross involving BCU73, PL172 and ALFA93 followed by pedigree selection. BCU 73 and ALF 93 are two-row exotic varieties released in India as malt barley variety, PL 172 is a six-row feed barley variety released by PAU, Ludhiana. DWR39 is two-row barley and posses' high level of resistance against leaf blight. It has erect growth habit with green foliage at vegetative stage and usually takes 75–78 days to flower and is early in maturity. Flag leaf, leaf sheath and ear are non-waxy. The number of grains/ spike varies from 28–30. The grains are bold, oval shaped with 47 g. 1000-grain weight. The performance of quality attributes (beta glucan and wort viscosity) in comparison to the check DWR28 are given in Table 3.

Table 1. Quality traits of DWR37 and check (DWR28) in NWPZ*

Traits	DWR37			DWR28(check)		
	2000-01	2001-02	**Mean**	2000-01	2001-02	**Mean**
Husk (%)	10.50	9.30	**9.90**	11.50	10.30	**10.90**
Beta glucan content (%)	4.72	4.22	**4.47**	5.57	5.52	**5.55**

* = Mean values of two locations in 2000-01 and three locations in 2001-02

Table 2. Quality traits of DWR38 (Barley Network Nurseries/ Trials)

Traits	DWR38 (BK9907)			BCU73** /DWR28(C)		
	99-00*	00-01	Mean	99-00*	00-01	Mean
Hectolitre Weight (Kg/ hl)	68	68	68	66	61	63.5

* Malt Barley Observation Nursery (MBON) data for the year 1999-00
** Check BCU73 was used, as DWR28 was included later on in the trials as check.

Table 3. Quality traits of DWR39 and check (DWR28) in NWPZ*

Traits	DWR39			DWR28 (C)		
	00-01	01-02	Mean	00-01	01-02	Mean
Beta glucan content (%)	4.33	4.25	**4.29**	5.57	5.52	**5.545**
Wort Viscosity (m pas)	1.472	1.436	**1.454**	1.610	1.663	**1.6365**

* = Mean values of two locations in 2000-01 and three locations in 2001-02

Barley Genotypes with Resistance to Yellow Rust and Leaf Blight

RPS Verma, B Sarkar and DP Singh
Directorate of Wheat Research, PB No. 158, Agrasain Marg, Karnal 132 001 (Haryana)

DWR44 (INGR No. 04090; IC 443613)

DWR 44 is a two-row barley genotype highly resistant against yellow rust both at seedling and adult plant stages. It is resistant (at seedling stage) against all the races of yellow rust prevalent in India and complete resistance at adult plant stage at a number of hot spot locations under barley network testing of All India Coordinated Wheat and Barley Improvement Programme (Table 1). It was developed through hybridisation between two-row barley varieties Clipper with six-row variety BH 75, followed by pedigree method of selection. It is erect in growth habit, with plant height of 95 cm with medium maturity duration. The ear colour at maturity is light yellow, parallel in shape with 24-26-grains/spike. The grains are medium bold in size and elongated in shape with 46 g. 1000-grain weight. It can function as an important source of resistance against yellow rust (Table 1).

Table 1. Reaction of DWR44 to yellow (stripe) rust in coordinated disease screening nurseries

Year	SRT[1]			APR[2]
	Yellow	Brown	Black	Yellow
2000-01*	–	–	–	5MS(2.0)
2001-02	Resistant to all	Resistant to all	Resistant to all	00 (0.0)

* =tested as BK019 in MBON disease screening nursery during 2000-01 and as DWR44 in national barley diseases screening nursery (NBDSN) during 2001-02

1. Seedling resistance test against individual pathotypes of yellow, brown and black rusts
2. Reaction in plant pathological nurseries under artificial screening at hot spot locations

DWR47 (INGR No. 04091; IC 443614)

DWR 47 is barley genotype resistant against leaf blight in the two-row barley background. It was developed through hybridisation between two-row and six-row varieties, Clipper and K 508, followed by pedigree selection. The genotype has erect growth habit with medium tall plant and late in maturity. Number of grain/spike varies from 28-30 with 49 g. 1000-grain weight. Grain colour is yellow, medium bold and elongated in shape. This genotype showed minimum reaction to leaf blight amongst 112 entries tested under NBDSN at six hot spot locations (Table 1) under AICW&BIP. Most genotypes tested in the hot spot locations are susceptible to leaf blights, therefore DWR 47 can be used as source in breeding for leaf blight resistance.

Table 2: Reaction of DWR47 to leaf blight in coordinated disease screening nurseries

Year	Highest score	
	DWR47	Check
2001-02*	01	45
2002-03**	24	99

(The reactions up to 35 on double-digit system (reaction on the flag and next to flag leaf) are considered as resistant.) * = IBRSN data (BK104= DWR47); ** = NBDSN data

JCR/TRS-510 (INGR No. 04093; IC258253), Chenopod (*Chenopodium album* L.) Germplasm with Brown Seeds

JC Rana[1], VD Verma[1], K Pradheep[1] and TR Sharma[2]
1. National Bureau of Plant Genetic Resources, Regional Station, Shimla 171 004 Himachal Pradesh
2. Centre of Hill Bioresources and Biotechnology, CSK HP Krishi Vishwavidyalaya, Palampur 176 062, Himachal Pradesh.

The chenopod is extensively used as leafy vegetable in the hills and plains. However, the cultivation is decreasing because of low yield, seed shattering, small seed size and black seed colour. Generally, Chenopodium album seed is black in colour. The germplasm accession, 'IC258253' collected from Pangi subdivision of Chamba district in Himachal Pradesh was found to have brown seed colour. This is the only accession with brown seed among more than 100 accessions maintained at the station. Chenopod is generally consumed either as unleavened bread or flour mixed with wheat flour. Occasionally whole grain is cooked with rice. The black

Barley Genotypes with Resistance to Yellow Rust and Leaf Blight

RPS Verma, B Sarkar and DP Singh
Directorate of Wheat Research, PB No. 158, Agrasain Marg, Karnal 132 001 (Haryana)

DWR44 (INGR No. 04090; IC 443613)

DWR 44 is a two-row barley genotype highly resistant against yellow rust both at seedling and adult plant stages. It is resistant (at seedling stage) against all the races of yellow rust prevalent in India and complete resistance at adult plant stage at a number of hot spot locations under barley network testing of All India Coordinated Wheat and Barley Improvement Programme (Table 1). It was developed through hybridisation between two-row barley varieties Clipper with six-row variety BH 75, followed by pedigree method of selection. It is erect in growth habit, with plant height of 95 cm with medium maturity duration. The ear colour at maturity is light yellow, parallel in shape with 24-26-grains/spike. The grains are medium bold in size and elongated in shape with 46 g. 1000-grain weight. It can function as an important source of resistance against yellow rust (Table 1).

Table 1. Reaction of DWR44 to yellow (stripe) rust in coordinated disease screening nurseries

Year	SRT[1]			APR[2]
	Yellow	Brown	Black	Yellow
2000-01*	–	–	–	5MS(2.0)
2001-02	Resistant to all	Resistant to all	Resistant to all	00 (0.0)

* =tested as BK019 in MBON disease screening nursery during 2000-01 and as DWR44 in national barley diseases screening nursery (NBDSN) during 2001-02

1. Seedling resistance test against individual pathotypes of yellow, brown and black rusts
2. Reaction in plant pathological nurseries under artificial screening at hot spot locations

DWR47 (INGR No. 04091; IC 443614)

DWR 47 is barley genotype resistant against leaf blight in the two-row barley background. It was developed through hybridisation between two-row and six-row varieties, Clipper and K 508, followed by pedigree selection. The genotype has erect growth habit with medium tall plant and late in maturity. Number of grain/spike varies from 28-30 with 49 g. 1000-grain weight. Grain colour is yellow, medium bold and elongated in shape. This genotype showed minimum reaction to leaf blight amongst 112 entries tested under NBDSN at six hot spot locations (Table 1) under AICW&BIP. Most genotypes tested in the hot spot locations are susceptible to leaf blights, therefore DWR 47 can be used as source in breeding for leaf blight resistance.

Table 2: Reaction of DWR47 to leaf blight in coordinated disease screening nurseries

Year	Highest score	
	DWR47	Check
2001-02*	01	45
2002-03**	24	99

(The reactions up to 35 on double-digit system (reaction on the flag and next to flag leaf) are considered as resistant.) * = IBRSN data (BK104= DWR47); ** = NBDSN data

JCR/TRS-510 (INGR No. 04093; IC258253), Chenopod (*Chenopodium album* L.) Germplasm with Brown Seeds

JC Rana[1], VD Verma[1], K Pradheep[1] and TR Sharma[2]
1. National Bureau of Plant Genetic Resources, Regional Station, Shimla 171 004 Himachal Pradesh
2. Centre of Hill Bioresources and Biotechnology, CSK HP Krishi Vishwavidyalaya, Palampur 176 062, Himachal Pradesh.

The chenopod is extensively used as leafy vegetable in the hills and plains. However, the cultivation is decreasing because of low yield, seed shattering, small seed size and black seed colour. Generally, Chenopodium album seed is black in colour. The germplasm accession, 'IC258253' collected from Pangi subdivision of Chamba district in Himachal Pradesh was found to have brown seed colour. This is the only accession with brown seed among more than 100 accessions maintained at the station. Chenopod is generally consumed either as unleavened bread or flour mixed with wheat flour. Occasionally whole grain is cooked with rice. The black

colour of seed is not preferred, as it gives black flour and releases black seed coat when cooked with rice. Therefore, brown or white seed colours are preferred. Hence, germplasm with brown or white seed colour can help increase area under cultivation. JCR/TRS-510 is high yielding with medium plant height, a desirable attribute and was therefore, included in the trials of AICRP on UC in 2004. Table 1 lists the characteristic features.

Table 1. Characteristic features of IC329457

Characters	Mean	Characters	Mean
Plant height (cm)	182.60	1000 seed wt. (g)	0.59
Leaf length (cm)	6.85	Seed yield/plant (g)	23.46
Leaf width (cm)	3.00	Early plant vigour	Very Good
No. of primary branches	7.00	Leaf shape	Ovate to lanceolate
Inflorescence length	36.7	Stem colour	Red
Petiole length	2.6	Seed shedding	Moderate
Days to 50% flowering	89	Stem branching	Very good
Days to 80% maturity	133	Seed shape	Round
Average seed length (mm)	1.28	Seed colour	Brown
Average seed thickness (mm)	0.66	Inflorescence colour	Pink
Average seed diameter (mm)	1.24	Inflorescence shape	Globose

1409A &B (INGR No. 04094; IC432861 and IC432862), Sorghum (*Sorghum bicolor* L.) Germplasm with Cytoplasmic Male Sterility

BN Narkhede[1], JV Patil[1], SB Chaudhary[1], SB Wandhekar[1], VM Kulkarni[1], BB Thombare[1], MS Shinde, UG Kachole and BK Katule[2]

1. *Mahatma Phule Krishi Vidyapeeth, Rahuri 413 722 (Maharashtra)*
2. *Agricultural Research Station, Solapur (Maharashtra)*

1409A is a male sterile line with *Rabi* base, possessing a plant type of early maturity and medium height, resistance to shoot-fly and charcoal rot, high yielding with good grain and fodder characters. The plant material for the present programme consisted of three tropical 'B' lines viz., 42B, 104 B and 116 B and four temperate 'B' lines ICSB 52B, 85 B, ICSB 36209 and 88010 B. The crossings of three tropical 'B' lines with each of four temperate 'B' lines were made by hand emasculation and pollination. The resulting 12 hybrids were evaluated during *Rabi* 1995 in medium black soils under the Sorghum Improvement Project at Rahuri in rain-fed conditions. The segregating generation of F_2 and onward were advanced by planting in off-season, and simultaneously backcrossing was carried out by selecting desirable segregants. At F_3 generation, 16 individual plant selections from the cross, 104 B x ICSB 36209 were grown and evaluated. Subsequently at BC_4 and BC_5 generations the promising lines were isolated on the basis of sterility performance and photo-insensitiveness. Counter part of this 'B' line nicks well. The morphological characteristics of newly developed CMS 1409 A, are listed below in Table 1.

Table 1. Characteristic features of CMS 1409 A

Characters	Value
Pedigree	104 B x ICSB 36209
Plant height (cm)	145-150
Days to 50 % flowering	62-68
Days to maturity	108-110
Plant pigmentation	Non-tan
Mid rib colour	White
Leaf colour	Dark green
Internodes cover	Full
Panicle compactness	Semi-compact, long ear-head
Glumes colour	Yellowish
Glumes covering	¼ covering
Threshability	Easy
Awn	Awned
Seed colour and shape	Pearly white and round
Test weight (g)	30
Grain yield (kg/ha)	1500-1800
Resistance to shoot-fly	Tolerant

colour of seed is not preferred, as it gives black flour and releases black seed coat when cooked with rice. Therefore, brown or white seed colours are preferred. Hence, germplasm with brown or white seed colour can help increase area under cultivation. JCR/TRS-510 is high yielding with medium plant height, a desirable attribute and was therefore, included in the trials of AICRP on UC in 2004. Table 1 lists the characteristic features.

Table 1. Characteristic features of IC329457

Characters	Mean	Characters	Mean
Plant height (cm)	182.60	1000 seed wt. (g)	0.59
Leaf length (cm)	6.85	Seed yield/plant (g)	23.46
Leaf width (cm)	3.00	Early plant vigour	Very Good
No. of primary branches	7.00	Leaf shape	Ovate to lanceolate
Inflorescence length	36.7	Stem colour	Red
Petiole length	2.6	Seed shedding	Moderate
Days to 50% flowering	89	Stem branching	Very good
Days to 80% maturity	133	Seed shape	Round
Average seed length (mm)	1.28	Seed colour	Brown
Average seed thickness (mm)	0.66	Inflorescence colour	Pink
Average seed diameter (mm)	1.24	Inflorescence shape	Globose

1409A &B (INGR No. 04094; IC432861 and IC432862), Sorghum (*Sorghum bicolor* L.) Germplasm with Cytoplasmic Male Sterility

BN Narkhede[1], JV Patil[1], SB Chaudhary[1], SB Wandhekar[1], VM Kulkarni[1], BB Thombare[1], MS Shinde, UG Kachole and BK Katule[2]

1. *Mahatma Phule Krishi Vidyapeeth, Rahuri 413 722 (Maharashtra)*
2. *Agricultural Research Station, Solapur (Maharashtra)*

1409A is a male sterile line with *Rabi* base, possessing a plant type of early maturity and medium height, resistance to shoot-fly and charcoal rot, high yielding with good grain and fodder characters. The plant material for the present programme consisted of three tropical 'B' lines viz., 42B, 104 B and 116 B and four temperate 'B' lines ICSB 52B, 85 B, ICSB 36209 and 88010 B. The crossings of three tropical 'B' lines with each of four temperate 'B' lines were made by hand emasculation and pollination. The resulting 12 hybrids were evaluated during *Rabi* 1995 in medium black soils under the Sorghum Improvement Project at Rahuri in rain-fed conditions. The segregating generation of F_2 and onward were advanced by planting in off-season, and simultaneously backcrossing was carried out by selecting desirable segregants. At F_3 generation, 16 individual plant selections from the cross, 104 B x ICSB 36209 were grown and evaluated. Subsequently at BC_4 and BC_5 generations the promising lines were isolated on the basis of sterility performance and photo-insensitiveness. Counter part of this 'B' line nicks well. The morphological characteristics of newly developed CMS 1409 A, are listed below in Table 1.

Table 1. Characteristic features of CMS 1409 A

Characters	Value
Pedigree	104 B x ICSB 36209
Plant height (cm)	145-150
Days to 50 % flowering	62-68
Days to maturity	108-110
Plant pigmentation	Non-tan
Mid rib colour	White
Leaf colour	Dark green
Internodes cover	Full
Panicle compactness	Semi-compact, long ear-head
Glumes colour	Yellowish
Glumes covering	¼ covering
Threshability	Easy
Awn	Awned
Seed colour and shape	Pearly white and round
Test weight (g)	30
Grain yield (kg/ha)	1500-1800
Resistance to shoot-fly	Tolerant

RMM-12 (INGR No. 04095; IC432859), Moth Bean [*Vigna aconitifolia* (Jacq) Marechal] Germplasm with Single Stem and Early Maturity

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

Moth bean (*Vigna aconitifolia* Jacq. Marechal) is one of the favoured crops of arid zone. The un-branched mutant RMM-12, having cluster of pods at the main stem was isolated in M_2 generation (1997) from seeds irradiated with 30 kR at the Central Arid Zone Research Institute, Jodhpur. It was stabilized through M_3 and M_4 generations and evaluated for various traits. The distinguishing features of the mutant are, its upright, straight growth habit having only main stem and complete lack of branches. In a replicated yield trial during *Kharif* 2001 (327.6 mm rainfall through 15 days), this mutant yielded 600 kg ha^{-1}, registering 24.1% yield increase over the parental variety. Probably, it was due to high harvest index and synchronous maturity suited for mechanical harvesting. The erect habit makes it suitable for inter cropping and mix cropping.

During *Kharif* 1999, nutrient movements of this mutant were compared with some of the genotypes at the critical growth period following Roemer and Schenk (1998) method. The mutant showed maximum influx of Na ions to the tune of 0.14 mol/ cm root/ second x 10^{-15}, whereas other genotypes barring RMO-257 showed the influx of Na ions in range of 0.07 to 0.10 mol/ cm root/ second x 10^{-15} (Kumar *et al.* 2001). Higher influx or uptake rate of Na ions may contribute to salt tolerance potential. However, further studies are required on genetics of branching habits, salt tolerance and to evaluate its performance under intercropping and mix cropping systems.

References

Roemer W and Schenk H (1998) Influence of genotype on phosphate uptake and utilization efficiencies in spring barley. *European Journal of Agronomy* **8**: 215-224.

Kumar D and Tarafdar JC (2001) Genotypic differences for nutrient influx in moth bean under rain-fed conditions. In: *Diamond Jubilee Symposium on Hundred Years of Post-Mendelian Genetics and Plant Breeding- Retrospect and Prospects*, 6-9 November 2001, New Delhi, Abst No. VS VI-61, pp 191.

Imparipinnate Mutant (INGR No. 04097; IC 323372), Groundnut (*Arachis hypogaea* L.) Germplasm with Imparipinnate Leaves and Small Leaflet

SH Patil
Bhabha Atomic Research Centre, Trombay, Mumbai 400 085 (Maharashtra)

Many mutants induced by X-rays were produced in groundnut at the Bhabha Atomic Research Centre, Trombay (Patil, 1966). Of the several mutants generated under this programme there was a mutant with imparipinnate leaves. It has as many as eight accessory leaflets unlike two in the parent. About 25 percent of the leaves were imparipinnate and had smaller leaflets. Occasionally, funnel shaped leaflets were also observed. The height of the mutant and its sibs was shorter than the parents. It has smaller pods with shallow constrictions and prominent beak. Kernel colour was fleshy unlike rosy in the control/ parents.

Genetic studies showed a wide range of phenotypic ratios (3:1 to 40:1) with an average of 6.5:1. The genotypic segregation over 200 progenies indicated an apparent preferential segregation for dominant type that is 109:101:30. According to Cadman (1942) 50 percent of the non-segregants are expected in duplex progeny. Occasional reversions to heterozygous states have been observed in one to two mutant progenies

References

Cadman CH (1942) Autotetraploid inheritance in the potato: some new evidence. *J Genet* **44**: 33-52.

Patil SH (1966) Mutation induced in groundnut by X-rays. In: *Symposium on Impact of Mandelism* p 334-348.

RMM-12 (INGR No. 04095; IC432859), Moth Bean [*Vigna aconitifolia* (Jacq) Marechal] Germplasm with Single Stem and Early Maturity

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

Moth bean (*Vigna aconitifolia* Jacq. Marechal) is one of the favoured crops of arid zone. The un-branched mutant RMM-12, having cluster of pods at the main stem was isolated in M_2 generation (1997) from seeds irradiated with 30 kR at the Central Arid Zone Research Institute, Jodhpur. It was stabilized through M_3 and M_4 generations and evaluated for various traits. The distinguishing features of the mutant are, its upright, straight growth habit having only main stem and complete lack of branches. In a replicated yield trial during *Kharif* 2001 (327.6 mm rainfall through 15 days), this mutant yielded 600 kg ha^{-1}, registering 24.1% yield increase over the parental variety. Probably, it was due to high harvest index and synchronous maturity suited for mechanical harvesting. The erect habit makes it suitable for inter cropping and mix cropping.

During *Kharif* 1999, nutrient movements of this mutant were compared with some of the genotypes at the critical growth period following Roemer and Schenk (1998) method. The mutant showed maximum influx of Na ions to the tune of 0.14 mol/ cm root/ second x 10^{-15}, whereas other genotypes barring RMO-257 showed the influx of Na ions in range of 0.07 to 0.10 mol/ cm root/ second x 10^{-15} (Kumar *et al.* 2001). Higher influx or uptake rate of Na ions may contribute to salt tolerance potential. However, further studies are required on genetics of branching habits, salt tolerance and to evaluate its performance under intercropping and mix cropping systems.

References

Roemer W and Schenk H (1998) Influence of genotype on phosphate uptake and utilization efficiencies in spring barley. *European Journal of Agronomy* **8**: 215-224.

Kumar D and Tarafdar JC (2001) Genotypic differences for nutrient influx in moth bean under rain-fed conditions. In: *Diamond Jubilee Symposium on Hundred Years of Post-Mendelian Genetics and Plant Breeding- Retrospect and Prospects*, 6-9 November 2001, New Delhi, Abst No. VS VI-61, pp 191.

Imparipinnate Mutant (INGR No. 04097; IC 323372), Groundnut (*Arachis hypogaea* L.) Germplasm with Imparipinnate Leaves and Small Leaflet

SH Patil
Bhabha Atomic Research Centre, Trombay, Mumbai 400 085 (Maharashtra)

Many mutants induced by X-rays were produced in groundnut at the Bhabha Atomic Research Centre, Trombay (Patil, 1966). Of the several mutants generated under this programme there was a mutant with imparipinnate leaves. It has as many as eight accessory leaflets unlike two in the parent. About 25 percent of the leaves were imparipinnate and had smaller leaflets. Occasionally, funnel shaped leaflets were also observed. The height of the mutant and its sibs was shorter than the parents. It has smaller pods with shallow constrictions and prominent beak. Kernel colour was fleshy unlike rosy in the control/ parents.

Genetic studies showed a wide range of phenotypic ratios (3:1 to 40:1) with an average of 6.5:1. The genotypic segregation over 200 progenies indicated an apparent preferential segregation for dominant type that is 109:101:30. According to Cadman (1942) 50 percent of the non-segregants are expected in duplex progeny. Occasional reversions to heterozygous states have been observed in one to two mutant progenies

References

Cadman CH (1942) Autotetraploid inheritance in the potato: some new evidence. *J Genet* **44**: 33-52.

Patil SH (1966) Mutation induced in groundnut by X-rays. In: *Symposium on Impact of Mandelism* p 334-348.

Suppressed Branch Mutant (INGR No. 04098; IC 323373), Groundnut (*Arachis hypogaea* L.) Germplasm

SH Patil and Chandra Mouli
Bhabha Atomic Research Centre, Trombay, Mumbai 400 085 (Maharashtra)

A new mutant with suppressed branches was isolated in groundnut after gamma-irradiation at the Bhabha Atomic Research Centre, Trombay, Mumbai (Mouli and Patil, 1976). The mutant is characterised by suppressed primary branches that can usually be identified after six weeks of sowing. In addition, the mutant leaves are larger than those of parent variety, because of suppressed vegetative growth of the branches. Concurrently there is a gradual reduction in size of the leaves on the suppressed branches from the basal nodes to the tip, where they are very small. The flowering pattern is also altered in the mutant. The basal three to four nodes are vegetative like in the parent TG-2; subsequently, however, the development of vegetative and reproductive buds in the leaf axils of the mutant stem is unique. It has one to three reproductive nodes, which alternate with six to eight vegetative nodes. Beyond 13 or 14 nodes the axils generally have reproductive buds and the top eight to ten nodes have highly suppressed buds. Pods in the mutants are extremely reduced in autumn growing season compared to almost normal in the spring (Table 1). The mutant's pods are similar to those of TG-2, but their shells are thicker and kernel smaller thereby reducing the shelling percentage. The genetic study revealed that a pair of recessive genes, *bsp/bsp* governs the suppressed branching character.

Table 1. Comparative characteristics of normal and mutant plants in autumn and spring growing seasons

Characteristics	Autumn		Spring	
	TG-2	Mutant	TG-2	Mutant
Germination (%)	96	98	95	95
Plant height (cm)	70 ± 1.5	60 ± 0.8	43 ± 2.0	45 ± 1.2
Branch length (cm)	84 ± 2.3	10 ± 1.2	45 ± 3.5	25 ± 2.8
Leaflet size (cm) (length x width)	6.5 x 3.3	7.8 x 4.1	5.8 x 3.3	6.3 x 3.6
Number of branches (n+1) + (n+2)	8 + 12	7 + 0	6 + 7	6 + 0
Mutant (days)	100	100	100	100
Number of pods (1+2 seeded)	8 + 50	2 + 5	5 + 47	4 + 38
Shelling (%)	84	75	Go	71
10 kernel wt (gm)	36 0.5±	32 ± 0.4	41 ± 0.5	36 ± 0.5
Flowering pattern on stem	Sequential	Altered	Sequential	Altered

References

Mouli C and Patil SH (1976) Gamma-ray-induced mutant with suppressed branches in the peanut. *The Journal of Heredity* **67:** 322-324.

BIO-YSR (INGR No. 04099; IC 443623), Mustard (*Brassica juncea* L.) Germplasm with White Rust Resistance, Yellow Seed and High Yield and Oil Content

RK Katiyar and R Chamola
National Research Centre on Plant Biotechnology, Indian Agricultural Research Institute, New Delhi 110 012

White rust caused by *Albugo candida* is the second most serious fungal disease of *Brassicas'*, occurring in the form of white pustules (spots) on the lower surface of older leaves. This results in distortion of floral and growing parts of branches (hypertrophy or stag-head), leading to substantial yield losses. The National Research Centre on Plant Biotechnology, New Delhi has developed a highly resistant strain, BIO-YSR, using somaclonal variation followed by selection. The hypocotyl region of early seedling of an exotic *Brassica juncea* germplasm, BEC-286, was used as the ex-plant for tissue culture. The soma-clone (BIO-YSR) showed high degree of resistance to white rust when tested under natural and artificial conditions in the national disease nursery trial by the All India Co-ordinated Research Project on Rapeseed & Mustard (Table 1) over the years.

BIO-YSR possesses yellow, bold seeds (5.0g/1000 seeds) with nearly 3 to 4% more oil (43 to 44%) than most of the present day commercially released varieties (38–40%). The plant grows up to a height of 200 cm in the north and northwest parts of the country. It has strong, lodging resistant pods. The cup shaped leaves and the pale green colour of this genotype can function

Suppressed Branch Mutant (INGR No. 04098; IC 323373), Groundnut (*Arachis hypogaea* L.) Germplasm

SH Patil and Chandra Mouli
Bhabha Atomic Research Centre, Trombay, Mumbai 400 085 (Maharashtra)

A new mutant with suppressed branches was isolated in groundnut after gamma-irradiation at the Bhabha Atomic Research Centre, Trombay, Mumbai (Mouli and Patil, 1976). The mutant is characterised by suppressed primary branches that can usually be identified after six weeks of sowing. In addition, the mutant leaves are larger than those of parent variety, because of suppressed vegetative growth of the branches. Concurrently there is a gradual reduction in size of the leaves on the suppressed branches from the basal nodes to the tip, where they are very small. The flowering pattern is also altered in the mutant. The basal three to four nodes are vegetative like in the parent TG-2; subsequently, however, the development of vegetative and reproductive buds in the leaf axils of the mutant stem is unique. It has one to three reproductive nodes, which alternate with six to eight vegetative nodes. Beyond 13 or 14 nodes the axils generally have reproductive buds and the top eight to ten nodes have highly suppressed buds. Pods in the mutants are extremely reduced in autumn growing season compared to almost normal in the spring (Table 1). The mutant's pods are similar to those of TG-2, but their shells are thicker and kernel smaller thereby reducing the shelling percentage. The genetic study revealed that a pair of recessive genes, *bsp/bsp* governs the suppressed branching character.

Table 1. Comparative characteristics of normal and mutant plants in autumn and spring growing seasons

Characteristics	Autumn		Spring	
	TG-2	Mutant	TG-2	Mutant
Germination (%)	96	98	95	95
Plant height (cm)	70 ± 1.5	60 ± 0.8	43 ± 2.0	45 ± 1.2
Branch length (cm)	84 ± 2.3	10 ± 1.2	45 ± 3.5	25 ± 2.8
Leaflet size (cm) (length x width)	6.5 x 3.3	7.8 x 4.1	5.8 x 3.3	6.3 x 3.6
Number of branches (n+1) + (n+2)	8 + 12	7 + 0	6 + 7	6 + 0
Mutant (days)	100	100	100	100
Number of pods (1+2 seeded)	8 + 50	2 + 5	5 + 47	4 + 38
Shelling (%)	84	75	Go	71
10 kernel wt (gm)	36 0.5±	32 ± 0.4	41 ± 0.5	36 ± 0.5
Flowering pattern on stem	Sequential	Altered	Sequential	Altered

References

Mouli C and Patil SH (1976) Gamma-ray-induced mutant with suppressed branches in the peanut. *The Journal of Heredity* **67:** 322-324.

BIO-YSR (INGR No. 04099; IC 443623), Mustard (*Brassica juncea* L.) Germplasm with White Rust Resistance, Yellow Seed and High Yield and Oil Content

RK Katiyar and R Chamola
National Research Centre on Plant Biotechnology, Indian Agricultural Research Institute, New Delhi 110 012

White rust caused by *Albugo candida* is the second most serious fungal disease of *Brassicas'*, occurring in the form of white pustules (spots) on the lower surface of older leaves. This results in distortion of floral and growing parts of branches (hypertrophy or stag-head), leading to substantial yield losses. The National Research Centre on Plant Biotechnology, New Delhi has developed a highly resistant strain, BIO-YSR, using somaclonal variation followed by selection. The hypocotyl region of early seedling of an exotic *Brassica juncea* germplasm, BEC-286, was used as the ex-plant for tissue culture. The soma-clone (BIO-YSR) showed high degree of resistance to white rust when tested under natural and artificial conditions in the national disease nursery trial by the All India Co-ordinated Research Project on Rapeseed & Mustard (Table 1) over the years.

BIO-YSR possesses yellow, bold seeds (5.0g/1000 seeds) with nearly 3 to 4% more oil (43 to 44%) than most of the present day commercially released varieties (38–40%). The plant grows up to a height of 200 cm in the north and northwest parts of the country. It has strong, lodging resistant pods. The cup shaped leaves and the pale green colour of this genotype can function

as phenotypic markers for identification. It matures about 3 weeks earlier than its parent (BEC-286), fitting well into Indian cropping patterns. It out-yielded the best commercial variety (Varuna) by 8.3 to 17.3% in the all India co-ordinated varietal trial, in 1993-94. It is being used as source of white rust resistance, yellow seed and high oil content coupled with reasonably higher productivity.

Table 1. Comparative performance of BIO-YSR, against white rust over different years in National Disease Nursery Trial (AICRP)

Strain	White rust infection score			Av. Score	Yield (Kg/Ha)		Oil (%)	1000-seed wt
	99-2000	2000-01	2001-02		Zone-II	Zone-III		
BIO-YSR	0.35	0.7	0.4	0.48	2154	2000	42.0	4.7
	–	0.0	0.9	0.45				
Varuna								
(Check)	1.94	0.9	2.1	1.65	1741	1710	38.6	4.2
	–	1.0	5.0	3.00				

Fasciation Mutant (INGR No. 04100; IC436078), Sunflower (*Helianthus annuus* L.) Germplasm

Sanjay J Jambhulkar
Bhabha Atomic Research Centre, Trombay, Mumbai 400 085 (Maharashtra)

To induce variability, seeds of sunflower variety 'Surya' were treated with Gamma rays and a fasciation mutant was isolated from the 200Gy dose treatment at the Nuclear Agriculture & Biotechnology Division, Bhabha Atomic Research Centre, Mumbai. The fasciation mutation looks like fusion of 3-4 sunflower plants. It bears small and large number of leaves (~120) on flattened stem with disrupted phyllotaxy, more leaf area (6850 cm^2), and more fresh leaf biomass (203g/plant) than control parent. The flower head also looks like fusion of 3-4 flower heads without round boundaries for ray and disc florets. Fasciation is controlled by single recessive nuclear gene denoted as *sf*[1] (sunflower fasciation one). It could be exploited in basic studies to understand the mechanism of fasciation .

Reference

Jambhulkar SJ (2002) Growth morphology and inheritance of fasciation mutation in sunflower. *J Genet & Breed* **56:** 327-330.

ARG CMS and ARG CMS (maintainer) (INGR No. 04101; IC438345 & IC438346): a Sunflower (*Helianthus annuus* L.) Cytoplasmic Male Sterile Line Involving *Helianthus argophyllus*

AJ Prabhakaran and M Sujatha
Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

ARG CMS is a new cytoplasmic male sterile (CMS) in sunflower derived from interspecific hybridisation between *H. argophyllus* x cv. Morden and backcrossing with cultivated parent at the Directorate of Oilseed Research, Rajendranagar, Hyderabad. It has short stature (85 cm) and is un-branched with medium size leaves. Ray and disc florets are yellow. Capitulum is of medium size (12.5 cm). It is an early duration type with 50% flowering in 45-50 days and maturity in 85-90 days. Seeds are medium sized, well-filled and dark black in colour. This CMS source is being used in the hybrid-breeding programme for conversion of promising inbreds for good combining ability.

as phenotypic markers for identification. It matures about 3 weeks earlier than its parent (BEC-286), fitting well into Indian cropping patterns. It out-yielded the best commercial variety (Varuna) by 8.3 to 17.3% in the all India co-ordinated varietal trial, in 1993-94. It is being used as source of white rust resistance, yellow seed and high oil content coupled with reasonably higher productivity.

Table 1. Comparative performance of BIO-YSR, against white rust over different years in National Disease Nursery Trial (AICRP)

Strain	White rust infection score			Av. Score	Yield (Kg/Ha)		Oil (%)	1000-seed wt
	99-2000	2000-01	2001-02		Zone-II	Zone-III		
BIO-YSR	0.35	0.7	0.4	0.48	2154	2000	42.0	4.7
	–	0.0	0.9	0.45				
Varuna								
(Check)	1.94	0.9	2.1	1.65	1741	1710	38.6	4.2
	–	1.0	5.0	3.00				

Fasciation Mutant (INGR No. 04100; IC436078), Sunflower (*Helianthus annuus* L.) Germplasm

Sanjay J Jambhulkar
Bhabha Atomic Research Centre, Trombay, Mumbai 400 085 (Maharashtra)

To induce variability, seeds of sunflower variety 'Surya' were treated with Gamma rays and a fasciation mutant was isolated from the 200Gy dose treatment at the Nuclear Agriculture & Biotechnology Division, Bhabha Atomic Research Centre, Mumbai. The fasciation mutation looks like fusion of 3-4 sunflower plants. It bears small and large number of leaves (~120) on flattened stem with disrupted phyllotaxy, more leaf area (6850 cm^2), and more fresh leaf biomass (203g/plant) than control parent. The flower head also looks like fusion of 3-4 flower heads without round boundaries for ray and disc florets. Fasciation is controlled by single recessive nuclear gene denoted as *sf*[1] (sunflower fasciation one). It could be exploited in basic studies to understand the mechanism of fasciation .

Reference

Jambhulkar SJ (2002) Growth morphology and inheritance of fasciation mutation in sunflower. *J Genet & Breed* **56:** 327-330.

ARG CMS and ARG CMS (maintainer) (INGR No. 04101; IC438345 & IC438346): a Sunflower (*Helianthus annuus* L.) Cytoplasmic Male Sterile Line Involving *Helianthus argophyllus*

AJ Prabhakaran and M Sujatha
Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

ARG CMS is a new cytoplasmic male sterile (CMS) in sunflower derived from interspecific hybridisation between *H. argophyllus* x cv. Morden and backcrossing with cultivated parent at the Directorate of Oilseed Research, Rajendranagar, Hyderabad. It has short stature (85 cm) and is un-branched with medium size leaves. Ray and disc florets are yellow. Capitulum is of medium size (12.5 cm). It is an early duration type with 50% flowering in 45-50 days and maturity in 85-90 days. Seeds are medium sized, well-filled and dark black in colour. This CMS source is being used in the hybrid-breeding programme for conversion of promising inbreds for good combining ability.

as phenotypic markers for identification. It matures about 3 weeks earlier than its parent (BEC-286), fitting well into Indian cropping patterns. It out-yielded the best commercial variety (Varuna) by 8.3 to 17.3% in the all India co-ordinated varietal trial, in 1993-94. It is being used as source of white rust resistance, yellow seed and high oil content coupled with reasonably higher productivity.

Table 1. Comparative performance of BIO-YSR, against white rust over different years in National Disease Nursery Trial (AICRP)

Strain	White rust infection score			Av. Score	Yield (Kg/Ha)		Oil (%)	1000-seed wt
	99-2000	2000-01	2001-02		Zone-II	Zone-III		
BIO-YSR	0.35	0.7	0.4	0.48	2154	2000	42.0	4.7
	–	0.0	0.9	0.45				
Varuna								
(Check)	1.94	0.9	2.1	1.65	1741	1710	38.6	4.2
	–	1.0	5.0	3.00				

Fasciation Mutant (INGR No. 04100; IC436078), Sunflower (*Helianthus annuus* L.) Germplasm

Sanjay J Jambhulkar
Bhabha Atomic Research Centre, Trombay, Mumbai 400 085 (Maharashtra)

To induce variability, seeds of sunflower variety 'Surya' were treated with Gamma rays and a fasciation mutant was isolated from the 200Gy dose treatment at the Nuclear Agriculture & Biotechnology Division, Bhabha Atomic Research Centre, Mumbai. The fasciation mutation looks like fusion of 3-4 sunflower plants. It bears small and large number of leaves (~120) on flattened stem with disrupted phyllotaxy, more leaf area (6850 cm^2), and more fresh leaf biomass (203g/plant) than control parent. The flower head also looks like fusion of 3-4 flower heads without round boundaries for ray and disc florets. Fasciation is controlled by single recessive nuclear gene denoted as *sf*[1] (sunflower fasciation one). It could be exploited in basic studies to understand the mechanism of fasciation .

Reference

Jambhulkar SJ (2002) Growth morphology and inheritance of fasciation mutation in sunflower. *J Genet & Breed* **56:** 327-330.

ARG CMS and ARG CMS (maintainer) (INGR No. 04101; IC438345 & IC438346): a Sunflower (*Helianthus annuus* L.) Cytoplasmic Male Sterile Line Involving *Helianthus argophyllus*

AJ Prabhakaran and M Sujatha
Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

ARG CMS is a new cytoplasmic male sterile (CMS) in sunflower derived from interspecific hybridisation between *H. argophyllus* x cv. Morden and backcrossing with cultivated parent at the Directorate of Oilseed Research, Rajendranagar, Hyderabad. It has short stature (85 cm) and is un-branched with medium size leaves. Ray and disc florets are yellow. Capitulum is of medium size (12.5 cm). It is an early duration type with 50% flowering in 45-50 days and maturity in 85-90 days. Seeds are medium sized, well-filled and dark black in colour. This CMS source is being used in the hybrid-breeding programme for conversion of promising inbreds for good combining ability.

White Pollen Sunflower (INGR No. 04102; IC443609) Interspecific Derivative (*Helianthus annuus* x *H. divaricatus* L)

M Sujatha and AJ Prabakaran
Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

The new genotype with white pollen sunflower is derived from interspecific hybridisation between cultivated sunflower and *H. divaricatus* followed by backcrossing. In the BC_4F_2 population of this cross, it was selected at the Directorate of Oilseed Research, Rajendranagar, Hyderabad. The pollen produced are pure white and in abundance, turning creamy after drying. Invariably, the white pollen producing plants possessed lemon yellow coloured ray florets and distinct cup shaped leaves unlike the plants that segregated for yellow pollen, which had normal yellow ray florets. The white pollens are viable, highly fertile, functional and germinate readily *in vivo*. Sister plant mating and selfing of white pollen producing plants resulted in the development of lines breeding true for this trait. Genetic studies indicated that the trait is under the control of monogenic recessive genes. The white pollen could serves as a genetic marker and also as a useful model in studies on gene regulation with regard to flavonoid biosynthetic pathway.

RG 2722 (INGR No. 04103; IC306138), Castor (*Ricinus communis* L.) Germplasm with Resistance to *Macrophomina* Root Rot

K Anjani
Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

RG 2722 is a *Macrophomina* root rot resistant wild castor germplasm accession collected from Andaman and Nicobar islands in the year 2000 and characterised, evaluated and screened at the Directorate of Oilseeds Research Rajendranagar, Hyderabad. The screening against root rot in root rot sick plot in 2001-02, 2002-03 and 2003-04 showed that it has stable resistance to root rot in all the years under root rot sick conditions. It has purple stem, no bloom on plant, high node number and medium size spiny capsules.

RG 1608 (INGR No. 04104; IC373978), Castor (*Ricinus communis* L) Germplasm with Resistance to *Fusarium* Wilt

K Anjani
Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

RG 1608 is a wilt (*Fusarium ricini*) resistant wild castor germplasm accession collected from Bihar in 1992 and characterised, evaluated and screened at the Directorate of Oilseeds Research, Rajendranagar, Hyderabad. With an objective of producing uniform line, selections were made in the initial segregating progenies of RG 1608. Selected progenies were subjected to selfing to bring in reasonable uniformity. This line was screened against wilt in wilt sick plots at two locations under the All India Coordinated Research Project on Castor in 1997-98 and 2002-03. It showed stable resistance to wilt in both the years. Its resistance was reconfirmed using root-tip dip technique under very high disease pressure, in pots. It has red stem, bloom on stem and lower surface of the leaf, very high node number and medium size spiny capsules.

White Pollen Sunflower (INGR No. 04102; IC443609) Interspecific Derivative (*Helianthus annuus* x *H. divaricatus* L)

M Sujatha and AJ Prabakaran
Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

The new genotype with white pollen sunflower is derived from interspecific hybridisation between cultivated sunflower and *H. divaricatus* followed by backcrossing. In the BC_4F_2 population of this cross, it was selected at the Directorate of Oilseed Research, Rajendranagar, Hyderabad. The pollen produced are pure white and in abundance, turning creamy after drying. Invariably, the white pollen producing plants possessed lemon yellow coloured ray florets and distinct cup shaped leaves unlike the plants that segregated for yellow pollen, which had normal yellow ray florets. The white pollens are viable, highly fertile, functional and germinate readily *in vivo*. Sister plant mating and selfing of white pollen producing plants resulted in the development of lines breeding true for this trait. Genetic studies indicated that the trait is under the control of monogenic recessive genes. The white pollen could serves as a genetic marker and also as a useful model in studies on gene regulation with regard to flavonoid biosynthetic pathway.

RG 2722 (INGR No. 04103; IC306138), Castor (*Ricinus communis* L.) Germplasm with Resistance to *Macrophomina* Root Rot

K Anjani
Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

RG 2722 is a *Macrophomina* root rot resistant wild castor germplasm accession collected from Andaman and Nicobar islands in the year 2000 and characterised, evaluated and screened at the Directorate of Oilseeds Research Rajendranagar, Hyderabad. The screening against root rot in root rot sick plot in 2001-02, 2002-03 and 2003-04 showed that it has stable resistance to root rot in all the years under root rot sick conditions. It has purple stem, no bloom on plant, high node number and medium size spiny capsules.

RG 1608 (INGR No. 04104; IC373978), Castor (*Ricinus communis* L) Germplasm with Resistance to *Fusarium* Wilt

K Anjani
Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

RG 1608 is a wilt (*Fusarium ricini*) resistant wild castor germplasm accession collected from Bihar in 1992 and characterised, evaluated and screened at the Directorate of Oilseeds Research, Rajendranagar, Hyderabad. With an objective of producing uniform line, selections were made in the initial segregating progenies of RG 1608. Selected progenies were subjected to selfing to bring in reasonable uniformity. This line was screened against wilt in wilt sick plots at two locations under the All India Coordinated Research Project on Castor in 1997-98 and 2002-03. It showed stable resistance to wilt in both the years. Its resistance was reconfirmed using root-tip dip technique under very high disease pressure, in pots. It has red stem, bloom on stem and lower surface of the leaf, very high node number and medium size spiny capsules.

White Pollen Sunflower (INGR No. 04102; IC443609) Interspecific Derivative (*Helianthus annuus* x *H. divaricatus* L)

M Sujatha and AJ Prabakaran
Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

The new genotype with white pollen sunflower is derived from interspecific hybridisation between cultivated sunflower and *H. divaricatus* followed by backcrossing. In the BC_4F_2 population of this cross, it was selected at the Directorate of Oilseed Research, Rajendranagar, Hyderabad. The pollen produced are pure white and in abundance, turning creamy after drying. Invariably, the white pollen producing plants possessed lemon yellow coloured ray florets and distinct cup shaped leaves unlike the plants that segregated for yellow pollen, which had normal yellow ray florets. The white pollens are viable, highly fertile, functional and germinate readily *in vivo*. Sister plant mating and selfing of white pollen producing plants resulted in the development of lines breeding true for this trait. Genetic studies indicated that the trait is under the control of monogenic recessive genes. The white pollen could serves as a genetic marker and also as a useful model in studies on gene regulation with regard to flavonoid biosynthetic pathway.

RG 2722 (INGR No. 04103; IC306138), Castor (*Ricinus communis* L.) Germplasm with Resistance to *Macrophomina* Root Rot

K Anjani
Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

RG 2722 is a *Macrophomina* root rot resistant wild castor germplasm accession collected from Andaman and Nicobar islands in the year 2000 and characterised, evaluated and screened at the Directorate of Oilseeds Research Rajendranagar, Hyderabad. The screening against root rot in root rot sick plot in 2001-02, 2002-03 and 2003-04 showed that it has stable resistance to root rot in all the years under root rot sick conditions. It has purple stem, no bloom on plant, high node number and medium size spiny capsules.

RG 1608 (INGR No. 04104; IC373978), Castor (*Ricinus communis* L) Germplasm with Resistance to *Fusarium* Wilt

K Anjani
Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

RG 1608 is a wilt (*Fusarium ricini*) resistant wild castor germplasm accession collected from Bihar in 1992 and characterised, evaluated and screened at the Directorate of Oilseeds Research, Rajendranagar, Hyderabad. With an objective of producing uniform line, selections were made in the initial segregating progenies of RG 1608. Selected progenies were subjected to selfing to bring in reasonable uniformity. This line was screened against wilt in wilt sick plots at two locations under the All India Coordinated Research Project on Castor in 1997-98 and 2002-03. It showed stable resistance to wilt in both the years. Its resistance was reconfirmed using root-tip dip technique under very high disease pressure, in pots. It has red stem, bloom on stem and lower surface of the leaf, very high node number and medium size spiny capsules.

MCP 1-1 (INGR No. 04121; IC296551), Castor (*Ricinus communis* L.) Germplasm with Diverse Stable Pistillate Nature

Shambhoo Singh Solanki
Agricultural Research Station Mandor, Rajasthan Agricultural University, Jodhpur 342 304 (Rajasthan)

Inflorescence of castor is raceme and basically monoecious in nature. Lower part of raceme bears staminate flowers and upper, pistillate flowers. Castor lines, with only pistillate flowers are also available. Pistillate stock MCP-1-1 was isolated by selection from existing pistillate line MCP-1. The MCP-1 had unstable sex nature. The promising line was planted in summer season and normal season at the Agriculture Research Station, Mandor (Rajasthan Agriculture University), Jodhpur. In summer plants expressing optimum interspersed staminate flowers under high temperature were selected and planted in normal season. These were observed for the pistillateness and other yield contributing characters. MCP-1-1 is a diverse, good general combiner for seed yield and 100 seed weight (Anonymous 2003, Solanki, *et al.*, 2004) and a new source of pistillate flowers for heterosis breeding.

MCP-1-1 is characterized by mahogany colour stem and petiole, condensed nodes, deep cup shaped leaves, medium size spiny capsules and long primary raceme (60-65 cm) and 16-18 nodes up to primary raceme. It is waxy on dorsal as well as ventral sides of leaves, stem and other parts of plant; triple bloom; spike semi compact. This line also expressed high degree of pistillateness at S.K.Nagar, Sri Krashi Nagar Dhantiwada Unversity and Directorate of Oilseeds Research, Hyderabad indicating its wider adaptability and sex stability.

MCP-1-1 shows high degree of femaleness up to fifth/ sixth order of raceme development under summer season without monoeciousism and reversion in normal season making it ideal for castor hybrid development. It can be maintained by planting in summer season (last week of February to first week of March), the favourable temperature for expression of interspersed staminate flowers is around 31-34 °C. To grow crop, adoption of common production technology and irrigation at an interval of 8-12 days is recommended. Minimum isolation distance of 1000 m is required for production of breeder and foundation seeds during summer season.

References

Anonymous (2003) Annual Progress Report 1-4-1999 to 31-3-2003 (summarised). *Development of Hybrids Crops – Castor*, NATP (mission mode).

Solanki SS, VS Deora and DP Singh (2004). Combining ability of new castor, *Ricinus communis* L. pistillate line: MCP-1-1. *J. Oilseeds Res.*, **21**: 274-276.

IS-244/2/1 (INGR No. 04105; IC427812), Cotton (*Gossypium* Interspecific Hybrid) Apomictic Germplasm

AS Ansingkar[1], AW More[1], SS More[1] and PR Khdake[2]
1. Marathwada Agricultural University, Parbhani (Maharashtra)
2. Cotton Research Station, Nanded 431 604 (Maharashtra)

In BC_1 F_6 generation of interspecific cross involving (*G hirsutum* x *G barbadense*) x *G. arboreum* (colchiploid) backcrossed to *G. arboreum*, one of the segregant, IS-244/4/1 showed apomictic behaviour. Such kind of phenomenon is rarely reported in cotton, though it is common in polyploid species of Graminae, Rosaceae, Astraceae and in some intergeneric and interspecific crosses. The suspected apomictic line showed peculiar morphological features, such as dwarf stature, smaller leaf size, smaller boll size, round seeds, reduced stomata number and style length, flower size as compared to the tetraploid cultivars. Following observations confirmed the apomictic nature- progenies remained identical to respective mother plant without genetical variation, from BC_1 F_6 to BC_1 F_{14} generation, boll setting was observed, even when buds were emasculated before anthesis and selfed, and even after cutting of stigma and style, F_1 progenies from crosses between apomictic line and other lines having marker characters (petal spot, pigmented style) showed neither the marker nor the intermediate

MCP 1-1 (INGR No. 04121; IC296551), Castor (*Ricinus communis* L.) Germplasm with Diverse Stable Pistillate Nature

Shambhoo Singh Solanki
Agricultural Research Station Mandor, Rajasthan Agricultural University, Jodhpur 342 304 (Rajasthan)

Inflorescence of castor is raceme and basically monoecious in nature. Lower part of raceme bears staminate flowers and upper, pistillate flowers. Castor lines, with only pistillate flowers are also available. Pistillate stock MCP-1-1 was isolated by selection from existing pistillate line MCP-1. The MCP-1 had unstable sex nature. The promising line was planted in summer season and normal season at the Agriculture Research Station, Mandor (Rajasthan Agriculture University), Jodhpur. In summer plants expressing optimum interspersed staminate flowers under high temperature were selected and planted in normal season. These were observed for the pistillateness and other yield contributing characters. MCP-1-1 is a diverse, good general combiner for seed yield and 100 seed weight (Anonymous 2003, Solanki, *et al.*, 2004) and a new source of pistillate flowers for heterosis breeding.

MCP-1-1 is characterized by mahogany colour stem and petiole, condensed nodes, deep cup shaped leaves, medium size spiny capsules and long primary raceme (60-65 cm) and 16-18 nodes up to primary raceme. It is waxy on dorsal as well as ventral sides of leaves, stem and other parts of plant; triple bloom; spike semi compact. This line also expressed high degree of pistillateness at S.K.Nagar, Sri Krashi Nagar Dhantiwada Unversity and Directorate of Oilseeds Research, Hyderabad indicating its wider adaptability and sex stability.

MCP-1-1 shows high degree of femaleness up to fifth/ sixth order of raceme development under summer season without monoeciousism and reversion in normal season making it ideal for castor hybrid development. It can be maintained by planting in summer season (last week of February to first week of March), the favourable temperature for expression of interspersed staminate flowers is around 31-34 °C. To grow crop, adoption of common production technology and irrigation at an interval of 8-12 days is recommended. Minimum isolation distance of 1000 m is required for production of breeder and foundation seeds during summer season.

References

Anonymous (2003) Annual Progress Report 1-4-1999 to 31-3-2003 (summarised). *Development of Hybrids Crops – Castor*, NATP (mission mode).

Solanki SS, VS Deora and DP Singh (2004). Combining ability of new castor, *Ricinus communis* L. pistillate line: MCP-1-1. *J. Oilseeds Res.*, **21**: 274-276.

IS-244/2/1 (INGR No. 04105; IC427812), Cotton (*Gossypium* Interspecific Hybrid) Apomictic Germplasm

AS Ansingkar[1], AW More[1], SS More[1] and PR Khdake[2]
1. Marathwada Agricultural University, Parbhani (Maharashtra)
2. Cotton Research Station, Nanded 431 604 (Maharashtra)

In BC_1 F_6 generation of interspecific cross involving (*G hirsutum* x *G barbadense*) x *G. arboreum* (colchiploid) backcrossed to *G. arboreum*, one of the segregant, IS-244/4/1 showed apomictic behaviour. Such kind of phenomenon is rarely reported in cotton, though it is common in polyploid species of Graminae, Rosaceae, Astraceae and in some intergeneric and interspecific crosses. The suspected apomictic line showed peculiar morphological features, such as dwarf stature, smaller leaf size, smaller boll size, round seeds, reduced stomata number and style length, flower size as compared to the tetraploid cultivars. Following observations confirmed the apomictic nature- progenies remained identical to respective mother plant without genetical variation, from BC_1 F_6 to BC_1 F_{14} generation, boll setting was observed, even when buds were emasculated before anthesis and selfed, and even after cutting of stigma and style, F_1 progenies from crosses between apomictic line and other lines having marker characters (petal spot, pigmented style) showed neither the marker nor the intermediate

characters, but features identical to apomictic parent, In F_1 progenies, developed by crossing CMS 'A' line with apomictic genotype, despite selfing setting bolls took place, which is possible due to transfer of apomictic gene in CMS 'A' line, cytological investigation revealed aneuploidy nature of apomictic line with chromosome number varying form 26 to 45, because of cytological instability very less pollen sterility (35%) was recorded and that RAPD analysis of apomictic line showed identical banding pattern similar to their F_1.

IS-376/14/21 (INGR No. 04106; IC427815), Cotton (*Gossypium* Interspecific Hybrid) Germplasm with Resistance to Sucking Pest

AS Ansingkar[1], AW More[1], SS More[1] and PR Khdake[2]
1. Marathawada Agricultural University, Parbhani (Maharashtra)
2. Cotton Research Station, Nanded 431 604 (Maharashtra)

Desi cotton (*G. arboreum*) has inbuilt resistance to sucking pests due to their peculiar leaf anatomy. *Homoptera* pests including jassids have pre-set target to reach phloem element to suck sap by piercing stylet into lower epidermis. In *G. arboreum* distance to phloem from lower epidermis is relatively more and parenchyma cells are more compact compared to *G. hirustum*. Therefore, a breeding programme was initiated to incorporate these anatomical features of *G. arboreum* into *G. hirsutum* with an objective to get genotypes with multiple resistances against sucking pests. Hybridisation between *G. arboreum* and *G. hirsutum* led to identification of an introgressed genotype, IS-376/14/21 at the Marathawada Agricultural University. This recorded 30.2 m distance for first phloem element from the abaxial surface and was more by (7.3 m) 10-15 m than *G. hirsutum* check, NHH-44 (22.9 m). Leaf anatomical study revealed that the introgressed genotype had more compactly arranged parenchyma cells (number of cells per micron ranging between 11.6-11.7) matching with *G. arboreum*. Field observations in multi-location testing further indicated lesser mean population of sucking pests namely aphid, jassid, thrip and whitefly on IS-376/14/21 in comparison to *G. hirsutum* varieties. Further, it maintains green and healthy leaves throughout its life span indicating resistance to sucking pests.

dlpf (CMU 013) (INGR No. 04107; IC427817), Jute (*Corchorus capsularis* L.) Germplasm with Low Lignin, GA_3 (7 times lower than JRC 212) and Cellulose Fibre

Pratip Kumar Palit
Central Research Institute for Jute and Allied Fibres, Barrackpore, Kolkata 700 120 (West Bengal)

High lignin content of ligno-cellulose jute fibre does not allow making of fine fabric and other value added products. To develop low lignin jute fibre, an X-ray induced mutant line of jute (*Corchorus capsularis* L.) was produced and evaluated at the Central Research Institute for Jute and Allied Fibres, Barrackpore, resulting in identification of the CMU 013, one of the most undulated phenotype compared to its normal parent, JRC 212 for its growth, secondary fibre development and lignification of the fibre.

The mutant grew slower, had shorter internodes and yielded much less fibre after retting. The fibre of the mutant contains 50 percent less lignin and comparatively more cellulose then the normal type. Differentiation of primary and secondary vascular tissues through out the CMU 013 stem was regular and did not have secondary phloem fibre bundles as in JRC 212. Instead, a few thin-walled, less lignified fibre cells formed uni-or biseriate radial rows with in the phloem wedges of the middle stem. The lower and earliest developed part of the mutant stem had no lignified fibre cells. This developmental deficiency in lignification of fibre cells was correlated to a similar deficiency in phenyl-alanine ammonia lyase activity, but not peroxidase activity, in the bark tissue along the stem axis. In spite of severe reduction in lignin synthesis in the phloem cells this mutant functioned normally and bred true. This mutant, it has been designated as deficient lignified phloem fibre (*dlpf*) mutant. It can be used as a source to developed low lignin fibre jute varieties.

MCP 1-1 (INGR No. 04121; IC296551), Castor (*Ricinus communis* L.) Germplasm with Diverse Stable Pistillate Nature

Shambhoo Singh Solanki
Agricultural Research Station Mandor, Rajasthan Agricultural University, Jodhpur 342 304 (Rajasthan)

Inflorescence of castor is raceme and basically monoecious in nature. Lower part of raceme bears staminate flowers and upper, pistillate flowers. Castor lines, with only pistillate flowers are also available. Pistillate stock MCP-1-1 was isolated by selection from existing pistillate line MCP-1. The MCP-1 had unstable sex nature. The promising line was planted in summer season and normal season at the Agriculture Research Station, Mandor (Rajasthan Agriculture University), Jodhpur. In summer plants expressing optimum interspersed staminate flowers under high temperature were selected and planted in normal season. These were observed for the pistillateness and other yield contributing characters. MCP-1-1 is a diverse, good general combiner for seed yield and 100 seed weight (Anonymous 2003, Solanki, *et al.*, 2004) and a new source of pistillate flowers for heterosis breeding.

MCP-1-1 is characterized by mahogany colour stem and petiole, condensed nodes, deep cup shaped leaves, medium size spiny capsules and long primary raceme (60-65 cm) and 16-18 nodes up to primary raceme. It is waxy on dorsal as well as ventral sides of leaves, stem and other parts of plant; triple bloom; spike semi compact. This line also expressed high degree of pistillateness at S.K.Nagar, Sri Krashi Nagar Dhantiwada Unversity and Directorate of Oilseeds Research, Hyderabad indicating its wider adaptability and sex stability.

MCP-1-1 shows high degree of femaleness up to fifth/ sixth order of raceme development under summer season without monoeciousism and reversion in normal season making it ideal for castor hybrid development. It can be maintained by planting in summer season (last week of February to first week of March), the favourable temperature for expression of interspersed staminate flowers is around 31-34 °C. To grow crop, adoption of common production technology and irrigation at an interval of 8-12 days is recommended. Minimum isolation distance of 1000 m is required for production of breeder and foundation seeds during summer season.

References

Anonymous (2003) Annual Progress Report 1-4-1999 to 31-3-2003 (summarised). *Development of Hybrids Crops – Castor*, NATP (mission mode).

Solanki SS, VS Deora and DP Singh (2004). Combining ability of new castor, *Ricinus communis* L. pistillate line: MCP-1-1. *J. Oilseeds Res.*, **21**: 274-276.

IS-244/2/1 (INGR No. 04105; IC427812), Cotton (*Gossypium* Interspecific Hybrid) Apomictic Germplasm

AS Ansingkar[1], AW More[1], SS More[1] and PR Khdake[2]
1. Marathwada Agricultural University, Parbhani (Maharashtra)
2. Cotton Research Station, Nanded 431 604 (Maharashtra)

In BC_1 F_6 generation of interspecific cross involving (*G hirsutum* x *G barbadense*) x *G. arboreum* (colchiploid) backcrossed to *G. arboreum*, one of the segregant, IS-244/4/1 showed apomictic behaviour. Such kind of phenomenon is rarely reported in cotton, though it is common in polyploid species of Graminae, Rosaceae, Astraceae and in some intergeneric and interspecific crosses. The suspected apomictic line showed peculiar morphological features, such as dwarf stature, smaller leaf size, smaller boll size, round seeds, reduced stomata number and style length, flower size as compared to the tetraploid cultivars. Following observations confirmed the apomictic nature- progenies remained identical to respective mother plant without genetical variation, from BC_1 F_6 to BC_1 F_{14} generation, boll setting was observed, even when buds were emasculated before anthesis and selfed, and even after cutting of stigma and style, F_1 progenies from crosses between apomictic line and other lines having marker characters (petal spot, pigmented style) showed neither the marker nor the intermediate

characters, but features identical to apomictic parent, In F_1 progenies, developed by crossing CMS 'A' line with apomictic genotype, despite selfing setting bolls took place, which is possible due to transfer of apomictic gene in CMS 'A' line, cytological investigation revealed aneuploidy nature of apomictic line with chromosome number varying form 26 to 45, because of cytological instability very less pollen sterility (35%) was recorded and that RAPD analysis of apomictic line showed identical banding pattern similar to their F_1.

IS-376/14/21 (INGR No. 04106; IC427815), Cotton (*Gossypium* Interspecific Hybrid) Germplasm with Resistance to Sucking Pest

AS Ansingkar[1], AW More[1], SS More[1] and PR Khdake[2]
1. Marathawada Agricultural University, Parbhani (Maharashtra)
2. Cotton Research Station, Nanded 431 604 (Maharashtra)

Desi cotton (*G. arboreum*) has inbuilt resistance to sucking pests due to their peculiar leaf anatomy. *Homoptera* pests including jassids have pre-set target to reach phloem element to suck sap by piercing stylet into lower epidermis. In *G. arboreum* distance to phloem from lower epidermis is relatively more and parenchyma cells are more compact compared to *G. hirustum*. Therefore, a breeding programme was initiated to incorporate these anatomical features of *G. arboreum* into *G. hirsutum* with an objective to get genotypes with multiple resistances against sucking pests. Hybridisation between *G. arboreum* and *G. hirsutum* led to identification of an introgressed genotype, IS-376/14/21 at the Marathawada Agricultural University. This recorded 30.2 m distance for first phloem element from the abaxial surface and was more by (7.3 m) 10-15 m than *G. hirsutum* check, NHH-44 (22.9 m). Leaf anatomical study revealed that the introgressed genotype had more compactly arranged parenchyma cells (number of cells per micron ranging between 11.6-11.7) matching with *G. arboreum*. Field observations in multi-location testing further indicated lesser mean population of sucking pests namely aphid, jassid, thrip and whitefly on IS-376/14/21 in comparison to *G. hirsutum* varieties. Further, it maintains green and healthy leaves throughout its life span indicating resistance to sucking pests.

dlpf (CMU 013) (INGR No. 04107; IC427817), Jute (*Corchorus capsularis* L.) Germplasm with Low Lignin, GA_3 (7 times lower than JRC 212) and Cellulose Fibre

Pratip Kumar Palit
Central Research Institute for Jute and Allied Fibres, Barrackpore, Kolkata 700 120 (West Bengal)

High lignin content of ligno-cellulose jute fibre does not allow making of fine fabric and other value added products. To develop low lignin jute fibre, an X-ray induced mutant line of jute (*Corchorus capsularis* L.) was produced and evaluated at the Central Research Institute for Jute and Allied Fibres, Barrackpore, resulting in identification of the CMU 013, one of the most undulated phenotype compared to its normal parent, JRC 212 for its growth, secondary fibre development and lignification of the fibre.

The mutant grew slower, had shorter internodes and yielded much less fibre after retting. The fibre of the mutant contains 50 percent less lignin and comparatively more cellulose then the normal type. Differentiation of primary and secondary vascular tissues through out the CMU 013 stem was regular and did not have secondary phloem fibre bundles as in JRC 212. Instead, a few thin-walled, less lignified fibre cells formed uni-or biseriate radial rows with in the phloem wedges of the middle stem. The lower and earliest developed part of the mutant stem had no lignified fibre cells. This developmental deficiency in lignification of fibre cells was correlated to a similar deficiency in phenyl-alanine ammonia lyase activity, but not peroxidase activity, in the bark tissue along the stem axis. In spite of severe reduction in lignin synthesis in the phloem cells this mutant functioned normally and bred true. This mutant, it has been designated as deficient lignified phloem fibre (*dlpf*) mutant. It can be used as a source to developed low lignin fibre jute varieties.

characters, but features identical to apomictic parent, In F_1 progenies, developed by crossing CMS 'A' line with apomictic genotype, despite selfing setting bolls took place, which is possible due to transfer of apomictic gene in CMS 'A' line, cytological investigation revealed aneuploidy nature of apomictic line with chromosome number varying form 26 to 45, because of cytological instability very less pollen sterility (35%) was recorded and that RAPD analysis of apomictic line showed identical banding pattern similar to their F_1.

IS-376/14/21 (INGR No. 04106; IC427815), Cotton (*Gossypium* Interspecific Hybrid) Germplasm with Resistance to Sucking Pest

AS Ansingkar[1], AW More[1], SS More[1] and PR Khdake[2]
1. Marathawada Agricultural University, Parbhani (Maharashtra)
2. Cotton Research Station, Nanded 431 604 (Maharashtra)

Desi cotton (*G. arboreum*) has inbuilt resistance to sucking pests due to their peculiar leaf anatomy. *Homoptera* pests including jassids have pre-set target to reach phloem element to suck sap by piercing stylet into lower epidermis. In *G. arboreum* distance to phloem from lower epidermis is relatively more and parenchyma cells are more compact compared to *G. hirustum*. Therefore, a breeding programme was initiated to incorporate these anatomical features of *G. arboreum* into *G. hirsutum* with an objective to get genotypes with multiple resistances against sucking pests. Hybridisation between *G. arboreum* and *G. hirsutum* led to identification of an introgressed genotype, IS-376/14/21 at the Marathawada Agricultural University. This recorded 30.2 m distance for first phloem element from the abaxial surface and was more by (7.3 m) 10-15 m than *G. hirsutum* check, NHH-44 (22.9 m). Leaf anatomical study revealed that the introgressed genotype had more compactly arranged parenchyma cells (number of cells per micron ranging between 11.6-11.7) matching with *G. arboreum*. Field observations in multi-location testing further indicated lesser mean population of sucking pests namely aphid, jassid, thrip and whitefly on IS-376/14/21 in comparison to *G. hirsutum* varieties. Further, it maintains green and healthy leaves throughout its life span indicating resistance to sucking pests.

dlpf (CMU 013) (INGR No. 04107; IC427817), Jute (*Corchorus capsularis* L.) Germplasm with Low Lignin, GA_3 (7 times lower than JRC 212) and Cellulose Fibre

Pratip Kumar Palit
Central Research Institute for Jute and Allied Fibres, Barrackpore, Kolkata 700 120 (West Bengal)

High lignin content of ligno-cellulose jute fibre does not allow making of fine fabric and other value added products. To develop low lignin jute fibre, an X-ray induced mutant line of jute (*Corchorus capsularis* L.) was produced and evaluated at the Central Research Institute for Jute and Allied Fibres, Barrackpore, resulting in identification of the CMU 013, one of the most undulated phenotype compared to its normal parent, JRC 212 for its growth, secondary fibre development and lignification of the fibre.

The mutant grew slower, had shorter internodes and yielded much less fibre after retting. The fibre of the mutant contains 50 percent less lignin and comparatively more cellulose then the normal type. Differentiation of primary and secondary vascular tissues through out the CMU 013 stem was regular and did not have secondary phloem fibre bundles as in JRC 212. Instead, a few thin-walled, less lignified fibre cells formed uni-or biseriate radial rows with in the phloem wedges of the middle stem. The lower and earliest developed part of the mutant stem had no lignified fibre cells. This developmental deficiency in lignification of fibre cells was correlated to a similar deficiency in phenyl-alanine ammonia lyase activity, but not peroxidase activity, in the bark tissue along the stem axis. In spite of severe reduction in lignin synthesis in the phloem cells this mutant functioned normally and bred true. This mutant, it has been designated as deficient lignified phloem fibre (*dlpf*) mutant. It can be used as a source to developed low lignin fibre jute varieties.

characters, but features identical to apomictic parent, In F_1 progenies, developed by crossing CMS 'A' line with apomictic genotype, despite selfing setting bolls took place, which is possible due to transfer of apomictic gene in CMS 'A' line, cytological investigation revealed aneuploidy nature of apomictic line with chromosome number varying form 26 to 45, because of cytological instability very less pollen sterility (35%) was recorded and that RAPD analysis of apomictic line showed identical banding pattern similar to their F_1.

IS-376/14/21 (INGR No. 04106; IC427815), Cotton (*Gossypium* Interspecific Hybrid) Germplasm with Resistance to Sucking Pest

AS Ansingkar[1], AW More[1], SS More[1] and PR Khdake[2]
1. Marathawada Agricultural University, Parbhani (Maharashtra)
2. Cotton Research Station, Nanded 431 604 (Maharashtra)

Desi cotton (*G. arboreum*) has inbuilt resistance to sucking pests due to their peculiar leaf anatomy. *Homoptera* pests including jassids have pre-set target to reach phloem element to suck sap by piercing stylet into lower epidermis. In *G. arboreum* distance to phloem from lower epidermis is relatively more and parenchyma cells are more compact compared to *G. hirustum*. Therefore, a breeding programme was initiated to incorporate these anatomical features of *G. arboreum* into *G. hirsutum* with an objective to get genotypes with multiple resistances against sucking pests. Hybridisation between *G. arboreum* and *G. hirsutum* led to identification of an introgressed genotype, IS-376/14/21 at the Marathawada Agricultural University. This recorded 30.2 m distance for first phloem element from the abaxial surface and was more by (7.3 m) 10-15 m than *G. hirsutum* check, NHH-44 (22.9 m). Leaf anatomical study revealed that the introgressed genotype had more compactly arranged parenchyma cells (number of cells per micron ranging between 11.6-11.7) matching with *G. arboreum*. Field observations in multi-location testing further indicated lesser mean population of sucking pests namely aphid, jassid, thrip and whitefly on IS-376/14/21 in comparison to *G. hirsutum* varieties. Further, it maintains green and healthy leaves throughout its life span indicating resistance to sucking pests.

dlpf (CMU 013) (INGR No. 04107; IC427817), Jute (*Corchorus capsularis* L.) Germplasm with Low Lignin, GA_3 (7 times lower than JRC 212) and Cellulose Fibre

Pratip Kumar Palit
Central Research Institute for Jute and Allied Fibres, Barrackpore, Kolkata 700 120 (West Bengal)

High lignin content of ligno-cellulose jute fibre does not allow making of fine fabric and other value added products. To develop low lignin jute fibre, an X-ray induced mutant line of jute (*Corchorus capsularis* L.) was produced and evaluated at the Central Research Institute for Jute and Allied Fibres, Barrackpore, resulting in identification of the CMU 013, one of the most undulated phenotype compared to its normal parent, JRC 212 for its growth, secondary fibre development and lignification of the fibre.

The mutant grew slower, had shorter internodes and yielded much less fibre after retting. The fibre of the mutant contains 50 percent less lignin and comparatively more cellulose then the normal type. Differentiation of primary and secondary vascular tissues through out the CMU 013 stem was regular and did not have secondary phloem fibre bundles as in JRC 212. Instead, a few thin-walled, less lignified fibre cells formed uni-or biseriate radial rows with in the phloem wedges of the middle stem. The lower and earliest developed part of the mutant stem had no lignified fibre cells. This developmental deficiency in lignification of fibre cells was correlated to a similar deficiency in phenyl-alanine ammonia lyase activity, but not peroxidase activity, in the bark tissue along the stem axis. In spite of severe reduction in lignin synthesis in the phloem cells this mutant functioned normally and bred true. This mutant, it has been designated as deficient lignified phloem fibre (*dlpf*) mutant. It can be used as a source to developed low lignin fibre jute varieties.

CSD 137 (INGR No. 04108; IC427827), Sesbania (*Sesbania aculeata* Pers.) Germplasm with High Foliage and Sodicity Tolerance

RK Singh[1], RK Gautam[1] and B Mishra[2]
1. Central Soil Salinity Research Institute, Kachhwa Road, Karnal 132 001 (Haryana)
2. Directorate of Rice Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

Sesbania aculeata commonly called as 'Dhaincha' is an ideal and cheap biological resource to improve the physico-chemical properties of salt affected soils. Its incorporation in sodic soils not only increases the fertility through green manuring, but also hastens the reclamation process of sodic soils and is considered an effective supplement to chemical amendments. Screening of 140 collections of *Sesbania aculeata* and *S. rostrata* collected from various parts of the country at the Central Soil Salinity Research Institute led to the identification of a *S. aculeata* genotype, CSD 137, which consistently gives high fresh foliage yield in sodic soils. CSD137 is a local collection made from village Birharu, tehsil, Kheragarh, district Agra.

CSD 137 has shown consistent foliage yield superiority under different sodicity stress level (from pH_2 9.2 to 9.7) in Haryana and U.P. Across sodicity stress levels it recorded 52, 70, 72, 99 and 123 gram of fresh foliage yield/ plant respectively at 40, 45, 55, and 60 days after sowing (Table 1). It attains a plant height of about 220 cm with 10 primary branches, 30 secondary branches, 180 pods/ plant, and 20.0 g test weight, and takes about 110 days for pod bearing. Thus 1.5 to 2 times more foliage yield could be incorporated in sodic soils for their fast reclamation and utilization.

Table 1. Green foliage yield (g/plant) of CSD 137 in sodic soils

Days after sowing	Sodic environments			
	L1 (pH_2~9.2)	L1 (pH_2~9.5)	L1 (pH_2~9.7)	Average
40	114 (70) *	37 (20)	4 (1)	52 (33.0)
45	151 (74)	41 (22)	17 (6)	70 (34.0)
50	155 (76)	44 (32)	18 (11)	72 (40.0)
55	156 (88)	96 (47)	46 (13)	99 (49.0)
60	161 (109)	154(71)	55 (47)	123 (76.0)
Average	147 (83)	74 (38)	28 (16)	

*The values within parenthesis are of lowest yielding genotype at each level.

MP/99-322 (INGR No. 04109; IC445068), Potato (*Solanum tuberosum* L.) Germplasm with High Starch and Dry Matter, Low Amylose, and Resistance to Late Blight

SK Pandey, P Manivel, SV Singh and Dinesh Kumar
Central Potato Research Institute, Shimla 171 001 (Himachal Pradesh)

MP/99-322 is the first Indian potato (*Solanum tuberosum* ssp. *tuberosum*) hybrid with higher starch content (> 17%), higher dry matter (>23%), low amylose content (< 27.3%), high amylopectin (>72.7%) and resistance to late blight. This hybrid was identified from the F_1 progeny of a cross MP/91-76 x MP/92-35 following the recurrent breeding selection method at the Central Potato Research Institute campus, Modipuram, Uttar Pradesh.

Morphologically, MP/99-322 is of medium height with open canopy; stem medium thick, green, and wings feebly developed and straight; leaflet width narrow, leaflet coalescence frequency low, rachis and midrib pigmentation absent; flowering profuse, floral stalk light purple, floral stalk-pedicel articulation poorly visible and located above the middle, calyx partially pigmented, bud green to light purple, corolla purple, corolla shape semi-stellate, anther yellow and cone normally developed, stylar length longer than stamen column and stigma bi-lobed; tuber oval/oblong, skin yellow, eyes shallow, eyebrows slightly raised, and flesh cream/pale yellow. Sprout purple/red-purple, shape conical, pubescence and tip closed. It yields between 26-30 t/ha in a crop of 90 days with 87-95% processing grade (>45 mm diameter) tubers and between 31-34 t/ha in a crop of 105 days with 90-95% processing grade tubers in West-Central plains at Modipuram. The hybrid has very high tuber dry matter vis-à-vis starch content at Modipuram in West-Central plains an area known for producing low dry matter potatoes (Table 1). Further, it has lower

CSD 137 (INGR No. 04108; IC427827), Sesbania (*Sesbania aculeata* Pers.) Germplasm with High Foliage and Sodicity Tolerance

RK Singh[1], RK Gautam[1] and B Mishra[2]
1. Central Soil Salinity Research Institute, Kachhwa Road, Karnal 132 001 (Haryana)
2. Directorate of Rice Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

Sesbania aculeata commonly called as 'Dhaincha' is an ideal and cheap biological resource to improve the physico-chemical properties of salt affected soils. Its incorporation in sodic soils not only increases the fertility through green manuring, but also hastens the reclamation process of sodic soils and is considered an effective supplement to chemical amendments. Screening of 140 collections of *Sesbania aculeata* and *S. rostrata* collected from various parts of the country at the Central Soil Salinity Research Institute led to the identification of a *S. aculeata* genotype, CSD 137, which consistently gives high fresh foliage yield in sodic soils. CSD137 is a local collection made from village Birharu, tehsil, Kheragarh, district Agra.

CSD 137 has shown consistent foliage yield superiority under different sodicity stress level (from pH_2 9.2 to 9.7) in Haryana and U.P. Across sodicity stress levels it recorded 52, 70, 72, 99 and 123 gram of fresh foliage yield/ plant respectively at 40, 45, 55, and 60 days after sowing (Table 1). It attains a plant height of about 220 cm with 10 primary branches, 30 secondary branches, 180 pods/ plant, and 20.0 g test weight, and takes about 110 days for pod bearing. Thus 1.5 to 2 times more foliage yield could be incorporated in sodic soils for their fast reclamation and utilization.

Table 1. Green foliage yield (g/plant) of CSD 137 in sodic soils

Days after sowing	Sodic environments			
	L1 (pH_2~9.2)	L1 (pH_2~9.5)	L1 (pH_2~9.7)	Average
40	114 (70) *	37 (20)	4 (1)	52 (33.0)
45	151 (74)	41 (22)	17 (6)	70 (34.0)
50	155 (76)	44 (32)	18 (11)	72 (40.0)
55	156 (88)	96 (47)	46 (13)	99 (49.0)
60	161 (109)	154(71)	55 (47)	123 (76.0)
Average	147 (83)	74 (38)	28 (16)	

*The values within parenthesis are of lowest yielding genotype at each level.

MP/99-322 (INGR No. 04109; IC445068), Potato (*Solanum tuberosum* L.) Germplasm with High Starch and Dry Matter, Low Amylose, and Resistance to Late Blight

SK Pandey, P Manivel, SV Singh and Dinesh Kumar
Central Potato Research Institute, Shimla 171 001 (Himachal Pradesh)

MP/99-322 is the first Indian potato (*Solanum tuberosum* ssp. *tuberosum*) hybrid with higher starch content (> 17%), higher dry matter (>23%), low amylose content (< 27.3%), high amylopectin (>72.7%) and resistance to late blight. This hybrid was identified from the F_1 progeny of a cross MP/91-76 x MP/92-35 following the recurrent breeding selection method at the Central Potato Research Institute campus, Modipuram, Uttar Pradesh.

Morphologically, MP/99-322 is of medium height with open canopy; stem medium thick, green, and wings feebly developed and straight; leaflet width narrow, leaflet coalescence frequency low, rachis and midrib pigmentation absent; flowering profuse, floral stalk light purple, floral stalk-pedicel articulation poorly visible and located above the middle, calyx partially pigmented, bud green to light purple, corolla purple, corolla shape semi-stellate, anther yellow and cone normally developed, stylar length longer than stamen column and stigma bi-lobed; tuber oval/oblong, skin yellow, eyes shallow, eyebrows slightly raised, and flesh cream/pale yellow. Sprout purple/red-purple, shape conical, pubescence and tip closed. It yields between 26-30 t/ha in a crop of 90 days with 87-95% processing grade (>45 mm diameter) tubers and between 31-34 t/ha in a crop of 105 days with 90-95% processing grade tubers in West-Central plains at Modipuram. The hybrid has very high tuber dry matter vis-à-vis starch content at Modipuram in West-Central plains an area known for producing low dry matter potatoes (Table 1). Further, it has lower

Table 1. Percent dry matter, starch, amylose and amylopectin in high dry matter hybrid MP/99-322

Hybrid/variety	Dry matter (%)	Starch (%)	Amylose (%)	Amylopectin (%)	Swelling* volume
MP/99-322	24.18	17.55	27.30	72.70	95.67
K. Chipsona-1	23.20	16.68	27.98	72.02	109.59
Atlantic	22.04	15.64	33.14	66.86	106.67

* mg/g of starch on moisture free basis

amylose content compared to the best control varieties and may be more useful for industrial use. It is resistant to late blight and yields between 22-25 t/ha in North-western hills at Kufri (H.P.) with very high dry matter (27-29%). West-Central plains are endowed with a long potato growing season and this medium maturing, high starch containing hybrid can, therefore, be grown in autumn for production of starch. It can be a good source in the breeding hybrid for high starch/dry matter content.

IISR-G-246 (Coll. No. 3513) (INGR No. 04110; IC432866), a Dwarf Ginger (*Zingiber officinale* Rosc.) Germplasm

B Sasikumar, K Johnson George and KV Saji
Indian Institute of Spices Research, P.O. Marikunnu, Kozhikode 673 012 (Kerala)

Ginger (*Z. officinale* R.) is an important spice and medicinal plant of export value. India is one of the major centres of diversity and has wide variability for yield and quality (Sasikumar *et al.*, 1999). The Indian Institute of Spices Research, Kozhikode maintains 756 accessions of *Zingiber* in its *ex situ* repository comprising landraces, improved varieties, putative wild relatives and the related species. IISR-G-246, is a putative wild type *Z. officinale* with dwarf plant type collected from Sabarimala hills, Pathanamthitta district, in the Western Ghats of Kerala. The accession has characteristic small rhizomes, dwarf plant stature, more tillers, small leaves, early maturity and high oil (Sasikumar *et al.*, 1995). The details of morpho-agronomic feature are listed in Table 1.

Table 1. Morpho-agronmic traits of IISR-G-246

Character	Value
Plant height (cm)	45.56
Tiller (no.)	11.20
Leaf number	19.60
Leaf length (cm)	24.68
Leaf width (cm)	2.58
Maturity (days)	198
Fresh yield (per 3 m^2 bed, kg)	7.08
Dry recovery (%)	19.6
Essential oil (%)	3.5
Fibre (%)	5.0
Oleoresin (%)	7.0

References

Sasikumar B, Krishnamoorthy B, Saji KV, Johnson K George, Peter KV and Ravindran PN (1999) Spices diversity and conservation of plants that yield major spices in India. *Plant Genetic Resources Newsletter* **118:** 19–26.

Sasikumar B, Johnson George K and John Zachariah T (1995) A note on a ginger type (*Z. officinale* R.) collected from Western Ghats. *J Spices & Aromatic Crops* **4**: 160–161.

Coll. No. 5455 (INGR No. 04111; IC370011), Black Pepper (*Piper nigrum* L.) Germplasm with High Oleoresin Content and Bold Berries

KV Saji, K Johnson George, B Sasikumar, John Zacharia and VA Parthasarathy
Indian Institute of Spices Research, P.O. Marikunnu, Kozhikode 673 012 (Kerala)

The genus *Piper* includes important cultivated species like *Piper nigrum* L. the black pepper and betel vine *P. betle* L. *Piper nigrum* is a native of Western Ghats. It is considered as the world's most important spice and rightly known as the "King of spices". Oleoresin is the major valuable product from pepper. It is a blend of volatile oil wax, pungent principle resinoids etc. It is used in food and pharmaceutical industry (Zachariah, 2000).

Table 1. Percent dry matter, starch, amylose and amylopectin in high dry matter hybrid MP/99-322

Hybrid/variety	Dry matter (%)	Starch (%)	Amylose (%)	Amylopectin (%)	Swelling* volume
MP/99-322	24.18	17.55	27.30	72.70	95.67
K. Chipsona-1	23.20	16.68	27.98	72.02	109.59
Atlantic	22.04	15.64	33.14	66.86	106.67

* mg/g of starch on moisture free basis

amylose content compared to the best control varieties and may be more useful for industrial use. It is resistant to late blight and yields between 22-25 t/ha in North-western hills at Kufri (H.P.) with very high dry matter (27-29%). West-Central plains are endowed with a long potato growing season and this medium maturing, high starch containing hybrid can, therefore, be grown in autumn for production of starch. It can be a good source in the breeding hybrid for high starch/dry matter content.

IISR-G-246 (Coll. No. 3513) (INGR No. 04110; IC432866), a Dwarf Ginger (*Zingiber officinale* Rosc.) Germplasm

B Sasikumar, K Johnson George and KV Saji
Indian Institute of Spices Research, P.O. Marikunnu, Kozhikode 673 012 (Kerala)

Ginger (*Z. officinale* R.) is an important spice and medicinal plant of export value. India is one of the major centres of diversity and has wide variability for yield and quality (Sasikumar *et al.*, 1999). The Indian Institute of Spices Research, Kozhikode maintains 756 accessions of *Zingiber* in its *ex situ* repository comprising landraces, improved varieties, putative wild relatives and the related species. IISR-G-246, is a putative wild type *Z. officinale* with dwarf plant type collected from Sabarimala hills, Pathanamthitta district, in the Western Ghats of Kerala. The accession has characteristic small rhizomes, dwarf plant stature, more tillers, small leaves, early maturity and high oil (Sasikumar *et al.*, 1995). The details of morpho-agronomic feature are listed in Table 1.

Table 1. Morpho-agronmic traits of IISR-G-246

Character	Value
Plant height (cm)	45.56
Tiller (no.)	11.20
Leaf number	19.60
Leaf length (cm)	24.68
Leaf width (cm)	2.58
Maturity (days)	198
Fresh yield (per 3 m^2 bed, kg)	7.08
Dry recovery (%)	19.6
Essential oil (%)	3.5
Fibre (%)	5.0
Oleoresin (%)	7.0

References

Sasikumar B, Krishnamoorthy B, Saji KV, Johnson K George, Peter KV and Ravindran PN (1999) Spices diversity and conservation of plants that yield major spices in India. *Plant Genetic Resources Newsletter* **118:** 19–26.

Sasikumar B, Johnson George K and John Zachariah T (1995) A note on a ginger type (*Z. officinale* R.) collected from Western Ghats. *J Spices & Aromatic Crops* **4**: 160–161.

Coll. No. 5455 (INGR No. 04111; IC370011), Black Pepper (*Piper nigrum* L.) Germplasm with High Oleoresin Content and Bold Berries

KV Saji, K Johnson George, B Sasikumar, John Zacharia and VA Parthasarathy
Indian Institute of Spices Research, P.O. Marikunnu, Kozhikode 673 012 (Kerala)

The genus *Piper* includes important cultivated species like *Piper nigrum* L. the black pepper and betel vine *P. betle* L. *Piper nigrum* is a native of Western Ghats. It is considered as the world's most important spice and rightly known as the "King of spices". Oleoresin is the major valuable product from pepper. It is a blend of volatile oil wax, pungent principle resinoids etc. It is used in food and pharmaceutical industry (Zachariah, 2000).

Table 1. Percent dry matter, starch, amylose and amylopectin in high dry matter hybrid MP/99-322

Hybrid/variety	Dry matter (%)	Starch (%)	Amylose (%)	Amylopectin (%)	Swelling* volume
MP/99-322	24.18	17.55	27.30	72.70	95.67
K. Chipsona-1	23.20	16.68	27.98	72.02	109.59
Atlantic	22.04	15.64	33.14	66.86	106.67

* mg/g of starch on moisture free basis

amylose content compared to the best control varieties and may be more useful for industrial use. It is resistant to late blight and yields between 22-25 t/ha in North-western hills at Kufri (H.P.) with very high dry matter (27-29%). West-Central plains are endowed with a long potato growing season and this medium maturing, high starch containing hybrid can, therefore, be grown in autumn for production of starch. It can be a good source in the breeding hybrid for high starch/dry matter content.

IISR-G-246 (Coll. No. 3513) (INGR No. 04110; IC432866), a Dwarf Ginger (*Zingiber officinale* Rosc.) Germplasm

B Sasikumar, K Johnson George and KV Saji
Indian Institute of Spices Research, P.O. Marikunnu, Kozhikode 673 012 (Kerala)

Ginger (*Z. officinale* R.) is an important spice and medicinal plant of export value. India is one of the major centres of diversity and has wide variability for yield and quality (Sasikumar *et al.*, 1999). The Indian Institute of Spices Research, Kozhikode maintains 756 accessions of *Zingiber* in its *ex situ* repository comprising landraces, improved varieties, putative wild relatives and the related species. IISR-G-246, is a putative wild type *Z. officinale* with dwarf plant type collected from Sabarimala hills, Pathanamthitta district, in the Western Ghats of Kerala. The accession has characteristic small rhizomes, dwarf plant stature, more tillers, small leaves, early maturity and high oil (Sasikumar *et al.*, 1995). The details of morpho-agronomic feature are listed in Table 1.

Table 1. Morpho-agronmic traits of IISR-G-246

Character	Value
Plant height (cm)	45.56
Tiller (no.)	11.20
Leaf number	19.60
Leaf length (cm)	24.68
Leaf width (cm)	2.58
Maturity (days)	198
Fresh yield (per 3 m^2 bed, kg)	7.08
Dry recovery (%)	19.6
Essential oil (%)	3.5
Fibre (%)	5.0
Oleoresin (%)	7.0

References

Sasikumar B, Krishnamoorthy B, Saji KV, Johnson K George, Peter KV and Ravindran PN (1999) Spices diversity and conservation of plants that yield major spices in India. *Plant Genetic Resources Newsletter* **118:** 19–26.

Sasikumar B, Johnson George K and John Zachariah T (1995) A note on a ginger type (*Z. officinale* R.) collected from Western Ghats. *J Spices & Aromatic Crops* **4**: 160–161.

Coll. No. 5455 (INGR No. 04111; IC370011), Black Pepper (*Piper nigrum* L.) Germplasm with High Oleoresin Content and Bold Berries

KV Saji, K Johnson George, B Sasikumar, John Zacharia and VA Parthasarathy
Indian Institute of Spices Research, P.O. Marikunnu, Kozhikode 673 012 (Kerala)

The genus *Piper* includes important cultivated species like *Piper nigrum* L. the black pepper and betel vine *P. betle* L. *Piper nigrum* is a native of Western Ghats. It is considered as the world's most important spice and rightly known as the "King of spices". Oleoresin is the major valuable product from pepper. It is a blend of volatile oil wax, pungent principle resinoids etc. It is used in food and pharmaceutical industry (Zachariah, 2000).

Among the 68 wild accessions collected from the silent valley and Nelliampathy forests of Western Ghats, those with the berries available in sufficient quantity were used for quality analysis. Oleoresin was extracted by acetone following ASTA (1968) and piperine by using HPLC- ISO (International Standards Organisation) (1993). Quantitative analysis revealed that accession 5455 (IC370011), collected form the Elam estate of Nelliampathy has significantly high oleoresin content (Table 1).

The Table 2 below summarises the morpho-agronomic characteristics of the accession 5455. The accession can be assessed for its direct utility as a planting material for high altitude areas or can be used in the black pepper improvement programme.

Table 1. Quality attributes of wild *Piper nigrum* from Silent Valley and Nelliampathy

Coll. No.	IC No.	Locality	Place	Piperine (%)	Oleoresin (%)
5616	369961	Sairandri	Silent Valley	1.27	10.7
5419	369916	Kummatanthodu	Silent Valley	2.58	13.79
5434	369985	Pathenthodu	Silent Valley	2.04	15.9
5441	369995	Panthenthodu	Silent Valley	5.56	17.57
5442	369996	Panthenthodu	Silent Valley	6.06	21.6
5455	370011	Elam Estate	Nelliampathy	0.1	28.15

Table 2. Morpho agronomic characteristics of collection 5455

Characters	Value
Orthotropic shoot tip colour	Dark Purple
Pubescence on stem	Absent
Leaf petiole	Grooved.
Leaf petiole length (cm)	6.6 0 (Range 4.0 to 8.0 cm).
Leaf length (cm)	13. 0 (Range 11.0 to 15.0 cm).
Leaf width (cm)	9.0 (Range 7.0 to 11.5 cm).
Leaf lamina shape	Cordate
Leaf base shape	Round
Leaf tip	Acuminate
Leaf margin	Even
Leaf venation	Acrodromous
Leaf texture	Glabrous- coreaceous
Leaf hairs	Absent
Berry size	Bold
Piperine (%)	0.10
Oleoresin (%) 28.15*	

* Oleoresin content in Piper generally ranges from 8-15%.

References

Zacharia JT (2000) On-farm processing of black pepper. In: Black Pepper (ed) PN Ravindran. *Harwoo Academic Publishers*, Netherlands p. 335-354.

International Standards Organisation (ISO) bulletin 11027. (1993) Determination of Piperine content-method using High Performance Liquid chromatography.

American Spice Trade Association (ASTA) (1968) *Official Analytical Methods* 2nd Ed. American Spice Trade Association, New York p. 21.

Coll. No. 197 (INGR No. 04112; IC438344), a Dwarf Clove (*Syzygium aromaticum* (L.) Merr. & Perry) Germplasm

B Krishnamoorthy, J Rema and PA Mathew
Indian Institute of Spices Research, P.O. Marikkunnu., Kozhikode 673 012 (Kerala)

Clove, *Syzygium aromaticum* (L.) Merr. & Perry belonging to family Myrtaceae, is an important tree-spice. It is indigenous to Moluccas Islands in Indonesia, and was introduced into India during the eighteenth century by the colonial rulers. Dried, aromatic and fully-grown unopened flower-bud of clove tree is the clove of commerce.

The Indian Institute of Spices Research, Calicut, Kerala has the mandate to collect, conserve, catalogue and evaluate clove germplasm and a total of 233 accessions has been collected and conserved in the field repository at the experimental farm of the Institute. Two 16 year old clove trees were located at Black Rock Estate, Kanyakumari district, Tamil Nadu, during a collection survey (Krishnamoorthy and Rema, 1995). These trees are dwarf, bushy and about 2 m tall with a canopy width of 5 m. The main trunk is only 0.6 m in height, with profuse branches. Branching starts just 60 cm above the ground level. Each tree yields about 3 kg dry clove per year. The fruits are reddish brown and smaller than normal type. The leaves are arranged in cluster and are longer, broader and thicker with very short internodes, as compared to ordinary clove. A mean of 33.3 leaves could be observed in 12 cm shoot length. The base of the petiole is purplish. The seeds from these trees were collected during the survey and seedlings raised at the institute. The seedlings also exhibited dwarf nature and are conserved at the Institute as acc.197. The morphological characters of the dwarf clove is presented in Table 1.

Among the 68 wild accessions collected from the silent valley and Nelliampathy forests of Western Ghats, those with the berries available in sufficient quantity were used for quality analysis. Oleoresin was extracted by acetone following ASTA (1968) and piperine by using HPLC- ISO (International Standards Organisation) (1993). Quantitative analysis revealed that accession 5455 (IC370011), collected form the Elam estate of Nelliampathy has significantly high oleoresin content (Table 1).

The Table 2 below summarises the morpho-agronomic characteristics of the accession 5455. The accession can be assessed for its direct utility as a planting material for high altitude areas or can be used in the black pepper improvement programme.

Table 1. Quality attributes of wild *Piper nigrum* from Silent Valley and Nelliampathy

Coll. No.	IC No.	Locality	Place	Piperine (%)	Oleoresin (%)
5616	369961	Sairandri	Silent Valley	1.27	10.7
5419	369916	Kummatanthodu	Silent Valley	2.58	13.79
5434	369985	Pathenthodu	Silent Valley	2.04	15.9
5441	369995	Panthenthodu	Silent Valley	5.56	17.57
5442	369996	Panthenthodu	Silent Valley	6.06	21.6
5455	370011	Elam Estate	Nelliampathy	0.1	28.15

Table 2. Morpho agronomic characteristics of collection 5455

Characters	Value
Orthotropic shoot tip colour	Dark Purple
Pubescence on stem	Absent
Leaf petiole	Grooved.
Leaf petiole length (cm)	6.6 0 (Range 4.0 to 8.0 cm).
Leaf length (cm)	13. 0 (Range 11.0 to 15.0 cm).
Leaf width (cm)	9.0 (Range 7.0 to 11.5 cm).
Leaf lamina shape	Cordate
Leaf base shape	Round
Leaf tip	Acuminate
Leaf margin	Even
Leaf venation	Acrodromous
Leaf texture	Glabrous- coreaceous
Leaf hairs	Absent
Berry size	Bold
Piperine (%)	0.10
Oleoresin (%) 28.15*	

* Oleoresin content in Piper generally ranges from 8-15%.

References

Zacharia JT (2000) On-farm processing of black pepper. In: Black Pepper (ed) PN Ravindran. *Harwoo Academic Publishers*, Netherlands p. 335-354.

International Standards Organisation (ISO) bulletin 11027. (1993) Determination of Piperine content-method using High Performance Liquid chromatography.

American Spice Trade Association (ASTA) (1968) *Official Analytical Methods* 2nd Ed. American Spice Trade Association, New York p. 21.

Coll. No. 197 (INGR No. 04112; IC438344), a Dwarf Clove (*Syzygium aromaticum* (L.) Merr. & Perry) Germplasm

B Krishnamoorthy, J Rema and PA Mathew
Indian Institute of Spices Research, P.O. Marikkunnu., Kozhikode 673 012 (Kerala)

Clove, *Syzygium aromaticum* (L.) Merr. & Perry belonging to family Myrtaceae, is an important tree-spice. It is indigenous to Moluccas Islands in Indonesia, and was introduced into India during the eighteenth century by the colonial rulers. Dried, aromatic and fully-grown unopened flower-bud of clove tree is the clove of commerce.

The Indian Institute of Spices Research, Calicut, Kerala has the mandate to collect, conserve, catalogue and evaluate clove germplasm and a total of 233 accessions has been collected and conserved in the field repository at the experimental farm of the Institute. Two 16 year old clove trees were located at Black Rock Estate, Kanyakumari district, Tamil Nadu, during a collection survey (Krishnamoorthy and Rema, 1995). These trees are dwarf, bushy and about 2 m tall with a canopy width of 5 m. The main trunk is only 0.6 m in height, with profuse branches. Branching starts just 60 cm above the ground level. Each tree yields about 3 kg dry clove per year. The fruits are reddish brown and smaller than normal type. The leaves are arranged in cluster and are longer, broader and thicker with very short internodes, as compared to ordinary clove. A mean of 33.3 leaves could be observed in 12 cm shoot length. The base of the petiole is purplish. The seeds from these trees were collected during the survey and seedlings raised at the institute. The seedlings also exhibited dwarf nature and are conserved at the Institute as acc.197. The morphological characters of the dwarf clove is presented in Table 1.

Table 1. Morphological characters of dwarf clove

Character	Value
Age	8 years
Habit	Shrub
Height	52.62 cm at 8th year (range: 35.0 cm to 67.0 cm)
Shape of tree	Bushy
Canopy	50 cm (range: 24.0 cm to 60.0 cm)
Petiole colour	Purple
Petiole length	2.3 cm (range 2.1 cm to 2.4 cm)
Leaf shape	Lanceolate
Leaf length	10.9 cm (range 8.9 cm to 11.2 cm)
Leaf margin	Wavy
Leaf texture	Glabrous

Reference

Krishnamoorthy B and J Rema (1995) Three promising morphological variants in clove (*Syzygium aromaticum* (L.) Merr. & Perry) from Tamil Nadu, *Indian J Spices and Aromatic Crops* **3**: 168.

Safed Musli (*Chlorophytum Borivilianum* Sant. & Fern) Germplasm with Fleshy Roots

KA Geetha, Satyabrata Maiti and Narendra Gajbhiye
National Research Centre for Medicinal and Aromatic Plants, Boriavi, Anand 387 310 (Gujarat)

NRCCB-1 (INGR No. 04113; IC 323367)

Safed musli (*Chlorophytum borivilianum* Sant. & Fern) is widely distributed in forests of Maharashtra, Gujarat, Rajasthan & Madhya Pradesh. It is being used as a raw material for preparation of many ayurvedic tonics and therefore it is in high demand. Under the research programme on development of superior varieties a large number of collections have been assembled at the National Research Centre on Medicinal & Aromatic Plant, Anand. Evaluation of these collections for various important traits resulted in identification of NRCCB-1 as one of the superior distinct genotype. It has fleshy long, blunt ended, dark coloured and compact bunch type roots and excellent storage quality. The other characters of this line are listed in Table 1.

Table 1. Morpho-agronomic characteristics of NRCCB-1

Characters	Value
Number of leaves / plant	33.00 +/-11.00
Leaf length (cm)	33.20 +/-2.72
Leaf breadth (cm)	2.22 +/- 0.18
Leaf base (cm)	1.15 +/- 0.13
Fleshy root yield/plant	54.90 +/-4.31
Fleshy root length (cm)	12.34 +/-1.63
Dry matter content (%)	25.63 +/-2.80
Number of fleshy root/ plant	15.63 +/-4.27
Fleshy root diameter (cm)	0.91 +/-0.05
Single fleshy root weight (g)	3.55 +/-0.50

NRCCB-2 (INGR No. 04114; IC323368)

The evaluation of collections assembled at the National Research Centre on Medicinal & Aromatic Plant, Anand for various important traits resulted in identification of another distinct superior genotype NRCCB-2. This genotype of safed musli (*Chlorophytum borivilianum* Sant. & Fern) has fleshy, short, blunt ended, light coloured and diverged type roots, and has excellent storage quality. The other relevant morphological traits recorded are listed below in Table 1.

Table 1. Morpho-agronomic characteristics of NRCCB-2

Characters	Value
Number of leaves/ plant	25.33 +/- 8.02
Leaf length (cm)	22.25 +/- 0.29
Leaf breadth (cm)	1.80 +/- 0.41
Leaf base (cm)	1.01 +/- 0.20
Fleshy root yield / plant (g)	46.61 +/- 20.41
Fleshy root length (cm)	7.76 +/- 0.75
Dry matter content (%)	24.28 +/-1.28
Number of fleshy root / plant	28.83 +/-14.44
Fleshy root diameter (cm)	0.80 +/- 0.05
Single fleshy root weight (g)	1.79 +/- 0.37

Table 1. Morphological characters of dwarf clove

Character	Value
Age	8 years
Habit	Shrub
Height	52.62 cm at 8th year (range: 35.0 cm to 67.0 cm)
Shape of tree	Bushy
Canopy	50 cm (range: 24.0 cm to 60.0 cm)
Petiole colour	Purple
Petiole length	2.3 cm (range 2.1 cm to 2.4 cm)
Leaf shape	Lanceolate
Leaf length	10.9 cm (range 8.9 cm to 11.2 cm)
Leaf margin	Wavy
Leaf texture	Glabrous

Reference

Krishnamoorthy B and J Rema (1995) Three promising morphological variants in clove (*Syzygium aromaticum* (L.) Merr. & Perry) from Tamil Nadu, *Indian J Spices and Aromatic Crops* **3**: 168.

Safed Musli (*Chlorophytum Borivilianum* Sant. & Fern) Germplasm with Fleshy Roots

KA Geetha, Satyabrata Maiti and Narendra Gajbhiye
National Research Centre for Medicinal and Aromatic Plants, Boriavi, Anand 387 310 (Gujarat)

NRCCB-1 (INGR No. 04113; IC 323367)

Safed musli (*Chlorophytum borivilianum* Sant. & Fern) is widely distributed in forests of Maharashtra, Gujarat, Rajasthan & Madhya Pradesh. It is being used as a raw material for preparation of many ayurvedic tonics and therefore it is in high demand. Under the research programme on development of superior varieties a large number of collections have been assembled at the National Research Centre on Medicinal & Aromatic Plant, Anand. Evaluation of these collections for various important traits resulted in identification of NRCCB-1 as one of the superior distinct genotype. It has fleshy long, blunt ended, dark coloured and compact bunch type roots and excellent storage quality. The other characters of this line are listed in Table 1.

Table 1. Morpho-agronomic characteristics of NRCCB-1

Characters	Value
Number of leaves / plant	33.00 +/-11.00
Leaf length (cm)	33.20 +/-2.72
Leaf breadth (cm)	2.22 +/- 0.18
Leaf base (cm)	1.15 +/- 0.13
Fleshy root yield/plant	54.90 +/-4.31
Fleshy root length (cm)	12.34 +/-1.63
Dry matter content (%)	25.63 +/-2.80
Number of fleshy root/ plant	15.63 +/-4.27
Fleshy root diameter (cm)	0.91 +/-0.05
Single fleshy root weight (g)	3.55 +/-0.50

NRCCB-2 (INGR No. 04114; IC323368)

The evaluation of collections assembled at the National Research Centre on Medicinal & Aromatic Plant, Anand for various important traits resulted in identification of another distinct superior genotype NRCCB-2. This genotype of safed musli (*Chlorophytum borivilianum* Sant. & Fern) has fleshy, short, blunt ended, light coloured and diverged type roots, and has excellent storage quality. The other relevant morphological traits recorded are listed below in Table 1.

Table 1. Morpho-agronomic characteristics of NRCCB-2

Characters	Value
Number of leaves/ plant	25.33 +/- 8.02
Leaf length (cm)	22.25 +/- 0.29
Leaf breadth (cm)	1.80 +/- 0.41
Leaf base (cm)	1.01 +/- 0.20
Fleshy root yield / plant (g)	46.61 +/- 20.41
Fleshy root length (cm)	7.76 +/- 0.75
Dry matter content (%)	24.28 +/-1.28
Number of fleshy root / plant	28.83 +/-14.44
Fleshy root diameter (cm)	0.80 +/- 0.05
Single fleshy root weight (g)	1.79 +/- 0.37

Elaichi (INGR No. 04115; IC427821), a Mango (*Mangifera indica* L.) Germplasm with Tolerance to Floral Malformation

S Rajan, Ram Kumar, SS Negi, AK Mishra, GC Sinha and IS Yadav
Central Institute for Subtropical Horticulture, Lucknow 227 107 (Uttar Pradesh)

Mango malformation is the most important disease of mango (*Mangifera indica* L.) causing considerable yield losses to mango production. Development or identification of genetic resistance to malformation is the only practical approach. A large number of mango germplasm has been assemble at the Central Institute for Subtropical Horticulture, Lucknow and was screened against malformation on a scale of 0-5 between 1994 & 1997. During the screening the cultivar, Elaichi was found completely free form floral and vegetative malformation. Elaichi, though has small (4.5 x 4.5 cm) fruit size, possesses several good characters , such as large number of fruits, high yield and regulated bearing with semi-dwarf canopy. The pulp, skin and stone ratio is about 8:1:1. This cultivar is being used in breeding programme to develop mango varieties resistant/ tolerant to malformation at the Central Institute for Subtropical Horticulture, Lucknow.

Wild Mango (INGR No. 04122; IC409079), a Natural Wild Germplasm of Mango (*Mangifera andamanica* King.) from Andaman Islands with Regular Bearing, Disease Resistance and Wood Value

DR Singh and RP Medhi
Central Agricultural Research Institute, Port Blair 744 101 (Andaman and Nicobar Islands)

The genus *Mangifera* belongs to the order Sapindales in the family Anacardiaceae. The genus *Mangifera* consists of 69 species, mostly restricted to tropical Asia. Wild mangoes occur in India, Sri Lanka, Bangladesh, Myanmar, India (Sikkim), Thailand, Korea, Vietnam, Laos, southern China, Malaysia, Singapore, Indonesia, Brunei, the Philippines, Papua New Guinea and the Solomon and Caroline Islands. In India, this genus was earlier known by six species, of which four, viz; *M andamanica, M. camptosperns, M. indica* and *M. nicobarica* were reported from the Andaman and Nicobar islands. *M. andamanica* is endemic and rare, distributed in the Andaman forest. It is found wild in south Andaman (Chouldari and Chidyatapu, as cited by Singh *et al.*, 2002). The species has been collected, conserved and multiplied at the Central Agricultural Research Institute, Port Blair.

It is a large tree of 30- 40 m height, leaves are 3-5 inch long, obovate to broadly oblanceolate or elliptic, lateral nerves 10-12 pairs, curving upwards, petioles 0.5-1 inch long, channelled, flowers ¼ inch in diameter; petals twice as long as the lanceolate sepals and drupe 1-1.5 inch long (Table 1). Fruits are small, yellowish orange in colour and ripen in March-April. The fruits are free from pests and diseases (Medhi and Singh, 2004). The fruits are good source of vitamin A and C (98.50 mg/ 100g) with TSS 8.60 percent. The total sugar and reducing sugars in the fruit was 3.47 and 1.51 percent respectively (Singh *et al.*, 2005). The tree has a long straight bole with maximum canopy located at the top. The rootstock can be used in resistance breeding (Singh *et al.*, 2002-03) and wood for timber purpose.

Table 1. Some salient features of *Mangifera andamanica* King

Features	Value
Fruit Shape	Plum shaped
Fruit Surface	Smooth
Fruit weight (g)	18.30
Colour of the fruit	Yellowish Orange
Length/ Breadth of the fruit	3.62/ 2.76
Colour of the cotyledon	Lavender
Surface of the stone	Hairy
Weight of the stone	4.02
Pulp (%)	57.05
Juice (%)	42.73
TSS (%)	8.6
Acidity	0.37
Total Sugar (%)	3.47
Reducing Sugar (%)	1.51
Vitamin C mg/100g	98.50

Elaichi (INGR No. 04115; IC427821), a Mango (*Mangifera indica* L.) Germplasm with Tolerance to Floral Malformation

S Rajan, Ram Kumar, SS Negi, AK Mishra, GC Sinha and IS Yadav
Central Institute for Subtropical Horticulture, Lucknow 227 107 (Uttar Pradesh)

Mango malformation is the most important disease of mango (*Mangifera indica* L.) causing considerable yield losses to mango production. Development or identification of genetic resistance to malformation is the only practical approach. A large number of mango germplasm has been assemble at the Central Institute for Subtropical Horticulture, Lucknow and was screened against malformation on a scale of 0-5 between 1994 & 1997. During the screening the cultivar, Elaichi was found completely free form floral and vegetative malformation. Elaichi, though has small (4.5 x 4.5 cm) fruit size, possesses several good characters , such as large number of fruits, high yield and regulated bearing with semi-dwarf canopy. The pulp, skin and stone ratio is about 8:1:1. This cultivar is being used in breeding programme to develop mango varieties resistant/ tolerant to malformation at the Central Institute for Subtropical Horticulture, Lucknow.

Wild Mango (INGR No. 04122; IC409079), a Natural Wild Germplasm of Mango (*Mangifera andamanica* King.) from Andaman Islands with Regular Bearing, Disease Resistance and Wood Value

DR Singh and RP Medhi
Central Agricultural Research Institute, Port Blair 744 101 (Andaman and Nicobar Islands)

The genus *Mangifera* belongs to the order Sapindales in the family Anacardiaceae. The genus *Mangifera* consists of 69 species, mostly restricted to tropical Asia. Wild mangoes occur in India, Sri Lanka, Bangladesh, Myanmar, India (Sikkim), Thailand, Korea, Vietnam, Laos, southern China, Malaysia, Singapore, Indonesia, Brunei, the Philippines, Papua New Guinea and the Solomon and Caroline Islands. In India, this genus was earlier known by six species, of which four, viz; *M andamanica, M. camptosperns, M. indica* and *M. nicobarica* were reported from the Andaman and Nicobar islands. *M. andamanica* is endemic and rare, distributed in the Andaman forest. It is found wild in south Andaman (Chouldari and Chidyatapu, as cited by Singh *et al.*, 2002). The species has been collected, conserved and multiplied at the Central Agricultural Research Institute, Port Blair.

It is a large tree of 30- 40 m height, leaves are 3-5 inch long, obovate to broadly oblanceolate or elliptic, lateral nerves 10-12 pairs, curving upwards, petioles 0.5-1 inch long, channelled, flowers ¼ inch in diameter; petals twice as long as the lanceolate sepals and drupe 1-1.5 inch long (Table 1). Fruits are small, yellowish orange in colour and ripen in March-April. The fruits are free from pests and diseases (Medhi and Singh, 2004). The fruits are good source of vitamin A and C (98.50 mg/ 100g) with TSS 8.60 percent. The total sugar and reducing sugars in the fruit was 3.47 and 1.51 percent respectively (Singh *et al.*, 2005). The tree has a long straight bole with maximum canopy located at the top. The rootstock can be used in resistance breeding (Singh *et al.*, 2002-03) and wood for timber purpose.

Table 1. Some salient features of *Mangifera andamanica* King

Features	Value
Fruit Shape	Plum shaped
Fruit Surface	Smooth
Fruit weight (g)	18.30
Colour of the fruit	Yellowish Orange
Length/ Breadth of the fruit	3.62/ 2.76
Colour of the cotyledon	Lavender
Surface of the stone	Hairy
Weight of the stone	4.02
Pulp (%)	57.05
Juice (%)	42.73
TSS (%)	8.6
Acidity	0.37
Total Sugar (%)	3.47
Reducing Sugar (%)	1.51
Vitamin C mg/100g	98.50

References

Medhi RP and DR Singh (2004) *Wild Mangoes of Andaman and Nicobar Islands*. Published by Director, CARI, Port Blair.

Singh DB, BL Attri, RP Medhi, MA Suryanarayan and TVRS Sharma (2002) *Under Utilized Fruits of Andaman and Nicobar islands*, Published by Director, CARI, Port Blair, p-9

Singh DR, RP Medhi, S Senani, RB Rai and R Senthil Kumar (2005) *Nutritional Aspects of Under Utilized Fruits of Andaman and Nicobar Islands. Research Bulletin No.17* Published by Director, CARI, Port Blair, p-57.

Singh DR, BL Attri, RP Medhi, Kissan Swaroop and VB Pandey (2002-03) *"Andaman Nicobar mein phal utpadan ka bhavishya" Krishika*. Published by Director, CARI Port Blair, p-29

Hybrid Guava, *Psidium molle* x *P guajava* (INGR No. 04116; IC427822), with Resistance to Guava Wilt

S Rajan, Ram Kumar, AK Mishra and SS Negi

Central Institute for Subtropical Horticulture, Lucknow 227 107 (Uttar Pradesh)

All varieties of *Psidium guajava* are susceptible to wilt diseases. *Psidium molle* has field resistance against the guava wilt, because of having tough textured plant. It can be used as a rootstock, but its poor rooting habit interferes in it multiplication. Therefore, a hybrid population was raised from a cross, *Psidium molle* x *P guajava* and was screened against the guava wilt at the Central Institute for Subtropical Horticulture, Lucknow. It was screened against guava wilt by growing the F_1 population in wilt sick plot and repeated inoculation with standardised stem hole inoculation technique with potent guava wilt pathogen *viz., Gliocladium roseum, Fusarium oxysporum* and *F. solani.* None of the plant of the F_1 hybrid showed wilting and therefore were considered resistance. Thus *Psidium molle* and F_1 hybrid between *Psidium molle* x *P guajava* can be used a source of guava wilt resistance.

Ornamental Jatropha Interspecific Hybrids (*Jatropha curcas* x *J. integerrima*)

M Sujatha and AJ Prabakaran

Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

Soumya (INGR No. 04117; IC427819)

Soumya is an ornamental Jatropha interspecific hybrid (*Jatropha curcas* x *J. integerrima*) with pink flower and continuous flowering. The Directorate of Oilseed Research, Hyderabad developed it through interspecific hybridisation. *J. curcas* and *J. integerrima* are two economically important species. The F_1 hybrids are vigorous, freely flowering, luxuriant and morphologically intermediate between the two parents. The distinctness of the hybrids lies in the petal colour and the continuous flower bearing character. Unlike the parents, bearing yellowish-green and crimson-red, flowers Soumya has pink flowers. The robust and attractive plant type and pink colours are added advantages as an ornamental plant compared to *J. integerrima,* which has sparse branching and relatively few flowers. The hybrids can be easily propagated through stem cuttings. Backcrossing of the hybrids with *J. curcas* resulted in progeny with improved fruit and seed characteristics and hence, offers promise in improvement of *J. curcas*. The hybrids are adaptable for diverse situations including poor soils.

Swetha (INGR No. 04118; IC427820)

Swetha is another ornamental Jatropha interspecific hybrid (*Jatropha curcas* x *J. integerrima*) with white flower and continuous flowering. It is a sister line developed through interspecific hybridisation between two economically important species viz., *J. curcas* and *J. integerrima*. The F_1 hybrids are vigorous, freely flowering, luxuriant and morphologically intermediate. Unlike the parents they have white flowers. The more robust and attractive plant type of the hybrid white flowers adds to ornamental value compared to parents. The hybrids can be easily propagated through stem cuttings. Backcrossing of the hybrids with *J. curcas* resulted in progeny with improved fruit and seed characteristics and hence, offers promise for improvement of *J. curcas* per se. The hybrids are adaptable for diverse situations including poor soils.

References

Medhi RP and DR Singh (2004) *Wild Mangoes of Andaman and Nicobar Islands*. Published by Director, CARI, Port Blair.

Singh DB, BL Attri, RP Medhi, MA Suryanarayan and TVRS Sharma (2002) *Under Utilized Fruits of Andaman and Nicobar islands*, Published by Director, CARI, Port Blair, p-9

Singh DR, RP Medhi, S Senani, RB Rai and R Senthil Kumar (2005) *Nutritional Aspects of Under Utilized Fruits of Andaman and Nicobar Islands. Research Bulletin No.17* Published by Director, CARI, Port Blair, p-57.

Singh DR, BL Attri, RP Medhi, Kissan Swaroop and VB Pandey (2002-03) *"Andaman Nicobar mein phal utpadan ka bhavishya" Krishika*. Published by Director, CARI Port Blair, p-29

Hybrid Guava, *Psidium molle* x *P guajava* (INGR No. 04116; IC427822), with Resistance to Guava Wilt

S Rajan, Ram Kumar, AK Mishra and SS Negi

Central Institute for Subtropical Horticulture, Lucknow 227 107 (Uttar Pradesh)

All varieties of *Psidium guajava* are susceptible to wilt diseases. *Psidium molle* has field resistance against the guava wilt, because of having tough textured plant. It can be used as a rootstock, but its poor rooting habit interferes in it multiplication. Therefore, a hybrid population was raised from a cross, *Psidium molle* x *P guajava* and was screened against the guava wilt at the Central Institute for Subtropical Horticulture, Lucknow. It was screened against guava wilt by growing the F_1 population in wilt sick plot and repeated inoculation with standardised stem hole inoculation technique with potent guava wilt pathogen *viz., Gliocladium roseum, Fusarium oxysporum* and *F. solani.* None of the plant of the F_1 hybrid showed wilting and therefore were considered resistance. Thus *Psidium molle* and F_1 hybrid between *Psidium molle* x *P guajava* can be used a source of guava wilt resistance.

Ornamental Jatropha Interspecific Hybrids (*Jatropha curcas* x *J. integerrima*)

M Sujatha and AJ Prabakaran

Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

Soumya (INGR No. 04117; IC427819)

Soumya is an ornamental Jatropha interspecific hybrid (*Jatropha curcas* x *J. integerrima*) with pink flower and continuous flowering. The Directorate of Oilseed Research, Hyderabad developed it through interspecific hybridisation. *J. curcas* and *J. integerrima* are two economically important species. The F_1 hybrids are vigorous, freely flowering, luxuriant and morphologically intermediate between the two parents. The distinctness of the hybrids lies in the petal colour and the continuous flower bearing character. Unlike the parents, bearing yellowish-green and crimson-red, flowers Soumya has pink flowers. The robust and attractive plant type and pink colours are added advantages as an ornamental plant compared to *J. integerrima,* which has sparse branching and relatively few flowers. The hybrids can be easily propagated through stem cuttings. Backcrossing of the hybrids with *J. curcas* resulted in progeny with improved fruit and seed characteristics and hence, offers promise in improvement of *J. curcas*. The hybrids are adaptable for diverse situations including poor soils.

Swetha (INGR No. 04118; IC427820)

Swetha is another ornamental Jatropha interspecific hybrid (*Jatropha curcas* x *J. integerrima*) with white flower and continuous flowering. It is a sister line developed through interspecific hybridisation between two economically important species viz., *J. curcas* and *J. integerrima*. The F_1 hybrids are vigorous, freely flowering, luxuriant and morphologically intermediate. Unlike the parents they have white flowers. The more robust and attractive plant type of the hybrid white flowers adds to ornamental value compared to parents. The hybrids can be easily propagated through stem cuttings. Backcrossing of the hybrids with *J. curcas* resulted in progeny with improved fruit and seed characteristics and hence, offers promise for improvement of *J. curcas* per se. The hybrids are adaptable for diverse situations including poor soils.

References

Medhi RP and DR Singh (2004) *Wild Mangoes of Andaman and Nicobar Islands*. Published by Director, CARI, Port Blair.

Singh DB, BL Attri, RP Medhi, MA Suryanarayan and TVRS Sharma (2002) *Under Utilized Fruits of Andaman and Nicobar islands*, Published by Director, CARI, Port Blair, p-9

Singh DR, RP Medhi, S Senani, RB Rai and R Senthil Kumar (2005) *Nutritional Aspects of Under Utilized Fruits of Andaman and Nicobar Islands. Research Bulletin No.17* Published by Director, CARI, Port Blair, p-57.

Singh DR, BL Attri, RP Medhi, Kissan Swaroop and VB Pandey (2002-03) *"Andaman Nicobar mein phal utpadan ka bhavishya" Krishika*. Published by Director, CARI Port Blair, p-29

Hybrid Guava, *Psidium molle* x *P guajava* (INGR No. 04116; IC427822), with Resistance to Guava Wilt

S Rajan, Ram Kumar, AK Mishra and SS Negi

Central Institute for Subtropical Horticulture, Lucknow 227 107 (Uttar Pradesh)

All varieties of *Psidium guajava* are susceptible to wilt diseases. *Psidium molle* has field resistance against the guava wilt, because of having tough textured plant. It can be used as a rootstock, but its poor rooting habit interferes in it multiplication. Therefore, a hybrid population was raised from a cross, *Psidium molle* x *P guajava* and was screened against the guava wilt at the Central Institute for Subtropical Horticulture, Lucknow. It was screened against guava wilt by growing the F_1 population in wilt sick plot and repeated inoculation with standardised stem hole inoculation technique with potent guava wilt pathogen *viz., Gliocladium roseum, Fusarium oxysporum* and *F. solani.* None of the plant of the F_1 hybrid showed wilting and therefore were considered resistance. Thus *Psidium molle* and F_1 hybrid between *Psidium molle* x *P guajava* can be used a source of guava wilt resistance.

Ornamental Jatropha Interspecific Hybrids (*Jatropha curcas* x *J. integerrima*)

M Sujatha and AJ Prabakaran

Directorate of Oilseed Research, Rajendranagar, Hyderabad 500 030 (Andhra Pradesh)

Soumya (INGR No. 04117; IC427819)

Soumya is an ornamental Jatropha interspecific hybrid (*Jatropha curcas* x *J. integerrima*) with pink flower and continuous flowering. The Directorate of Oilseed Research, Hyderabad developed it through interspecific hybridisation. *J. curcas* and *J. integerrima* are two economically important species. The F_1 hybrids are vigorous, freely flowering, luxuriant and morphologically intermediate between the two parents. The distinctness of the hybrids lies in the petal colour and the continuous flower bearing character. Unlike the parents, bearing yellowish-green and crimson-red, flowers Soumya has pink flowers. The robust and attractive plant type and pink colours are added advantages as an ornamental plant compared to *J. integerrima,* which has sparse branching and relatively few flowers. The hybrids can be easily propagated through stem cuttings. Backcrossing of the hybrids with *J. curcas* resulted in progeny with improved fruit and seed characteristics and hence, offers promise in improvement of *J. curcas*. The hybrids are adaptable for diverse situations including poor soils.

Swetha (INGR No. 04118; IC427820)

Swetha is another ornamental Jatropha interspecific hybrid (*Jatropha curcas* x *J. integerrima*) with white flower and continuous flowering. It is a sister line developed through interspecific hybridisation between two economically important species viz., *J. curcas* and *J. integerrima*. The F_1 hybrids are vigorous, freely flowering, luxuriant and morphologically intermediate. Unlike the parents they have white flowers. The more robust and attractive plant type of the hybrid white flowers adds to ornamental value compared to parents. The hybrids can be easily propagated through stem cuttings. Backcrossing of the hybrids with *J. curcas* resulted in progeny with improved fruit and seed characteristics and hence, offers promise for improvement of *J. curcas* per se. The hybrids are adaptable for diverse situations including poor soils.

Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of **ICAR in its XIVth meeting held on 11th August 2005** at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 34 germplasm lines out of the 105 proposals considered.

T 1471 (Kodiyan) (INGR No. 05001; IC471839), Rice (*Oryza sativa*) Germplasm with Anaerobic Respiration Tolerant Seedling

BC Patra and RK Sarkar
Central Rice Research Institute, Cuttack 753 006 (Orissa)

The rice germplasm, namely, T-1471 (Ac. No. 1631, Kodiyan, INGR No. 05001, IC471839), a photosensitive cultivar was collected from the farmer's field in Malabar region of erstwhile Madras Presidency and identified at the Central Rice Research Institute, Cuttack. This germplasm line provides a new source of anaerobic seedling tolerance. In the rain-fed lowland rice ecosystem, direct seeding is common as the land gets submerged after the first monsoon showers. Direct seeding induces robustness so that the seedlings can avoid complete submergence in the peak monsoon months of July-August. However, there is substantial and heavy loss when there is torrential rain followed by early flooding. Kodiyan is a potentially valuable germplasm line, which sustains early flooding even after 5 days of sowing/ planting and also grows well under anaerobic condition (Sarkar and Das, 2003). Besides, this germplasm would be of immense use as a valuable gene source in irrigated rice where wet direct seeding is practiced instead of transplanting. Although wet sowing is more economical than transplanting, 3 major constraints, viz. inconsistent seedling establishment, greater weed infestation and higher lodging incidence create hindrances in adopting this technology. Anaerobic seedling establishment can solve these problems (Sarkar *et al.*, 1999). The morpho-agronomic traits of the germplasm are described in Table 1.

Table 1. Chief descriptive morphological characteristics of rice germplasm T-1471 (Kodiyan, AC-1631)

Characteristics	T-1471(Kodiyan)
Height of 21 days old seedling (cm)	34
Leaf length(cm)	44.8
Leaf width(cm)	1.1
Ligule length (cm)	2.2
Culm length (cm)	116.8
Culm number	7.6
Culm strength	Strong
Stigma colour	White
Awn	Absent
Panicle length(cm)	27.4
Grain length(mm)	9.4
Grain breadth(mm)	4.0
l/b ratio	2.35
1000 grain weight(gm)	26.2
Grain shape	Medium
Maturity duration(days)	143
Aroma	Absent
Coleoptile, basal leaf sheath & ligule colour	Green
Panicle exertion	Partly exerted
Panicle type	Intermediate

References

Sarkar RK and S Das (2003) Yield of rain-fed lowland rice with medium water depth under anaerobic direct seeding and transplanting. *Trop Agric* **43**: 192-198.

Sarkar RK, SK Bera and RN De (1999) Rice (*Oryza sativa*) cultivars for anaerobic seeding *Indian J of Agric Sci* **69**: 73-76.

* *Communicated by Dr. Anurudh Kumar Singh, Member Secretary, Plant Germplasm Registration Committee, National Bureau of Plant Genetic Resources, Indian Council of Agricultural Research, Pusa Campus, New Delhi*

Plant Germplasm Registration Notice*

The Plant Germplasm Registration Committee of **ICAR in its XIVth meeting held on 11th August 2005** at the National Bureau of Plant Genetic Resources, New Delhi approved the registration of following 34 germplasm lines out of the 105 proposals considered.

T 1471 (Kodiyan) (INGR No. 05001; IC471839), Rice (*Oryza sativa*) Germplasm with Anaerobic Respiration Tolerant Seedling

BC Patra and RK Sarkar
Central Rice Research Institute, Cuttack 753 006 (Orissa)

The rice germplasm, namely, T-1471 (Ac. No. 1631, Kodiyan, INGR No. 05001, IC471839), a photosensitive cultivar was collected from the farmer's field in Malabar region of erstwhile Madras Presidency and identified at the Central Rice Research Institute, Cuttack. This germplasm line provides a new source of anaerobic seedling tolerance. In the rain-fed lowland rice ecosystem, direct seeding is common as the land gets submerged after the first monsoon showers. Direct seeding induces robustness so that the seedlings can avoid complete submergence in the peak monsoon months of July-August. However, there is substantial and heavy loss when there is torrential rain followed by early flooding. Kodiyan is a potentially valuable germplasm line, which sustains early flooding even after 5 days of sowing/ planting and also grows well under anaerobic condition (Sarkar and Das, 2003). Besides, this germplasm would be of immense use as a valuable gene source in irrigated rice where wet direct seeding is practiced instead of transplanting. Although wet sowing is more economical than transplanting, 3 major constraints, viz. inconsistent seedling establishment, greater weed infestation and higher lodging incidence create hindrances in adopting this technology. Anaerobic seedling establishment can solve these problems (Sarkar *et al.*, 1999). The morpho-agronomic traits of the germplasm are described in Table 1.

Table 1. Chief descriptive morphological characteristics of rice germplasm T-1471 (Kodiyan, AC-1631)

Characteristics	T-1471(Kodiyan)
Height of 21 days old seedling (cm)	34
Leaf length(cm)	44.8
Leaf width(cm)	1.1
Ligule length (cm)	2.2
Culm length (cm)	116.8
Culm number	7.6
Culm strength	Strong
Stigma colour	White
Awn	Absent
Panicle length(cm)	27.4
Grain length(mm)	9.4
Grain breadth(mm)	4.0
l/b ratio	2.35
1000 grain weight(gm)	26.2
Grain shape	Medium
Maturity duration(days)	143
Aroma	Absent
Coleoptile, basal leaf sheath & ligule colour	Green
Panicle exertion	Partly exerted
Panicle type	Intermediate

References

Sarkar RK and S Das (2003) Yield of rain-fed lowland rice with medium water depth under anaerobic direct seeding and transplanting. *Trop Agric* **43**: 192-198.

Sarkar RK, SK Bera and RN De (1999) Rice (*Oryza sativa*) cultivars for anaerobic seeding *Indian J of Agric Sci* **69**: 73-76.

* *Communicated by Dr. Anurudh Kumar Singh, Member Secretary, Plant Germplasm Registration Committee, National Bureau of Plant Genetic Resources, Indian Council of Agricultural Research, Pusa Campus, New Delhi*

Pusa 1460-01-32-6-7-67 (IET-18990) (INGR No. 05002; IC522199), Basmati Rice (*Oryza sativa*) Germplasm with more Aroma, Free from Grain Chalkiness and Resistance to Bacterial Blight

VP Singh, AK Singh, SS Atwal, T Mohapatra, Minu Joseph, S Gopala Krishnan, KR Pandey and Jayshree Gopalakrishna
Division of Genetics, Indian Agricultural Research Institute, New Delhi 110 012

Pusa Basmati-1 the first semi dwarf high yielding, early maturing variety having key Basmati quality characteristics, released in 1989 is very popular with the cultivators, traders, exporters and consumers. However, it is highly susceptible to bacterial blight (BB) caused by *Xanthomonas oryzae* pv *oryzae* resulting into loss of yield and quality. Pusa 1460 has been developed at the Indian Agricultural Research Institute, New Delhi through marker assisted pyramiding of xa13 and Xa21 in the background of Pusa Basmati-1 through backcross pedigree method using IRBB55 as the donor for resistance (Joseph *et al.*, 2004). Based on molecular marker analysis Pusa 1460 is 96% similar to Pusa Basmati-1, combining excellent grain and cooking quality characteristics with high yield. It has been registered for BB resistance, more aroma and non-chalky grains.

It is semi dwarf (90-95cm) with sturdy stem, semi erect flag leaf and penultimate leaf with dark green foliage and free from purple pigmentation on any plant part. Grains are long slender with short awns. Panicles remain below the flag leaf. It was entered in Initial Varietal Trial Basmati in *Kharif* 2004. It gave 18% higher yield then Taraori Basmati in the Basmati growing region. In Haryana, which has the largest area under Pusa Basmati-1, it has given 28.3% and 95.55% more yield over Pusa Basmati-1 and Taraori Basmati respectively. Pusa 1460 was tested at 12 locations for bacterial blight and found resistant (Table 1). It can be successfully grown like any other semi-dwarf high yielding basmati varieties.

Table 1. Bacterial blight score in promising Basmati nominations in Initial Varietal Trials (Basmati) (*Kharif* 2004)

Locations	IET 18990	IET 18973	IET 18983	IET 18993	Ajaya*	PB1+
Chiplima	7	3	5	7	5	5
Faizabad	9	7	5	7	7	3
Martuteru	3	9	9	9	5	9
Raipur	3	7	7	7	7	7
Varanasi	1	1	3	1	3	5
Ludhiana I	3	NA	9	9	3	9
Ludhiana III	3	9	9	9	3	9
Ludhiana VI	3	5	9	9	3	9
DRR	9	9	9	9	3	7
Karjat	3	3	3	3	2	8
Patna	5	5	3	9	3	7
Nellore	5	9	5	3	5	5
AV. SI	4.5	5.5	6.3	6.8	4.0	6.9

Source: Screening Nurseries 2004, Insect Pest and Diseases, AICRIP, Directorate of Rice Research, Rajendranagar, Hyderabad 500 030 A.P. India.
* Resistant Check, + Susceptible Check

References

Joseph M, S Gopalakrishnan, RK Sharma, VP Singh, AK Singh, NK Singh, T Mohapatra (2004) Combining bacterial blight resistance and Basmati quality characteristics by phenotypic and molecular marker-assisted selection in rice. *Molecular Breeding* **13:** 377-387.

Wheat Genetic Stocks with Multiple Resistances

Dibendu Dutta, M Prashar, SC Bhardwaj and RN Brahma
Directorate of Wheat Research, Regional Station, Flowerdale, Shimla (Himachal Pradesh)

FLW 11 (INGR No. 05003; IC470825), Wheat (*Triticum aestivum*) germplasm with Multiple Rust Resistances

FLW11 was derived from the cross between WH542 and Hobbit at the Directorate of Wheat Research, Regional Station, Flowerdale. In addition to resistance gene from the winter wheat Hobbit, it also carries *Lr26, Sr31* and *Yr9* from WH542. This stock is completely resistant to yellow and black rusts. This stock has amber seed with test weight of 40 g, average plant height of 88 cm, and matures in about 120 days. This stock has good agronomic characteristics and high yield potential.

FLW 12 (INGR No. 05004; IC470826), Wheat (*Triticum aestivum*) Germplasm with Multiple Rust Resistances

FLW12 was derived from the cross between UP2338 and Mega at the Directorate of Wheat Research, Regional

Pusa 1460-01-32-6-7-67 (IET-18990) (INGR No. 05002; IC522199), Basmati Rice (*Oryza sativa*) Germplasm with more Aroma, Free from Grain Chalkiness and Resistance to Bacterial Blight

VP Singh, AK Singh, SS Atwal, T Mohapatra, Minu Joseph, S Gopala Krishnan, KR Pandey and Jayshree Gopalakrishna
Division of Genetics, Indian Agricultural Research Institute, New Delhi 110 012

Pusa Basmati-1 the first semi dwarf high yielding, early maturing variety having key Basmati quality characteristics, released in 1989 is very popular with the cultivators, traders, exporters and consumers. However, it is highly susceptible to bacterial blight (BB) caused by *Xanthomonas oryzae* pv *oryzae* resulting into loss of yield and quality. Pusa 1460 has been developed at the Indian Agricultural Research Institute, New Delhi through marker assisted pyramiding of xa13 and Xa21 in the background of Pusa Basmati-1 through backcross pedigree method using IRBB55 as the donor for resistance (Joseph *et al.*, 2004). Based on molecular marker analysis Pusa 1460 is 96% similar to Pusa Basmati-1, combining excellent grain and cooking quality characteristics with high yield. It has been registered for BB resistance, more aroma and non-chalky grains.

It is semi dwarf (90-95cm) with sturdy stem, semi erect flag leaf and penultimate leaf with dark green foliage and free from purple pigmentation on any plant part. Grains are long slender with short awns. Panicles remain below the flag leaf. It was entered in Initial Varietal Trial Basmati in *Kharif* 2004. It gave 18% higher yield then Taraori Basmati in the Basmati growing region. In Haryana, which has the largest area under Pusa Basmati-1, it has given 28.3% and 95.55% more yield over Pusa Basmati-1 and Taraori Basmati respectively. Pusa 1460 was tested at 12 locations for bacterial blight and found resistant (Table 1). It can be successfully grown like any other semi-dwarf high yielding basmati varieties.

Table 1. Bacterial blight score in promising Basmati nominations in Initial Varietal Trials (Basmati) (*Kharif* 2004)

Locations	IET 18990	IET 18973	IET 18983	IET 18993	Ajaya*	PB1+
Chiplima	7	3	5	7	5	5
Faizabad	9	7	5	7	7	3
Martuteru	3	9	9	9	5	9
Raipur	3	7	7	7	7	7
Varanasi	1	1	3	1	3	5
Ludhiana I	3	NA	9	9	3	9
Ludhiana III	3	9	9	9	3	9
Ludhiana VI	3	5	9	9	3	9
DRR	9	9	9	9	3	7
Karjat	3	3	3	3	2	8
Patna	5	5	3	9	3	7
Nellore	5	9	5	3	5	5
AV. SI	4.5	5.5	6.3	6.8	4.0	6.9

Source: Screening Nurseries 2004, Insect Pest and Diseases, AICRIP, Directorate of Rice Research, Rajendranagar, Hyderabad 500 030 A.P. India.
* Resistant Check, + Susceptible Check

References

Joseph M, S Gopalakrishnan, RK Sharma, VP Singh, AK Singh, NK Singh, T Mohapatra (2004) Combining bacterial blight resistance and Basmati quality characteristics by phenotypic and molecular marker-assisted selection in rice. *Molecular Breeding* **13:** 377-387.

Wheat Genetic Stocks with Multiple Resistances

Dibendu Dutta, M Prashar, SC Bhardwaj and RN Brahma
Directorate of Wheat Research, Regional Station, Flowerdale, Shimla (Himachal Pradesh)

FLW 11 (INGR No. 05003; IC470825), Wheat (*Triticum aestivum*) germplasm with Multiple Rust Resistances

FLW11 was derived from the cross between WH542 and Hobbit at the Directorate of Wheat Research, Regional Station, Flowerdale. In addition to resistance gene from the winter wheat Hobbit, it also carries *Lr26, Sr31* and *Yr9* from WH542. This stock is completely resistant to yellow and black rusts. This stock has amber seed with test weight of 40 g, average plant height of 88 cm, and matures in about 120 days. This stock has good agronomic characteristics and high yield potential.

FLW 12 (INGR No. 05004; IC470826), Wheat (*Triticum aestivum*) Germplasm with Multiple Rust Resistances

FLW12 was derived from the cross between UP2338 and Mega at the Directorate of Wheat Research, Regional

Station, Flowerdale. Yellow rust resistance from exotic winter wheat Mega was incorporated in to UP2338. This stock was completely resistant to yellow rust and black rust. In addition to yellow rust resistance genes from Mega, it also carries *Lr26, Sr31* and *Yr9* from UP2338. It has non-amber seed with long spikes and test weight of 43 g, average plant height about 125cm and matures in about 125 days. Yield per meter row was less than the check PBW343.

FLW 13 (INGR No. 05005; IC470827), Wheat (*Triticum aestivum*) Germplasm with Multiple Rust Resistances

FLW13 was derived from the cross between WH542 and *Yr15*(CN25087) at the Directorate of Wheat Research, Regional Station, Flowerdale. Yellow rust resistance gene derived from *Triticum turgidum* var. *dicoccoides* conferring complete seedling resistance to all stripe rust pathotypes. This stock is resistant to yellow rust. It has amber seed with test weight of 50 g and average plant height of about 100cm. It matures in about 115 days. Yield per meter row was good.

FLW 15 (INGR No. 05006; IC470828), Wheat (*Triticum aestivum*) Germplasm with Multiple Rust Resistances

FLW15 was derived through pedigree selection from the cross between PBW343 and Tc+*Lr32* at the Directorate of Wheat Research, Regional Station, Flowerdale. The average height of this stock was about 90cm and it matures in 120 days. It was completely resistant to brown and black rusts and to predominant pathotypes of yellow rust. It has amber seed with test weight of 45 g with good yield potential.

RNB 1001 (INGR No. 05007; IC470829), Wheat (*Triticum aestivum*) Germplasm with Novel Genes for Resistance to Brown, Black and Yellow Rust

RN Brahma, Bendu Dutta, M Prashar, SC Bhardwaj, M Siwaswamy and Aloka Saikia
Directorate of Wheat Research, Regional Station, Flowerdale, Shimla (Himachal Pradesh)

RNB1001 was derived from the cross between WH542 and Hobbit at the Indian Agricultural Research Institute, Regional Station, Wellington. RNB1001 is completely resistant to brown rust and is likely to carry new/novel rust resistance gene. It is also resistant to black and yellow rusts. This line is agronomically superior with good grain and yield attributes. This stock has amber seed with test weight of 40 g and average height about 100 cm. It matures very early.

Male Sterile Line in Wheat

SMS Tomar, Bhanwar Singh, Vinod and Rajendra Singh
Indian Agricultural Research Institute, New Delhi 110 012

Work carried out in some countries (Bruns and Peterson, 1998) has shown that the wheat hybrids out yield pure lines by 10-15 per cent under narrow row spacing and low seed rates. In India, hybrids have been developed by private sector and are being cultivated in small area under marginal environments. Out of many pollination control systems, the cytoplasmic genic male sterility system though cumbersome, provide useful and ecofriendly approach for hybrid seed production. However, significant effect of cytoplasmic x nuclear interaction on some traits in positive or negative direction has been observed (Ekiz and Konzak, 1991). Therefore, heterosis breeding through cytoplasmic male sterility-fertility restorer system needs to be explored (Tomar and Anbalagan, 2004). The availability of stable cytoplasmic male sterile lines and effective restorers is an essential pre-requisite for hybrid wheat breeding programme. All the three A (male sterile) B (maintainer) and R (restorer) lines are needed for successful hybrid seed production. Therefore, a programme for development of cytoplasmic male sterile lines at the Indian Agricultural Research Institute, New Delhi was initiated resulting in identification of following distinct lines in combination of other desirable traits.

Station, Flowerdale. Yellow rust resistance from exotic winter wheat Mega was incorporated in to UP2338. This stock was completely resistant to yellow rust and black rust. In addition to yellow rust resistance genes from Mega, it also carries *Lr26, Sr31* and *Yr9* from UP2338. It has non-amber seed with long spikes and test weight of 43 g, average plant height about 125cm and matures in about 125 days. Yield per meter row was less than the check PBW343.

FLW 13 (INGR No. 05005; IC470827), Wheat (*Triticum aestivum*) Germplasm with Multiple Rust Resistances

FLW13 was derived from the cross between WH542 and *Yr15*(CN25087) at the Directorate of Wheat Research, Regional Station, Flowerdale. Yellow rust resistance gene derived from *Triticum turgidum* var. *dicoccoides* conferring complete seedling resistance to all stripe rust pathotypes. This stock is resistant to yellow rust. It has amber seed with test weight of 50 g and average plant height of about 100cm. It matures in about 115 days. Yield per meter row was good.

FLW 15 (INGR No. 05006; IC470828), Wheat (*Triticum aestivum*) Germplasm with Multiple Rust Resistances

FLW15 was derived through pedigree selection from the cross between PBW343 and Tc+*Lr32* at the Directorate of Wheat Research, Regional Station, Flowerdale. The average height of this stock was about 90cm and it matures in 120 days. It was completely resistant to brown and black rusts and to predominant pathotypes of yellow rust. It has amber seed with test weight of 45 g with good yield potential.

RNB 1001 (INGR No. 05007; IC470829), Wheat (*Triticum aestivum*) Germplasm with Novel Genes for Resistance to Brown, Black and Yellow Rust

RN Brahma, Bendu Dutta, M Prashar, SC Bhardwaj, M Siwaswamy and Aloka Saikia
Directorate of Wheat Research, Regional Station, Flowerdale, Shimla (Himachal Pradesh)

RNB1001 was derived from the cross between WH542 and Hobbit at the Indian Agricultural Research Institute, Regional Station, Wellington. RNB1001 is completely resistant to brown rust and is likely to carry new/novel rust resistance gene. It is also resistant to black and yellow rusts. This line is agronomically superior with good grain and yield attributes. This stock has amber seed with test weight of 40 g and average height about 100 cm. It matures very early.

Male Sterile Line in Wheat

SMS Tomar, Bhanwar Singh, Vinod and Rajendra Singh
Indian Agricultural Research Institute, New Delhi 110 012

Work carried out in some countries (Bruns and Peterson, 1998) has shown that the wheat hybrids out yield pure lines by 10-15 per cent under narrow row spacing and low seed rates. In India, hybrids have been developed by private sector and are being cultivated in small area under marginal environments. Out of many pollination control systems, the cytoplasmic genic male sterility system though cumbersome, provide useful and ecofriendly approach for hybrid seed production. However, significant effect of cytoplasmic x nuclear interaction on some traits in positive or negative direction has been observed (Ekiz and Konzak, 1991). Therefore, heterosis breeding through cytoplasmic male sterility-fertility restorer system needs to be explored (Tomar and Anbalagan, 2004). The availability of stable cytoplasmic male sterile lines and effective restorers is an essential pre-requisite for hybrid wheat breeding programme. All the three A (male sterile) B (maintainer) and R (restorer) lines are needed for successful hybrid seed production. Therefore, a programme for development of cytoplasmic male sterile lines at the Indian Agricultural Research Institute, New Delhi was initiated resulting in identification of following distinct lines in combination of other desirable traits.

Station, Flowerdale. Yellow rust resistance from exotic winter wheat Mega was incorporated in to UP2338. This stock was completely resistant to yellow rust and black rust. In addition to yellow rust resistance genes from Mega, it also carries *Lr26, Sr31* and *Yr9* from UP2338. It has non-amber seed with long spikes and test weight of 43 g, average plant height about 125cm and matures in about 125 days. Yield per meter row was less than the check PBW343.

FLW 13 (INGR No. 05005; IC470827), Wheat (*Triticum aestivum*) Germplasm with Multiple Rust Resistances

FLW13 was derived from the cross between WH542 and *Yr15*(CN25087) at the Directorate of Wheat Research, Regional Station, Flowerdale. Yellow rust resistance gene derived from *Triticum turgidum* var. *dicoccoides* conferring complete seedling resistance to all stripe rust pathotypes. This stock is resistant to yellow rust. It has amber seed with test weight of 50 g and average plant height of about 100cm. It matures in about 115 days. Yield per meter row was good.

FLW 15 (INGR No. 05006; IC470828), Wheat (*Triticum aestivum*) Germplasm with Multiple Rust Resistances

FLW15 was derived through pedigree selection from the cross between PBW343 and Tc+*Lr32* at the Directorate of Wheat Research, Regional Station, Flowerdale. The average height of this stock was about 90cm and it matures in 120 days. It was completely resistant to brown and black rusts and to predominant pathotypes of yellow rust. It has amber seed with test weight of 45 g with good yield potential.

RNB 1001 (INGR No. 05007; IC470829), Wheat (*Triticum aestivum*) Germplasm with Novel Genes for Resistance to Brown, Black and Yellow Rust

RN Brahma, Bendu Dutta, M Prashar, SC Bhardwaj, M Siwaswamy and Aloka Saikia
Directorate of Wheat Research, Regional Station, Flowerdale, Shimla (Himachal Pradesh)

RNB1001 was derived from the cross between WH542 and Hobbit at the Indian Agricultural Research Institute, Regional Station, Wellington. RNB1001 is completely resistant to brown rust and is likely to carry new/novel rust resistance gene. It is also resistant to black and yellow rusts. This line is agronomically superior with good grain and yield attributes. This stock has amber seed with test weight of 40 g and average height about 100 cm. It matures very early.

Male Sterile Line in Wheat

SMS Tomar, Bhanwar Singh, Vinod and Rajendra Singh
Indian Agricultural Research Institute, New Delhi 110 012

Work carried out in some countries (Bruns and Peterson, 1998) has shown that the wheat hybrids out yield pure lines by 10-15 per cent under narrow row spacing and low seed rates. In India, hybrids have been developed by private sector and are being cultivated in small area under marginal environments. Out of many pollination control systems, the cytoplasmic genic male sterility system though cumbersome, provide useful and ecofriendly approach for hybrid seed production. However, significant effect of cytoplasmic x nuclear interaction on some traits in positive or negative direction has been observed (Ekiz and Konzak, 1991). Therefore, heterosis breeding through cytoplasmic male sterility-fertility restorer system needs to be explored (Tomar and Anbalagan, 2004). The availability of stable cytoplasmic male sterile lines and effective restorers is an essential pre-requisite for hybrid wheat breeding programme. All the three A (male sterile) B (maintainer) and R (restorer) lines are needed for successful hybrid seed production. Therefore, a programme for development of cytoplasmic male sterile lines at the Indian Agricultural Research Institute, New Delhi was initiated resulting in identification of following distinct lines in combination of other desirable traits.

Pusa 2022A & HW 2022 (B line) (INGR No. 05008; IC524013 & IC524282), Wheat (*Triticum aestivum*) Germplasm with Cytoplasmic Male Sterility and Resistance to Rust

Cytoplasmic male sterile line Pusa 2022 A carries cytoplasm from *Triticum araraticum* (2n=4x=28, genome AAGG). The characteristic feature of Pusa 2022A is that it has club shaped ear head and exhibits resistance to leaf rust. It has got desirable plant height suitable for hybrid seed production. Its maintainer is HW 2022 a backcross derivative of WH 147 (commercial cultivar in Central India) carrying highly effective rust resistance genes Sr 26 – Sr 24/Lr 24 from *Agropyron elongatum.*

Pusa 2019A/11 & HW 2019 (B line) (INGR No. 05009; IC524014 & IC524283), Wheat (*Triticum aestivum*) Germplasm with Cytoplasmic Male Sterility, Dwarfness and Resistance to Rust

Cytoplasmic male sterile lines Pusa 2019A/11 carry cytoplasm from *Triticum timopheevi* (2n=4x=28, genome AAGG). Its maintainer is a backcross line HW 2019 developed from a commercial cultivar WH 542. The backcross derivative of WH 542 is carrying 1BL.1RS translocation from *Secale cereale* and possesses complex genes Sr31Lr26Yr9Pm8. In addition, it carries highly effective rust resistance genes Sr24/Lr24 from *Agropyron elongatum.*

Pusa 2099A & HW 2099 (B line) (INGR No. 05010; IC524015 & IC524284), Wheat (*Triticum aestivum*) Germplasm with Cytoplasmic Male Sterility, High Grain Number per Spike and Resistance to all Three Rusts

Cytoplasmic male sterile lines Pusa 2099 A carries cytoplasm from *Triticum araraticum* (2n=4x=28, genome AAGG) and therefore it is a diverse line for hybrid seed production. Its maintainer is HW 2099, which carries highly effective resistance genes for all the three rusts. The characteristic features of this line are that it produces high grain number per/spike and possesses other desirable yield components.

Pusa 2338A/20 & UP 2338A/20 (B line) (INGR No. 05011; IC524016 & IC524285), Wheat (*Triticum aestivum*) Germplasm with Cytoplasmic Male Sterility, Non Synchrony and Resistance to Stem Rust

Cytoplasmic male sterile Pusa 2338A/20 carries cytoplasm from *Triticum timopheevi* (2n=4x=29, genome AAGG) and therefore it is a diverse line for hybrid seed production. The maintainer of Pusa 2338A/20 is a commercial cultivar, UP 2338, which carries a segment 1 BL.1RS from *Secale cereale* possessing the genes Sr31Lr26Yr9Pm8. The alien segment from rye is known for yield enhancement.

Pusa 2046A/8 & HW 2046 (B line) (INGR No. 05012; IC524017 & IC524286), Wheat (*Triticum aestivum*) Germplasm with Cytoplasmic Male Sterility, Waxy Bloom and Resistance to Leaf Rust

Cytoplasmic male sterile line Pusa 2046/8 carries cytoplasm from *Triticum timopheevi* (2n=4x=28, genome AAGG). The maintainer of this A line is HW 2046, which is a backcross derivative of HD2329 carrying highly effective rust resistance genes Sr 24/Lr 24 from *Agropyron elongatum.*

PWR 4099 (INGR No. 05013; EC414149), a New Restorer Wheat (*Triticum aestivum*) Germplasm of *timopheevi* and *araraticum* Cytoplasm

PWR 4099 (pedigree = CBHW-R CHN QI RR 925 OCHN S-4BV97 = EC 414149) is an exotic line, which restores complete fertility in the CMS lines carrying cytoplasms from *T. araraticum* and *T. timopheevi.* Genetic studies have revealed that PWR 4099 carries two genes with cumulative effect in fertility restoration. Also this line produce pollen in abundance and the flowering time also coincides with a few CMS lines. The line has also exhibited resistance to stripe rust. The ear is club shaped and the grain number per spike is also high.

PWR 4101 (INGR No. 05014; EC414148), a New Restorer Wheat (*Triticum aestivum*) Germplasm of *timopheevi* and *araraticum* Cytoplasm with Resistance to Yellow Rust

PWR 4101 (pedigree- CBHW-R CHN 89R 4294 OCHN S-2BV97, EC 414148) is an exotic line, which restores complete fertility in the cytoplasmic male sterile (CMS) lines carrying cytoplasms from *T. araraticum* and *T. timopheevi.* The genetic basis of fertility restoration in CMS lines of wheat and rice have been investigated extensively (Yang *et al.*, 1989; Nonaka, *et al.*, 1993; Tomar and Anbalagan, 2004), but it is still to be resolved for locally developed and adapted CMS and restorer lines. Any CMS system would be complete only when restorer genes are available. Genetic studies have revealed that PWR 4101 carried a single dominant gene for fertility restoration. This line produces pollen in abundance and the flowering time also coincides with a few CMS lines. The line has exhibited resistance to stripe rust. It is a diverse line as it differs from PWR 4099 with respect to fertility restorer genes and in various agronomic traits.

References

Bruns R and CJ Peterson (1988) Yield and stability factors associated with hybrid wheat. In: HJ Braun, F Altay, WE Kronstad, SPS Beniwal and A MacNab (eds) *Wheat: Prospects for Global improvement* Ankara 10-14 June 1996, Kluwer Academic Publishers, Drodecht, Netherlands p.23-27.

Ekiz H and CF Konzak (1991) Nuclear and cytoplasmic control of anther culture response in wheat. I. Analysis of alloplasmic lines. *Crop Sci* **31**: 1421-1427.

Nonaka S, K Toriyama, K Tsunewaki and T Shimada (1993) Breeding of male sterile lines and their maintainer lines by backcross method for wheat production using an Sv type cytoplasm and a 1BL.1RS chromosome. *Jap J Breed* **43**: 567-574

Tomar, SMS and S Anbalagan (2004) Characterisation of cytoplasmic male sterile lines in wheat (*Triticum aestivum* L.). *Indian J Genet* **64(3)**: 189-195.

Yang RC, NY Wang and KJ Liang (1989) Oryza nivara source of cytoplasmic male sterility (CMS) in rice. *Int Rice Res Newsletter* **14**: 5

Selection T2600 (INGR No. 05015; EC414148), Wheat (*Triticum aestivum*) Germplasm a New Source of Leaf and Stem Rust

SMS Tomar, Bhanwar Singh, Vinod and Rajendra Singh
Indian Agricultural Research Institute, New Delhi 110 012

Wheat rusts, particularly, leaf rust (*Puccinia triticina* syn. *Puccinia recondita tritici* Rob. Ex Desm.) occur world wide and are known to cause significant losses in wheat production. Leaf rust is highly variable and is known to have many patho-physiological races or biotypes. About 55 *Lr* genes providing resistance to a range of leaf rust pathotypes have been documented (Marais *et al.*, 2005). Amongst a large number of designated *Lr* genes, many have their origin in *Triticum aestivum* and most of them have become ineffective to virulent Indian pathotypes (Menon and Tomar, 2001). However, the resistance genes introgressed from alien species provided useful resistance to a broad spectrum of leaf rust pathotypes. But in recent past the resistance conferred by the genes, Lr9 (*Aegilops umbellulata*), Lr 19 (*Agropyron elongatum*) and Lr26 from *Secale cereale* has also been overcome by newly evolved biotypes, namely, 77-6, 77-8 and 77-1 respectively of 77 races. This has necessitated to hunt for new sources of resistance continuously, to combat the rust infection.

Triticum miliitnae, a free threshing mutant of *T. timopheevi* (2n=4x=28, genome, AAGG) exhibited complete resistance to Indian leaf rust races. Genetic resistance from *T. militinae* was introgressed to hexaploid wheat though cytogenetical manipulations at the Indian Agricultural Research Institute, New Delhi. Out of many derivatives, the selection T2600 showed resistance to a wide range of physiological races of leaf rust in seedling as well as in adult stage. Genetic studies revealed that resistance in selection T2600 is controlled by a single dominant gene, which is located in 6B chromosome (Nanthakumar and Tomar, 2002). Further, test of allelism indicated that the resistance imparted by selection T2600 is similar to that exhibited by *Aegilops umbellulata* derived gene Lr9, which is also located in chromosome 6B. Literature reveals that homologous group of VI chromosome is frequently involved in translocations; therefore, the resistance in selection T2600 may be diverse and will be useful in wheat breeding.

References

Menon MK and SMS Tomar (2001) *Aegilops*-derived specific genes in common wheat and their introgression into Indian bread wheat cultivars. *Indian J Genet* **61(2)**: 92-97.

Marais GF, B McCallum, JE Suyman, ZA Pretorius and AS Marais (2005) Leaf rust and stripe rust resistance genes Lr54 and Yr37 transferred to wheat from *Aegilops kotschyi Plant Breeding* **124**: 538-541.

Nanthakumar G and SMS Tomar (2002) Inheritance of *Triticum militinae* Zhuk derived leaf rust and stem rust resistance in common wheat. *Indian J Genet* **63(1)**: 18-23.

References

Bruns R and CJ Peterson (1988) Yield and stability factors associated with hybrid wheat. In: HJ Braun, F Altay, WE Kronstad, SPS Beniwal and A MacNab (eds) *Wheat: Prospects for Global improvement* Ankara 10-14 June 1996, Kluwer Academic Publishers, Drodecht, Netherlands p.23-27.

Ekiz H and CF Konzak (1991) Nuclear and cytoplasmic control of anther culture response in wheat. I. Analysis of alloplasmic lines. *Crop Sci* **31**: 1421-1427.

Nonaka S, K Toriyama, K Tsunewaki and T Shimada (1993) Breeding of male sterile lines and their maintainer lines by backcross method for wheat production using an Sv type cytoplasm and a 1BL.1RS chromosome. *Jap J Breed* **43**: 567-574

Tomar, SMS and S Anbalagan (2004) Characterisation of cytoplasmic male sterile lines in wheat (*Triticum aestivum* L.). *Indian J Genet* **64(3)**: 189-195.

Yang RC, NY Wang and KJ Liang (1989) Oryza nivara source of cytoplasmic male sterility (CMS) in rice. *Int Rice Res Newsletter* **14**: 5

Selection T2600 (INGR No. 05015; EC414148), Wheat (*Triticum aestivum*) Germplasm a New Source of Leaf and Stem Rust

SMS Tomar, Bhanwar Singh, Vinod and Rajendra Singh
Indian Agricultural Research Institute, New Delhi 110 012

Wheat rusts, particularly, leaf rust (*Puccinia triticina* syn. *Puccinia recondita tritici* Rob. Ex Desm.) occur world wide and are known to cause significant losses in wheat production. Leaf rust is highly variable and is known to have many patho-physiological races or biotypes. About 55 *Lr* genes providing resistance to a range of leaf rust pathotypes have been documented (Marais *et al.*, 2005). Amongst a large number of designated *Lr* genes, many have their origin in *Triticum aestivum* and most of them have become ineffective to virulent Indian pathotypes (Menon and Tomar, 2001). However, the resistance genes introgressed from alien species provided useful resistance to a broad spectrum of leaf rust pathotypes. But in recent past the resistance conferred by the genes, Lr9 (*Aegilops umbellulata*), Lr 19 (*Agropyron elongatum*) and Lr26 from *Secale cereale* has also been overcome by newly evolved biotypes, namely, 77-6, 77-8 and 77-1 respectively of 77 races. This has necessitated to hunt for new sources of resistance continuously, to combat the rust infection.

Triticum miliitnae, a free threshing mutant of *T. timopheevi* (2n=4x=28, genome, AAGG) exhibited complete resistance to Indian leaf rust races. Genetic resistance from *T. militinae* was introgressed to hexaploid wheat though cytogenetical manipulations at the Indian Agricultural Research Institute, New Delhi. Out of many derivatives, the selection T2600 showed resistance to a wide range of physiological races of leaf rust in seedling as well as in adult stage. Genetic studies revealed that resistance in selection T2600 is controlled by a single dominant gene, which is located in 6B chromosome (Nanthakumar and Tomar, 2002). Further, test of allelism indicated that the resistance imparted by selection T2600 is similar to that exhibited by *Aegilops umbellulata* derived gene Lr9, which is also located in chromosome 6B. Literature reveals that homologous group of VI chromosome is frequently involved in translocations; therefore, the resistance in selection T2600 may be diverse and will be useful in wheat breeding.

References

Menon MK and SMS Tomar (2001) *Aegilops*-derived specific genes in common wheat and their introgression into Indian bread wheat cultivars. *Indian J Genet* **61(2)**: 92-97.

Marais GF, B McCallum, JE Suyman, ZA Pretorius and AS Marais (2005) Leaf rust and stripe rust resistance genes Lr54 and Yr37 transferred to wheat from *Aegilops kotschyi Plant Breeding* **124**: 538-541.

Nanthakumar G and SMS Tomar (2002) Inheritance of *Triticum militinae* Zhuk derived leaf rust and stem rust resistance in common wheat. *Indian J Genet* **63(1)**: 18-23.

S 437-1 (INGR No. 05016; IC471842), Sorghum (*Sorghum bicolor*) Germplasm with Low Hydrocyanic Acid, High Protein and High *in vitro* Dry Matter Digestibility

SK Pahuja, RPS Grewal, Rajesh Yadav, Y Jindal, SR Pundir, YP Luthra, AS Rathi and SP Singh
Forage Research Section, CCS Haryana Agricultural University, Hisar 125 004 (Haryana)

In forage sorghum for fodder quality and resistance to foliar diseases and insect-pests are the most important criteria for realizing animal performance for milk, meat and draft. The genotype S 437-1 developed at the Forage Research Section, CCS Haryana Agricultural University, Hisar is a superior line with low Hydrocyanic acid (HCN) content (88 ppm), high protein percentage (7.7 %) and high protein yield (9.70 q/ha). It has high *in vitro* Dry Matter Digestibility (IVDMD) per cent and high Digestible Dry Matter (DDM) yield, which are 7.7 % and 9.7 q/ha, respectively. Also, it expressed resistance against three major foliar diseases *viz.*, grey leaf spot, *Cercospora sorghi* (1.2 score), zonate leaf spot, *Gloeocercospora sorghi* (1.5 score) and sooty stripe, *Ramulispora sorghi* (1.6 score) and two most important insect-pests of forage sorghum, namely, shoot fly, *Atherigona soccata* (19% dead hearts) and stem borer, *Cochilo porrtellus* (25% dead hearts) at multi-location testing for 2 years *i.e.* 2002 and 2003 (Anonymous, 2002, 2003).

This genotype was developed through pedigree selection method from a cross between S 153/V 60-1 x *Sorghum roxburghii* / P-1-3-7-1-1. *S. roxburghii* has multiple resistances against insects and foliar diseases and V 60-1 possesses better quality traits. It is tall, juicy, tan type with dull green midrib and long anthers. It gives 413 q/ha of green fodder and 132 q/ha of dry matter yield. It is widely adapted and should be sown at the first available opportunity after first monsoon showers, preferably between 25th June and 10th July. Seed should be sown at a depth of 2.5–4.0 cm in rows 30 cm apart. Seed rate of 16-20 kg/acre helps to get maximum fodder yield. In irrigated areas, application of 32 kg N and 12 kg P_2O_5 per acre are recommended to get best returns. Half dose of nitrogen and full dose of P_2O_5 should be applied as basal dose and remaining nitrogen should be top dressed at 30-35 days after sowing. Water stagnation should be avoided. Need based one or two irrigation and weeding may be done at an interval of 15-20 days.

References

Anonymous (2002) Annual Report of All India Co-ordinated Sorghum Improvement Project, NRCS, Hyderabad.

Anonymous (2003) Annual Report of All India Co-ordinated Sorghum Improvement Project, NRCS, Hyderabad.

PBL-123 (INGR No. 05017; IC524012), Berseem (*Trifolium alexandrinum*) Germplasm with Purple Leaflet and Flowers

SM Beri and BL Bhardwaj
Punjab Agricultural University, Ludhiana (Punjab)

Importance of distinct and dominant markers to estimate the extent of natural cross pollination has been emphasised by many workers (Bogdan 1966, Jain 1979 and Sohoo *et al.*, 1988). In Egyptian clover purple flowered strains are rare and utilisation of this trait as a marker would help in understanding of the breeding behaviour of this species (Beri *et al.*, 2001). PBL-123, a purple flowered strain was found as a spontaneous mutant at the Punjab Agricultural University, Ludhiana. Its stem is comparatively hard and has more dry matter content compared to normal plants providing green fodder of improved nutritional quality. Its leaflets are purple green, longer and of narrow size at the time of flowering. It has bold seeds. It can be sown in the end of September, maturing by the end of May, thus supplying green fodder in repeated cuttings.

References

Beri SM, BL Bhardwaj and SR Sharma (2001) Natural Cross pollination in Egyptian clover. *Crop improve.* **28(2):** 191-194.

Bogdan AV (1966) Pollination and breeding behaviour in the *Trifolium ruepellianum* complex in Kenya. *The New Phytologist* **65**: 417-422.

Jain SK (1979) Estimation of out crossing rate – some alternative procedures *Crop Sci.* **19**: 23-26.

Sohoo MS, SM Beri and BL Bhardwaj (1988) Inheritance of purple flower colour in Egyptian clover *Trifolium alexandrinum J. Res. Punjab agri. Univ.* **25(1):** 6-8.

S 437-1 (INGR No. 05016; IC471842), Sorghum (*Sorghum bicolor*) Germplasm with Low Hydrocyanic Acid, High Protein and High *in vitro* Dry Matter Digestibility

SK Pahuja, RPS Grewal, Rajesh Yadav, Y Jindal, SR Pundir, YP Luthra, AS Rathi and SP Singh
Forage Research Section, CCS Haryana Agricultural University, Hisar 125 004 (Haryana)

In forage sorghum for fodder quality and resistance to foliar diseases and insect-pests are the most important criteria for realizing animal performance for milk, meat and draft. The genotype S 437-1 developed at the Forage Research Section, CCS Haryana Agricultural University, Hisar is a superior line with low Hydrocyanic acid (HCN) content (88 ppm), high protein percentage (7.7 %) and high protein yield (9.70 q/ha). It has high *in vitro* Dry Matter Digestibility (IVDMD) per cent and high Digestible Dry Matter (DDM) yield, which are 7.7 % and 9.7 q/ha, respectively. Also, it expressed resistance against three major foliar diseases *viz.*, grey leaf spot, *Cercospora sorghi* (1.2 score), zonate leaf spot, *Gloeocercospora sorghi* (1.5 score) and sooty stripe, *Ramulispora sorghi* (1.6 score) and two most important insect-pests of forage sorghum, namely, shoot fly, *Atherigona soccata* (19% dead hearts) and stem borer, *Cochilo porrtellus* (25% dead hearts) at multi-location testing for 2 years *i.e.* 2002 and 2003 (Anonymous, 2002, 2003).

This genotype was developed through pedigree selection method from a cross between S 153/V 60-1 x *Sorghum roxburghii* / P-1-3-7-1-1. *S. roxburghii* has multiple resistances against insects and foliar diseases and V 60-1 possesses better quality traits. It is tall, juicy, tan type with dull green midrib and long anthers. It gives 413 q/ha of green fodder and 132 q/ha of dry matter yield. It is widely adapted and should be sown at the first available opportunity after first monsoon showers, preferably between 25th June and 10th July. Seed should be sown at a depth of 2.5–4.0 cm in rows 30 cm apart. Seed rate of 16-20 kg/acre helps to get maximum fodder yield. In irrigated areas, application of 32 kg N and 12 kg P_2O_5 per acre are recommended to get best returns. Half dose of nitrogen and full dose of P_2O_5 should be applied as basal dose and remaining nitrogen should be top dressed at 30-35 days after sowing. Water stagnation should be avoided. Need based one or two irrigation and weeding may be done at an interval of 15-20 days.

References

Anonymous (2002) Annual Report of All India Co-ordinated Sorghum Improvement Project, NRCS, Hyderabad.

Anonymous (2003) Annual Report of All India Co-ordinated Sorghum Improvement Project, NRCS, Hyderabad.

PBL-123 (INGR No. 05017; IC524012), Berseem (*Trifolium alexandrinum*) Germplasm with Purple Leaflet and Flowers

SM Beri and BL Bhardwaj
Punjab Agricultural University, Ludhiana (Punjab)

Importance of distinct and dominant markers to estimate the extent of natural cross pollination has been emphasised by many workers (Bogdan 1966, Jain 1979 and Sohoo *et al.*, 1988). In Egyptian clover purple flowered strains are rare and utilisation of this trait as a marker would help in understanding of the breeding behaviour of this species (Beri *et al.*, 2001). PBL-123, a purple flowered strain was found as a spontaneous mutant at the Punjab Agricultural University, Ludhiana. Its stem is comparatively hard and has more dry matter content compared to normal plants providing green fodder of improved nutritional quality. Its leaflets are purple green, longer and of narrow size at the time of flowering. It has bold seeds. It can be sown in the end of September, maturing by the end of May, thus supplying green fodder in repeated cuttings.

References

Beri SM, BL Bhardwaj and SR Sharma (2001) Natural Cross pollination in Egyptian clover. *Crop improve.* **28(2):** 191-194.

Bogdan AV (1966) Pollination and breeding behaviour in the *Trifolium ruepellianum* complex in Kenya. *The New Phytologist* **65**: 417-422.

Jain SK (1979) Estimation of out crossing rate – some alternative procedures *Crop Sci.* **19**: 23-26.

Sohoo MS, SM Beri and BL Bhardwaj (1988) Inheritance of purple flower colour in Egyptian clover *Trifolium alexandrinum J. Res. Punjab agri. Univ.* **25(1):** 6-8.

NM-58 (INGR No. 05018; IC522204), a Non-lodging Type Sesame (*Sesamum indicum*) Germplasm

GSS Murty
Nuclear Agriculture and Biotechnology Division, Bhabha Atomic Research Centre, Trombay, Mumbai 400 085 (Maharashtra)

Lodging is a serious problem in crop plants. In sesame (*Sesamum indicum* Linn.), at the Bhabha Atomic Research Centre, Trombay, Mumbai, a stiff stem mutant (NM-58), non-lodging type was identified (Murty and Bhatia, 1987). It was isolated in M_2 generation after exposing the dry seeds of cv. N-8 to 600 Gy gamma rays followed by a treatment with 1% ethyl methane sulphonate for 3 h at 25°C. The mutant bred true in the M_3 and subsequent generations (Murty and Bhatia, 1987, Murty *et al.*, 1995).

The mutant has bushy habit, slower growth rate and is non-lodging compared to its parent. Although number of nodes on main stem is similar to that of parent, number of nodes per unit length is less along with shorter internode length, contributing to shorter plant height. It has bushy appearance due to more number of primary and secondary branches. Capsule size is slightly smaller, while number of capsules and seed yield per plant are similar to the parent. Anatomically, NM-58 has greater proportion of xylem both in ridges and furrows in the terminal and basal portions of stem compared to N-8. Besides, sclerenchymatous phloem fibres are seen in terminal portion of stem in NM-58, while in N-8 they are present only in basal portion. Cortex in NM-58 is comprised of collenchyma, while in N-8 only parenchyma is seen. These anatomical differences appear to contribute for stem stiffness in the mutant. Genetic studies on NM-58 revealed that the mutant trait is governed by duplicate recessive genes, for which gene symbols stf1 and stf2 are proposed (Murty *et al.*, 1995).

References

Murty GSS and CR Bhatia (1987) Lodging due to weak stem, a major problem in sesame improvement. *Sesame and Safflower Newsletter* **3:** 9-13.

Murty GSS, CK Salunkhe and DC Joshua (1995) Inheritance of an induced stiff stem mutant in sesame. *Sesame and Safflower Newsletter* **10:** 62-66.

Bollworm and Jassid Tolerant Diverse Cytoplasmic Strains

SL Ahuja[1], SK Banerjee[1], Jagmail Singh[3], P Singh[2], VV Singh[2], D Monga[2] and OP Tuteja[3]
1 Central Institute for Cotton Research Regional Station, Sirsa 125 055 (Haryana)
2 Central Institute for Cotton Research, Nagpur 440 010 (Maharashtra)
3 Division of Genetics, Indian Agricultural Research Institute, New Delhi 110 012

BN-ARB-16 (INGR No. 05020; IC471864): *G. hirsutum* Cotton, BN (Bikaneri Nerma) with *Gossypium arboreum* Cytoplasm

BN-ARB-16 is a genetic stock having *Gossypium arboreum* cytoplasm in *G. hirsutum* cotton BN (Bikaneri Nerma). It was developed at the Central Institute for cotton Research Regional Station, Sirsa through backcross method (BC_8 generations) using elemental line DES-ARB-16 deriving cytoplasmic background from *G. arboreum* as non-recurrent parent and BN (Bikaneri Nerma), a *G. hirsutum* with *latifolium* cytoplasm as recurrent parent. Exotic *arboreum* cytoplasm influences resistance to pests as reported by various workers (Meyer, 1973; Meredith, 1979 and Singh and Verma, 1982). BN-ARB-16 has higher amount of gossypol and flavanol content in leaves and higher amount of phenols in stem and low reducing sugars and total sugars in leaves (Ahuja *et al.*, 2001). Studies of Lulefer *et al.*, (1969); Deterline (1975); Leigh, (1975) and Agarwal *et al.* (1976) indicate that high amount of gossypol, flavanol and phenol contents in plant parts contribute to lower bollworm infestation, which was considerably low in BN-ARB-16 compared to Bikaneri Nerma. The fibre quality characteristics of BN-ARB-16 are at par with Bikaneri Nerma. Table 1 shows the distinctive morphological features, biochemical components, and yield and its contributing characters.

NM-58 (INGR No. 05018; IC522204), a Non-lodging Type Sesame (*Sesamum indicum*) Germplasm

GSS Murty
Nuclear Agriculture and Biotechnology Division, Bhabha Atomic Research Centre, Trombay, Mumbai 400 085 (Maharashtra)

Lodging is a serious problem in crop plants. In sesame (*Sesamum indicum* Linn.), at the Bhabha Atomic Research Centre, Trombay, Mumbai, a stiff stem mutant (NM-58), non-lodging type was identified (Murty and Bhatia, 1987). It was isolated in M_2 generation after exposing the dry seeds of cv. N-8 to 600 Gy gamma rays followed by a treatment with 1% ethyl methane sulphonate for 3 h at 25°C. The mutant bred true in the M_3 and subsequent generations (Murty and Bhatia, 1987, Murty *et al.*, 1995).

The mutant has bushy habit, slower growth rate and is non-lodging compared to its parent. Although number of nodes on main stem is similar to that of parent, number of nodes per unit length is less along with shorter internode length, contributing to shorter plant height. It has bushy appearance due to more number of primary and secondary branches. Capsule size is slightly smaller, while number of capsules and seed yield per plant are similar to the parent. Anatomically, NM-58 has greater proportion of xylem both in ridges and furrows in the terminal and basal portions of stem compared to N-8. Besides, sclerenchymatous phloem fibres are seen in terminal portion of stem in NM-58, while in N-8 they are present only in basal portion. Cortex in NM-58 is comprised of collenchyma, while in N-8 only parenchyma is seen. These anatomical differences appear to contribute for stem stiffness in the mutant. Genetic studies on NM-58 revealed that the mutant trait is governed by duplicate recessive genes, for which gene symbols stf1 and stf2 are proposed (Murty *et al.*, 1995).

References

Murty GSS and CR Bhatia (1987) Lodging due to weak stem, a major problem in sesame improvement. *Sesame and Safflower Newsletter* **3:** 9-13.

Murty GSS, CK Salunkhe and DC Joshua (1995) Inheritance of an induced stiff stem mutant in sesame. *Sesame and Safflower Newsletter* **10:** 62-66.

Bollworm and Jassid Tolerant Diverse Cytoplasmic Strains

SL Ahuja[1], SK Banerjee[1], Jagmail Singh[3], P Singh[2], VV Singh[2], D Monga[2] and OP Tuteja[3]
1 Central Institute for Cotton Research Regional Station, Sirsa 125 055 (Haryana)
2 Central Institute for Cotton Research, Nagpur 440 010 (Maharashtra)
3 Division of Genetics, Indian Agricultural Research Institute, New Delhi 110 012

BN-ARB-16 (INGR No. 05020; IC471864): *G. hirsutum* Cotton, BN (Bikaneri Nerma) with *Gossypium arboreum* Cytoplasm

BN-ARB-16 is a genetic stock having *Gossypium arboreum* cytoplasm in *G. hirsutum* cotton BN (Bikaneri Nerma). It was developed at the Central Institute for cotton Research Regional Station, Sirsa through backcross method (BC_8 generations) using elemental line DES-ARB-16 deriving cytoplasmic background from *G. arboreum* as non-recurrent parent and BN (Bikaneri Nerma), a *G. hirsutum* with *latifolium* cytoplasm as recurrent parent. Exotic *arboreum* cytoplasm influences resistance to pests as reported by various workers (Meyer, 1973; Meredith, 1979 and Singh and Verma, 1982). BN-ARB-16 has higher amount of gossypol and flavanol content in leaves and higher amount of phenols in stem and low reducing sugars and total sugars in leaves (Ahuja *et al.*, 2001). Studies of Lulefer *et al.*, (1969); Deterline (1975); Leigh, (1975) and Agarwal *et al.* (1976) indicate that high amount of gossypol, flavanol and phenol contents in plant parts contribute to lower bollworm infestation, which was considerably low in BN-ARB-16 compared to Bikaneri Nerma. The fibre quality characteristics of BN-ARB-16 are at par with Bikaneri Nerma. Table 1 shows the distinctive morphological features, biochemical components, and yield and its contributing characters.

Table 1. Distinctive morphological, biochemical features and yield of BN-ARB-16 and Bikaneri Nerma

Morphological features	BN-ARB-16			Bikaneri Nerma		
Plant type	Lanky/robust			Lanky		
Plant height (cm)	103.33			143.00		
Number of monopodial branches/plant	3.0			2.67		
Number of sympodial branches/plant	7.33			12.0		
Hairiness	Dense hairy			Hairy		
Colour	Brown			Light pink		
Lobing	Small (3 lobed)			Narrow		
Colour	Dark green			Medium green		
Nectary/leaf	1-3			1-2		
Bolls/plant	36.67			45.0		
Boll weight (g)	2.50			2.58		
Seed cotton yield/plant (g)	85.55			91.00		
Ginning Out Turn (%)	33.0			33.00		
Lint index (g)	3.69			3.49		
Shape	Oval pointed small boll			Oval		
Seeds/locule	6-7			8		
Fuzz colour	White			White		
Seed index (g)	7.50			7.1		
2.5% span length (mm)	25.5			26.7		
Uniformity ratio (%)	49.0			45.0		
Micronaire value 10^{-6} g/in	4.4			4.3		
Tenacity (g/tex) (3.2mm)	21.2			22.1		
Biochemical features	L	ST	SQ	L	ST	SQ
Gossypol (mg/g)	5.6	3.8	4.3	4.5	6.4	4.30
Reducing sugar (mg/g)	3.1	2.1	2.0	3.8	2.3	4.30
Flavanol (mg/g)	3.3	3.3	1.5	1.3	3.8	1.8
Total phenol (mg/g)	32.5	60.0	37.5	38.1	40.3	42.3
Total sugar (mg/g)	5.6	5.2	3.1	7.2	5.5	8.8
Bollworm incidence (%)	40.0 (39.1)			70.5 (59.7)		
Jassid grade	1.88			1.33		

Where L=leaves, ST= stem and SQ= square

BN-TOM-277 (INGR No. 05019; IC 471863): *G hirsutum* Cotton, BN (Bikaneri Nerma) with *Gossypium tomentosum* Cytoplasm

BN-TOM-277 is a genetic stock possessing *Gossypium tomentosum* cytoplasm in *G hirsutum* cotton BN (Bikaneri Nerma) developed at the Central Institute for cotton Research Regional Station, Sirsa through backcross method (BC_8 generations) using elemental line DES-TOM-277, deriving cytoplasmic background from *G tomentosum* used as non-recurrent parent and BN (Bikaneri Nerma), a *G hirsutum* with *latifolium* cytoplasm as recurrent parent. Exotic *tomentosum* cytoplasm has effect on resistance to pests (Meyer, 1973; Meredith, 1979 and Singh and Verma, 1982). BN-TOM-277 has higher amount of gossypol and flavanol contents in leaves and higher amount of phenols in stem and low reducing sugars and total sugars in leaves (Ahuja *et al.*, 2001). Lulefer *et al.*, (1969), Leigh (1975) and Agarwal *et al.*, (1976) has indicated that high amount of gossypol, flavanol and phenols contents contribute to lower bollworm infestation. The bollworm incidence and jassid infestation in BN-TOM-277 was considerably less compared to Bikaneri Nerma. BN-TOM-277 has fibre quality characteristics at par with Bikaneri Nerma. Table 2 presents comparative account of morphological characteristics, pest incidence, bio-chemical components, and yield and its contributing characters.

Table 2. Comparative account of BN-TOM-277 and Bikaneri Nerma characteristics

Morphological features	BN-TOM-277			Bikaneri Nerma		
Plant height (cm)	135			143.00		
Number of monopodial branches/plant	1.67			2.67		
Number of sympodial branches/plant	10.0			12.0		
Internodes length (cm)	6-10			5-10		
Colour	Dark green			Medium green		
Bolls/plant	42.67			45.0		
Boll weight (g)	2.75			2.58		
Seed cotton yield/plant (g)	84.67			91.00		
Ginning Out Turn (%)	33.00			33.00		
Lint index (g)	3.45			3.49		
Shape	Oval (pointed tip)			Oval		
Gossypol glands	8			8-10		
Seeds/locule	7-8			8		
Seed index (g)	7.0			7.1		
2.5% span length (mm)	25.0			26.7		
Uniformity ratio (%)	47.0			45.0		
Tenacity (g/tex) (3.2mm)	21.0			22.1		
Biochemical features	L	ST	SQ	L	ST	SQ
Gossypol (mg/g)	5.5	6.5	4.2	4.5	6.5	4.3
Flavanol (mg/g)	2.9	3.1	1.3	1.3	3.8	1.8
Total phenol (mg/g)	42.2	46.3	34.6	38.1	40.3	42.3
Total sugar (mg/g)	8.2	4.2	6.9	7.2	5.5	8.8
Bollworm incidence (%)	36.2 (37.2)			70.5 (59.7)		
Jassid grade	1.43			1.33		
Cytoplasmic background	*G. tomentosum*			*G. hirsutum*		

Where L=leaves, ST= stem and SQ= square

References

Agarwal RA, SK Banerjee, M Singh and KN Katiyar (1976) *Cotton Fibre Trop.* **31:** 217-221.

Ahuja SL, OP Tuteja and SK Banerjee (2001) Biochemical basis of resistance to bollworms and Jassid in cytotypes of *Gossypium hirsutum* cotton. *J Cott Res Dev* **15(1):** 87-92.

Leigh TF (1975) Insect resistance in cotton. What for future?. *Proc 28th Cott Insec Res Cotton Conf* p. 140-141.

Lukefar MJ, MJ Shaver and WL Parrot (1969) Sources and nature of resistance in *Gossypium hirsutum* to bollworms and tobacco budworms. *Proc Cott Improv Ecen Conf* p. 81-82.

SSH-1 (INGR No. 05021; IC5229943), Sugarcane and Sorghum Hybrid (*Sorghum bicolor* x *Saccharum officinarum*)

N Vijayan Nair

Sugarcane Breeding Institute, Coimbatore (Tamil Nadu)

The sugarcane hybrid (SSH-1/INGR No.05021) is the first ever *Sorghum bicolor* x *Saccharum* hybrid produced at Sugarcane Breeding Institute, Coimbatore with Sorghum as the female parent. The hybrid is unique, as it has sorghum cytoplasm. The pedigree of the clone is ICSA56 (Sorghum) x IJ 76316 (*Saccharum officinarum*). The hybrid is morphologically similar to the sugarcane parent, but with shorter plant type. Sorghum characters present in the hybrid included soft texture of the leaves, tight clasping of the leaf sheaths, presence of aerial roots and triangular ligule. Somatic chromosome number of the hybrid is 2n+66 indicating n+n transmission. Table 1 presents the detailed morphological characters of Sorghum x *Saccharum* hybrid.

Table 1. Morphological characters of *Sorghum bicolor* x *Saccharum* hybrid

Characters	Detail
Chromosome number	2n+66
Cane colour	Yellow
Cane thickness (cm)	1.6
Number of internodes	20
Internode length (cm)	5.0
No. of rows of root primordia	1
Bud groove	Present
Leaf length (cm)	110
Leaf width (cm)	2.4
Leaf texture	Soft
Leaf carriage	Open droopy
Leaf sheath clasping	Tight
Leaf shape	Triangular
Ligular process	Poorly developed
Aerial root	Present

Table 2. Comparative account of BN-TOM-277 and Bikaneri Nerma characteristics

Morphological features	BN-TOM-277			Bikaneri Nerma		
Plant height (cm)	135			143.00		
Number of monopodial branches/plant	1.67			2.67		
Number of sympodial branches/plant	10.0			12.0		
Internodes length (cm)	6-10			5-10		
Colour	Dark green			Medium green		
Bolls/plant	42.67			45.0		
Boll weight (g)	2.75			2.58		
Seed cotton yield/plant (g)	84.67			91.00		
Ginning Out Turn (%)	33.00			33.00		
Lint index (g)	3.45			3.49		
Shape	Oval (pointed tip)			Oval		
Gossypol glands	8			8-10		
Seeds/locule	7-8			8		
Seed index (g)	7.0			7.1		
2.5% span length (mm)	25.0			26.7		
Uniformity ratio (%)	47.0			45.0		
Tenacity (g/tex) (3.2mm)	21.0			22.1		
Biochemical features	L	ST	SQ	L	ST	SQ
Gossypol (mg/g)	5.5	6.5	4.2	4.5	6.5	4.3
Flavanol (mg/g)	2.9	3.1	1.3	1.3	3.8	1.8
Total phenol (mg/g)	42.2	46.3	34.6	38.1	40.3	42.3
Total sugar (mg/g)	8.2	4.2	6.9	7.2	5.5	8.8
Bollworm incidence (%)	36.2 (37.2)			70.5 (59.7)		
Jassid grade	1.43			1.33		
Cytoplasmic background	*G. tomentosum*			*G. hirsutum*		

Where L=leaves, ST= stem and SQ= square

References

Agarwal RA, SK Banerjee, M Singh and KN Katiyar (1976) *Cotton Fibre Trop.* **31:** 217-221.

Ahuja SL, OP Tuteja and SK Banerjee (2001) Biochemical basis of resistance to bollworms and Jassid in cytotypes of *Gossypium hirsutum* cotton. *J Cott Res Dev* **15(1):** 87-92.

Leigh TF (1975) Insect resistance in cotton. What for future?. *Proc 28th Cott Insec Res Cotton Conf* p. 140-141.

Lukefar MJ, MJ Shaver and WL Parrot (1969) Sources and nature of resistance in *Gossypium hirsutum* to bollworms and tobacco budworms. *Proc Cott Improv Ecen Conf* p. 81-82.

SSH-1 (INGR No. 05021; IC5229943), Sugarcane and Sorghum Hybrid (*Sorghum bicolor* x *Saccharum officinarum*)

N Vijayan Nair

Sugarcane Breeding Institute, Coimbatore (Tamil Nadu)

The sugarcane hybrid (SSH-1/INGR No.05021) is the first ever *Sorghum bicolor* x *Saccharum* hybrid produced at Sugarcane Breeding Institute, Coimbatore with Sorghum as the female parent. The hybrid is unique, as it has sorghum cytoplasm. The pedigree of the clone is ICSA56 (Sorghum) x IJ 76316 (*Saccharum officinarum*). The hybrid is morphologically similar to the sugarcane parent, but with shorter plant type. Sorghum characters present in the hybrid included soft texture of the leaves, tight clasping of the leaf sheaths, presence of aerial roots and triangular ligule. Somatic chromosome number of the hybrid is 2n+66 indicating n+n transmission. Table 1 presents the detailed morphological characters of Sorghum x *Saccharum* hybrid.

Table 1. Morphological characters of *Sorghum bicolor* x *Saccharum* hybrid

Characters	Detail
Chromosome number	2n+66
Cane colour	Yellow
Cane thickness (cm)	1.6
Number of internodes	20
Internode length (cm)	5.0
No. of rows of root primordia	1
Bud groove	Present
Leaf length (cm)	110
Leaf width (cm)	2.4
Leaf texture	Soft
Leaf carriage	Open droopy
Leaf sheath clasping	Tight
Leaf shape	Triangular
Ligular process	Poorly developed
Aerial root	Present

E/79-42 (INGR No. 05022; IC522200), a Combined Resistant for Cyst Nematodes and Late Blight Disease of Potato (*Solanum tuberosum*) Germplasm

KS Krishna Prasad, TA Joseph, SK Pandey, IA Khan, DB Singh
Central Potato Research Institute, Regional Station, Muthorai (Tamil Nadu)

The potato cyst nematode (*Globodera pallida* and *G. rostochiensis*) and the late blight (*Phytophthora infestans*) are the major productivity constraints in potato cultivation in Nilgiri hills of Tamil Nadu. Breeding for genetic resistance is the most effective and environment friendly way to manage such diseases. Screening of potato germplasm and advanced breeding lines at the Central Potato Research Institute, Regional Station Muthorai, Tamil Nadu, a hot spot for potato cyst nematode and late blight resulted in identification of the breeding line E/79-42 as a source of resistance to both the diseases. Considering that it has resistance to both it can be effectively used in breeding for resistance to control these diseases and thereby overcoming the yield constraint. It has white flowers with high pollen fertility. The tubers are of medium size, oval, white with shallow eyes. It matures in 125-135 days.

JW 96 (INGR No. 05023; IC524019), Potato (*Solanum tuberosum*) Germplasm with Early Maturity

Raj Kumar[1], GS Kang[1], Jai Gopal[2] and SK Pandey[2]
1 Crop Improvement Section, Central Potato Research Station, Post Bag No. 1, Model Town P.O., Jalandhar 144 003 (Punjab)
2 Crop Improvement Division, Central Potato Research Institute, Shimla 171 001 (Himachal Pradesh)

JW 96 is a selection from the progeny of the cross Kufri Jyoti x CP 1362. The cross was made at during 1984. The clone was selected from the progeny of this cross at the Central Potato Research Station, Jalandhar, Punjab. The breeding methodology is clonal selection from the cross between selected parents (Kumar, 2004).

Tubers of JW 96 are oval shape, white skin, large sized with shallow eyes and creamy flesh colour. JW 96 flowers profusely at Kufri. The flower is red purple. Plant is medium tall. Leaflets are ovate with entire margin. Under early (75 days) harvest, this germplasm accession yielded at par with best control Kufri Ashoka in Indian plains and plateau region in multi-location trials under All India Coordinated Potato Improvement Project from 1997-1998 to 2001-2002. It is moderately resistant to late blight

Reference

Raj Kumar (2004) Estimation of genetic variances and combining ability in potato (*Solanum tuberosum*). *Ind J Agric Sci* **74**: 544-547.

IHR 3315 (INGR No. 05024; IC526794), Chilli (*Capsicum annum*) Germplasm with Fertility Restorer Genes and Resistance to PvY and CMV

K Madhavi Reddy
Indian Institute of Horticultural Research, Bangalore (Karnataka)

IIHR 3315 is a pure-line selection from ICPN 11#7 identified at the Indian Institute of Horticultural Research, Bangalore, Bangalore. It is a fertility restorer line with good general combining ability and thereby very much suitable for exploitation of heterosis. Plants are medium tall, fruits are long 13.25 cm. Number of fruits per plant are 30 and number of seeds per fruit are 70-80. It is also resistance to PVY and CMA.

E/79-42 (INGR No. 05022; IC522200), a Combined Resistant for Cyst Nematodes and Late Blight Disease of Potato (*Solanum tuberosum*) Germplasm

KS Krishna Prasad, TA Joseph, SK Pandey, IA Khan, DB Singh
Central Potato Research Institute, Regional Station, Muthorai (Tamil Nadu)

The potato cyst nematode (*Globodera pallida* and *G. rostochiensis*) and the late blight (*Phytophthora infestans*) are the major productivity constraints in potato cultivation in Nilgiri hills of Tamil Nadu. Breeding for genetic resistance is the most effective and environment friendly way to manage such diseases. Screening of potato germplasm and advanced breeding lines at the Central Potato Research Institute, Regional Station Muthorai, Tamil Nadu, a hot spot for potato cyst nematode and late blight resulted in identification of the breeding line E/79-42 as a source of resistance to both the diseases. Considering that it has resistance to both it can be effectively used in breeding for resistance to control these diseases and thereby overcoming the yield constraint. It has white flowers with high pollen fertility. The tubers are of medium size, oval, white with shallow eyes. It matures in 125-135 days.

JW 96 (INGR No. 05023; IC524019), Potato (*Solanum tuberosum*) Germplasm with Early Maturity

Raj Kumar[1], GS Kang[1], Jai Gopal[2] and SK Pandey[2]
1 Crop Improvement Section, Central Potato Research Station, Post Bag No. 1, Model Town P.O., Jalandhar 144 003 (Punjab)
2 Crop Improvement Division, Central Potato Research Institute, Shimla 171 001 (Himachal Pradesh)

JW 96 is a selection from the progeny of the cross Kufri Jyoti x CP 1362. The cross was made at during 1984. The clone was selected from the progeny of this cross at the Central Potato Research Station, Jalandhar, Punjab. The breeding methodology is clonal selection from the cross between selected parents (Kumar, 2004).

Tubers of JW 96 are oval shape, white skin, large sized with shallow eyes and creamy flesh colour. JW 96 flowers profusely at Kufri. The flower is red purple. Plant is medium tall. Leaflets are ovate with entire margin. Under early (75 days) harvest, this germplasm accession yielded at par with best control Kufri Ashoka in Indian plains and plateau region in multi-location trials under All India Coordinated Potato Improvement Project from 1997-1998 to 2001-2002. It is moderately resistant to late blight

Reference

Raj Kumar (2004) Estimation of genetic variances and combining ability in potato (*Solanum tuberosum*). *Ind J Agric Sci* **74**: 544-547.

IHR 3315 (INGR No. 05024; IC526794), Chilli (*Capsicum annum*) Germplasm with Fertility Restorer Genes and Resistance to PvY and CMV

K Madhavi Reddy
Indian Institute of Horticultural Research, Bangalore (Karnataka)

IIHR 3315 is a pure-line selection from ICPN 11#7 identified at the Indian Institute of Horticultural Research, Bangalore, Bangalore. It is a fertility restorer line with good general combining ability and thereby very much suitable for exploitation of heterosis. Plants are medium tall, fruits are long 13.25 cm. Number of fruits per plant are 30 and number of seeds per fruit are 70-80. It is also resistance to PVY and CMA.

E/79-42 (INGR No. 05022; IC522200), a Combined Resistant for Cyst Nematodes and Late Blight Disease of Potato (*Solanum tuberosum*) Germplasm

KS Krishna Prasad, TA Joseph, SK Pandey, IA Khan, DB Singh
Central Potato Research Institute, Regional Station, Muthorai (Tamil Nadu)

The potato cyst nematode (*Globodera pallida* and *G. rostochiensis*) and the late blight (*Phytophthora infestans*) are the major productivity constraints in potato cultivation in Nilgiri hills of Tamil Nadu. Breeding for genetic resistance is the most effective and environment friendly way to manage such diseases. Screening of potato germplasm and advanced breeding lines at the Central Potato Research Institute, Regional Station Muthorai, Tamil Nadu, a hot spot for potato cyst nematode and late blight resulted in identification of the breeding line E/79-42 as a source of resistance to both the diseases. Considering that it has resistance to both it can be effectively used in breeding for resistance to control these diseases and thereby overcoming the yield constraint. It has white flowers with high pollen fertility. The tubers are of medium size, oval, white with shallow eyes. It matures in 125-135 days.

JW 96 (INGR No. 05023; IC524019), Potato (*Solanum tuberosum*) Germplasm with Early Maturity

Raj Kumar[1], GS Kang[1], Jai Gopal[2] and SK Pandey[2]
1 Crop Improvement Section, Central Potato Research Station, Post Bag No. 1, Model Town P.O., Jalandhar 144 003 (Punjab)
2 Crop Improvement Division, Central Potato Research Institute, Shimla 171 001 (Himachal Pradesh)

JW 96 is a selection from the progeny of the cross Kufri Jyoti x CP 1362. The cross was made at during 1984. The clone was selected from the progeny of this cross at the Central Potato Research Station, Jalandhar, Punjab. The breeding methodology is clonal selection from the cross between selected parents (Kumar, 2004).

Tubers of JW 96 are oval shape, white skin, large sized with shallow eyes and creamy flesh colour. JW 96 flowers profusely at Kufri. The flower is red purple. Plant is medium tall. Leaflets are ovate with entire margin. Under early (75 days) harvest, this germplasm accession yielded at par with best control Kufri Ashoka in Indian plains and plateau region in multi-location trials under All India Coordinated Potato Improvement Project from 1997-1998 to 2001-2002. It is moderately resistant to late blight

Reference

Raj Kumar (2004) Estimation of genetic variances and combining ability in potato (*Solanum tuberosum*). *Ind J Agric Sci* **74**: 544-547.

IHR 3315 (INGR No. 05024; IC526794), Chilli (*Capsicum annum*) Germplasm with Fertility Restorer Genes and Resistance to PvY and CMV

K Madhavi Reddy
Indian Institute of Horticultural Research, Bangalore (Karnataka)

IIHR 3315 is a pure-line selection from ICPN 11#7 identified at the Indian Institute of Horticultural Research, Bangalore, Bangalore. It is a fertility restorer line with good general combining ability and thereby very much suitable for exploitation of heterosis. Plants are medium tall, fruits are long 13.25 cm. Number of fruits per plant are 30 and number of seeds per fruit are 70-80. It is also resistance to PVY and CMA.

BWBH-3 (INGR No. 05025; IC526796), Brinjal (*Solanum melongena*) Germplasm with Combined Resistance to Bacterial Wilt

AT Sadashiva and TH Singh
Indian Institute of Horticultural Research, Bangalore (Karnataka)

BWBH–3 is an advanced breeding line with resistance to bacterial wilt. It was developed by crossing IIHR–3 with IIHR–322 at the Indian Institute of Horticultural Research, Bangalore. The plants are spreading type, fruits are long green in colour, weighing from 50-55 gm. It has been found to have high yield potential (60.29 tonnes per hectare).

Acc. No. 315 (INGR No. 05026; IC526796), Okra (*Abelmoschus esculentus*) Germplasm with Dwarf, Bushy Plant Type

Bijendra Singh, G Kalloo and Mathura Rai
Indian Institute of Vegetable Research, Varanasi (Uttar Pradesh)

Okra (*Abelmoschus esculentus* L.) is a medium to tall plant with multi-pickings valued for its tender and delicious fruits. Pickings of green fruit in okra becomes problem during the later stages of the crop when plant becomes tall and dense. Considering this, Okra No. 315 is identified at the Indian Institute of Vegetable Research, Varanasi with short internode's length (0.4 to 0.7 cm), dwarf plant type (12-15 cm) with bushy nature (2-3 effective branches). First flower appears from 3rd or 4th node at about 42 days after sowing. Plant bears 10-15 fruits per plant having 7-9 ridges. It was identified from gene pool of okra germplasm available at Indian Institute of Vegetable Research, Varanasi (Annual report, 2002-2003 and 2003-2004). It breeds true and can be utilized in breeding programme for development of dwarf variety with short inter-node length.

References

Indian Institute of Vegetable Research (2002) *Annual Report* (2002-2003), Indian Institute of Vegetable Research, Varanasi, India, 8 p.

Indian Institute of Vegetable Research (2003) *Annual Report* (2003-2004), Indian Institute of Vegetable Research, Varanasi, India, 17 p.

SA 90 (INGR No. 05027; IC526796), Pumpkin (*Cucurbita moschata*) Germplasm with High Carotenoid Content

Sudhakar Pandy, Mathura Rai and G Kalloo
Indian Institute of Vegetable Research, Varanasi (Uttar Pradesh)

SA 90 is high carotene content genotype developed through inbreeding at the Indian Institute of Vegetable Research, Varanasi. After collection, first two seasons SA 90 was maintained by sib mating /selfing. SA 90 was grown along with other 70 lines of pumpkin and analyzed for carotenoid content along with record morphological observations. The genotype SA-90 has 14.85mg (100 g edible portion) carotenoid and was considered as a promising line for carotenoid followed by Pumpkin-111(14.19mg), BP-14(13.61mg), IVPK-225(13.29mg) and IVPK-226(13.08mg). SA 90 is vigorous in vine growth. The signal plant bears 1.6 fruits, having the fruit weight 4.0-5.15 kg. The polar and equatorial circumference of fruit is 72cm and 85.5 cm, respectively. The flesh colour of fruit is dark yellow had 3.5 cm thickness. The shape of the fruit is flat round having the 3-4 month storage capacity at ambient room temperature. It is tolerant to pumpkin mosaic virus disease and fruit fly. This line with high carotenoid content may be utilized for further quality improvement of pumpkin through development of hybrids and varieties. These materials may be also utilized for study of gene action, development of mapping population and tagging.

BWBH-3 (INGR No. 05025; IC526796), Brinjal (*Solanum melongena*) Germplasm with Combined Resistance to Bacterial Wilt

AT Sadashiva and TH Singh
Indian Institute of Horticultural Research, Bangalore (Karnataka)

BWBH–3 is an advanced breeding line with resistance to bacterial wilt. It was developed by crossing IIHR–3 with IIHR–322 at the Indian Institute of Horticultural Research, Bangalore. The plants are spreading type, fruits are long green in colour, weighing from 50-55 gm. It has been found to have high yield potential (60.29 tonnes per hectare).

Acc. No. 315 (INGR No. 05026; IC526796), Okra (*Abelmoschus esculentus*) Germplasm with Dwarf, Bushy Plant Type

Bijendra Singh, G Kalloo and Mathura Rai
Indian Institute of Vegetable Research, Varanasi (Uttar Pradesh)

Okra (*Abelmoschus esculentus* L.) is a medium to tall plant with multi-pickings valued for its tender and delicious fruits. Pickings of green fruit in okra becomes problem during the later stages of the crop when plant becomes tall and dense. Considering this, Okra No. 315 is identified at the Indian Institute of Vegetable Research, Varanasi with short internode's length (0.4 to 0.7 cm), dwarf plant type (12-15 cm) with bushy nature (2-3 effective branches). First flower appears from 3rd or 4th node at about 42 days after sowing. Plant bears 10-15 fruits per plant having 7-9 ridges. It was identified from gene pool of okra germplasm available at Indian Institute of Vegetable Research, Varanasi (Annual report, 2002-2003 and 2003-2004). It breeds true and can be utilized in breeding programme for development of dwarf variety with short inter-node length.

References

Indian Institute of Vegetable Research (2002) *Annual Report* (2002-2003), Indian Institute of Vegetable Research, Varanasi, India, 8 p.

Indian Institute of Vegetable Research (2003) *Annual Report* (2003-2004), Indian Institute of Vegetable Research, Varanasi, India, 17 p.

SA 90 (INGR No. 05027; IC526796), Pumpkin (*Cucurbita moschata*) Germplasm with High Carotenoid Content

Sudhakar Pandy, Mathura Rai and G Kalloo
Indian Institute of Vegetable Research, Varanasi (Uttar Pradesh)

SA 90 is high carotene content genotype developed through inbreeding at the Indian Institute of Vegetable Research, Varanasi. After collection, first two seasons SA 90 was maintained by sib mating /selfing. SA 90 was grown along with other 70 lines of pumpkin and analyzed for carotenoid content along with record morphological observations. The genotype SA-90 has 14.85mg (100 g edible portion) carotenoid and was considered as a promising line for carotenoid followed by Pumpkin-111(14.19mg), BP-14(13.61mg), IVPK-225(13.29mg) and IVPK-226(13.08mg). SA 90 is vigorous in vine growth. The signal plant bears 1.6 fruits, having the fruit weight 4.0-5.15 kg. The polar and equatorial circumference of fruit is 72cm and 85.5 cm, respectively. The flesh colour of fruit is dark yellow had 3.5 cm thickness. The shape of the fruit is flat round having the 3-4 month storage capacity at ambient room temperature. It is tolerant to pumpkin mosaic virus disease and fruit fly. This line with high carotenoid content may be utilized for further quality improvement of pumpkin through development of hybrids and varieties. These materials may be also utilized for study of gene action, development of mapping population and tagging.

BWBH-3 (INGR No. 05025; IC526796), Brinjal (*Solanum melongena*) Germplasm with Combined Resistance to Bacterial Wilt

AT Sadashiva and TH Singh
Indian Institute of Horticultural Research, Bangalore (Karnataka)

BWBH–3 is an advanced breeding line with resistance to bacterial wilt. It was developed by crossing IIHR–3 with IIHR–322 at the Indian Institute of Horticultural Research, Bangalore. The plants are spreading type, fruits are long green in colour, weighing from 50-55 gm. It has been found to have high yield potential (60.29 tonnes per hectare).

Acc. No. 315 (INGR No. 05026; IC526796), Okra (*Abelmoschus esculentus*) Germplasm with Dwarf, Bushy Plant Type

Bijendra Singh, G Kalloo and Mathura Rai
Indian Institute of Vegetable Research, Varanasi (Uttar Pradesh)

Okra (*Abelmoschus esculentus* L.) is a medium to tall plant with multi-pickings valued for its tender and delicious fruits. Pickings of green fruit in okra becomes problem during the later stages of the crop when plant becomes tall and dense. Considering this, Okra No. 315 is identified at the Indian Institute of Vegetable Research, Varanasi with short internode's length (0.4 to 0.7 cm), dwarf plant type (12-15 cm) with bushy nature (2-3 effective branches). First flower appears from 3rd or 4th node at about 42 days after sowing. Plant bears 10-15 fruits per plant having 7-9 ridges. It was identified from gene pool of okra germplasm available at Indian Institute of Vegetable Research, Varanasi (Annual report, 2002-2003 and 2003-2004). It breeds true and can be utilized in breeding programme for development of dwarf variety with short inter-node length.

References

Indian Institute of Vegetable Research (2002) *Annual Report* (2002-2003), Indian Institute of Vegetable Research, Varanasi, India, 8 p.

Indian Institute of Vegetable Research (2003) *Annual Report* (2003-2004), Indian Institute of Vegetable Research, Varanasi, India, 17 p.

SA 90 (INGR No. 05027; IC526796), Pumpkin (*Cucurbita moschata*) Germplasm with High Carotenoid Content

Sudhakar Pandy, Mathura Rai and G Kalloo
Indian Institute of Vegetable Research, Varanasi (Uttar Pradesh)

SA 90 is high carotene content genotype developed through inbreeding at the Indian Institute of Vegetable Research, Varanasi. After collection, first two seasons SA 90 was maintained by sib mating /selfing. SA 90 was grown along with other 70 lines of pumpkin and analyzed for carotenoid content along with record morphological observations. The genotype SA-90 has 14.85mg (100 g edible portion) carotenoid and was considered as a promising line for carotenoid followed by Pumpkin-111(14.19mg), BP-14(13.61mg), IVPK-225(13.29mg) and IVPK-226(13.08mg). SA 90 is vigorous in vine growth. The signal plant bears 1.6 fruits, having the fruit weight 4.0-5.15 kg. The polar and equatorial circumference of fruit is 72cm and 85.5 cm, respectively. The flesh colour of fruit is dark yellow had 3.5 cm thickness. The shape of the fruit is flat round having the 3-4 month storage capacity at ambient room temperature. It is tolerant to pumpkin mosaic virus disease and fruit fly. This line with high carotenoid content may be utilized for further quality improvement of pumpkin through development of hybrids and varieties. These materials may be also utilized for study of gene action, development of mapping population and tagging.

Table 1. Total carotenoids content of 5 most important accession out of 70, based on maximum value

Traits	Range	Population mean	GCV	PCV	CV (%)	C Dat 5%	High value accessions
Beta carotene (mg/100g)	2.34-14.85	9.29	33.19	33.97	7.5	1.07	SA-90, Pumpkin-111, BP-14, IVPK-225, IVPK-226

References

Kubicki, B and B Walczak (1976) Variation and heritability of beta carotene content in some cultivar of the *cucurbita* species. *Genetica-Polonica* **17:** 531-544.

Ram D, Sudhakar Pandey, G Kalloo and MK Banerjee (2001) Vegetable germplasm collecting in West Bengal, India. *IPGRI, Newsletter for Asia, The Pacific and Oceania* **34:** 23

Pandey, Sudhakar, J Singh, AK Upadhaya, D Ram and Mathura Rai (2003). Ascorbate and Carotenoid Content in an Indian Collection of Pumpkin (*Cucurbita moschata* Duch. Ex. Poir.). *CGC Report* **26:** 51-53.

CARI Acc. 1 (INGR No. 05028; IC524021), *Morinda citrifolia* an Endemic Fruit of Andaman and Nicobar Islands

DR Singh and RB Rai

Central Agricultural Research Institute, Port Blair (Andaman and Nicobar Islands)

Indian mulberry, *Morinda citrifolia* belongs to the family Rubiaceae, subfamily Rubioideae. It is distributed in India, Indonesia, Hawaiian Islands, Australia, Eastern and Western Polynesia. *Morinda citrifolia* var. *citrifolia,* indigenous and distributed in Andaman & Nicobar Islands is researched at the Central Agricultural Research Institute, Port Blair. This species is found in disturbed forests, in dry to mosaic forests, in open areas near the shoreline, in pastures and in coconut plantations, around villages and wastelands. It is popularly called Noni and locally it is known as Lorang, Burma phal, Suraogi and Pongee phal. It is eaten as fruit and also used in local traditional system of medicine (Singh *et al.,* 2005).

It is a large evergreen shrub or tree attaining a height of 3-5 meters at maturity. Leaves are opposite, glossy, pinnately veined, oval shaped 25-28 cm long and 10-15 cm wide, flowers are perfect and occur in the leaf axils in clusters, corolla is white, 5-lobed, calyx 5 forming a truncated green rim. Stamens 5, ovary 2 inferior, fruits conical, yellowish white, fleshy 9.8 x 5.26 cm in diameter syncarp, soft and fetid when ripe. Seeds are brown, oblong with distinct air chamber.

It can grow on infertile soils as well in brackish tide pools near the coast. It is highly salt tolerant and is reported to gains nutritional benefit from the minerals contained in seawater (Nelson, 2005). The plants are thriving well in tsunami-affected land with the EC 6-15 dsm^{-1} and up to EC 30 dsm^{-1} has been studied in pot cultivation. It can withstand pH ranging from 4-5 to 8.5. The fruit is getting popular in a variety of forms- dried and crushed, juiced and bottled, or freeze-dried. It is being touted as a veritable cure in mitigating diabetes, cardiovascular disease, cancer, headaches, arthritis and a host of degenerative diseases, and also used in veterinary medicine (Dixon *et al.,* 1992). Nelson (2002) reported that in seed propagation of *Morinda citrifolia* without seed treatment, takes 6-12 months or more to germinate, whereas stem cuttings can be rooted within 1-2 months. Treatment with GA (800 ppm) produced cent per cent seed germination and cuttings treated with 4000 ppm IBA produced maximum percentage of rooted cuttings (Singh *et al.,* 2005)

Table 1. Nutrient Composition and analytical studies of *Morinda citrifolia* var. *citrifolia*

Sample	K[1]	Ca [1]	Mg [1]	Mn [1]	Cu[2]	Fe[2]	Juice[1]	TSS[3]	Acidity [1]	Vit C[4]
Leaf	0.1-0.1	0.5-0.6	0.1-0.10	4.5	2.2	Trace	–	–	–	–
M. Fruit	0.1-0.2	0.0004-.0006	0.01-0.05	1.56	11.9	10.7	39.0	8.4	0.1	139.1
R. fruit	0.0005-0.1	0.006-3.5	0.02-0.05	0.5-4.8	27.4	3.3-42	54.3	8.5	0.1	125-1

1 = %; 2 = ppm; 3 = °brix; 4 = mg/100g

Table 1. Total carotenoids content of 5 most important accession out of 70, based on maximum value

Traits	Range	Population mean	GCV	PCV	CV (%)	C Dat 5%	High value accessions
Beta carotene (mg/100g)	2.34-14.85	9.29	33.19	33.97	7.5	1.07	SA-90, Pumpkin-111, BP-14, IVPK-225, IVPK-226

References

Kubicki, B and B Walczak (1976) Variation and heritability of beta carotene content in some cultivar of the *cucurbita* species. *Genetica-Polonica* **17:** 531-544.

Ram D, Sudhakar Pandey, G Kalloo and MK Banerjee (2001) Vegetable germplasm collecting in West Bengal, India. *IPGRI, Newsletter for Asia, The Pacific and Oceania* **34:** 23

Pandey, Sudhakar, J Singh, AK Upadhaya, D Ram and Mathura Rai (2003). Ascorbate and Carotenoid Content in an Indian Collection of Pumpkin (*Cucurbita moschata* Duch. Ex. Poir.). *CGC Report* **26:** 51-53.

CARI Acc. 1 (INGR No. 05028; IC524021), *Morinda citrifolia* an Endemic Fruit of Andaman and Nicobar Islands

DR Singh and RB Rai

Central Agricultural Research Institute, Port Blair (Andaman and Nicobar Islands)

Indian mulberry, *Morinda citrifolia* belongs to the family Rubiaceae, subfamily Rubioideae. It is distributed in India, Indonesia, Hawaiian Islands, Australia, Eastern and Western Polynesia. *Morinda citrifolia* var. *citrifolia,* indigenous and distributed in Andaman & Nicobar Islands is researched at the Central Agricultural Research Institute, Port Blair. This species is found in disturbed forests, in dry to mosaic forests, in open areas near the shoreline, in pastures and in coconut plantations, around villages and wastelands. It is popularly called Noni and locally it is known as Lorang, Burma phal, Suraogi and Pongee phal. It is eaten as fruit and also used in local traditional system of medicine (Singh *et al.,* 2005).

It is a large evergreen shrub or tree attaining a height of 3-5 meters at maturity. Leaves are opposite, glossy, pinnately veined, oval shaped 25-28 cm long and 10-15 cm wide, flowers are perfect and occur in the leaf axils in clusters, corolla is white, 5-lobed, calyx 5 forming a truncated green rim. Stamens 5, ovary 2 inferior, fruits conical, yellowish white, fleshy 9.8 x 5.26 cm in diameter syncarp, soft and fetid when ripe. Seeds are brown, oblong with distinct air chamber.

It can grow on infertile soils as well in brackish tide pools near the coast. It is highly salt tolerant and is reported to gains nutritional benefit from the minerals contained in seawater (Nelson, 2005). The plants are thriving well in tsunami-affected land with the EC 6-15 dsm^{-1} and up to EC 30 dsm^{-1} has been studied in pot cultivation. It can withstand pH ranging from 4-5 to 8.5. The fruit is getting popular in a variety of forms- dried and crushed, juiced and bottled, or freeze-dried. It is being touted as a veritable cure in mitigating diabetes, cardiovascular disease, cancer, headaches, arthritis and a host of degenerative diseases, and also used in veterinary medicine (Dixon *et al.,* 1992). Nelson (2002) reported that in seed propagation of *Morinda citrifolia* without seed treatment, takes 6-12 months or more to germinate, whereas stem cuttings can be rooted within 1-2 months. Treatment with GA (800 ppm) produced cent per cent seed germination and cuttings treated with 4000 ppm IBA produced maximum percentage of rooted cuttings (Singh *et al.,* 2005)

Table 1. Nutrient Composition and analytical studies of *Morinda citrifolia* var. *citrifolia*

Sample	K[1]	Ca [1]	Mg [1]	Mn [1]	Cu[2]	Fe[2]	Juice[1]	TSS[3]	Acidity [1]	Vit C[4]
Leaf	0.1-0.1	0.5-0.6	0.1-0.10	4.5	2.2	Trace	–	–	–	–
M. Fruit	0.1-0.2	0.0004-.0006	0.01-0.05	1.56	11.9	10.7	39.0	8.4	0.1	139.1
R. fruit	0.0005-0.1	0.006-3.5	0.02-0.05	0.5-4.8	27.4	3.3-42	54.3	8.5	0.1	125-1

1 = %; 2 = ppm; 3 = °brix; 4 = mg/100g

References

Dixon, Anna R, McMillen, Heather, Etkin, L Nina (1999) Ferment This: The transformation of Noni, a traditional Polynesian medicine (*Morinda citrifolia*, Rubiaceae). *Economic Botany* **53(1)**: 51-68.

Nelson Scot C (2005) Species profiles for Pacific Island agroforestry "*Morinda citrifolia* (noni) Version 1.2 (www.traditionaltree.org).

Singh DR, RB Rai (2005) Effect of growth regulators in rooting of stem cuttings of *Morinda citrifolia* var. *citrifolia* in Bay islands. *Intl J Noni Res* **1(1)**: 17-22.

Singh, DR and RB Rai (2005) Influence of Gibberllic acid on seed germination in Noni (*Morinda citrifolia* Linn.) of Andamans. *Intl J Noni Res* **1(1)**: 31-35.

Acc. C 1 (INGR No. 05029; IC370415), Chinese Cassia or Cinnamon *(Cinnamomum cassia)* Germplasm with High Oleoresin Content

B Krishnamoorthy, J Rema and PA Mathew
Indian Institute of Spices Research, Kozhikode (Kerala)

Cinnamomum cassia Blume (Syn. *C. aromaticum* Nees), of family Lauraceae known as cassia cinnamon or Chinese cassia. It is a medium sized and straight trunked evergreen tree reaching a height of about 20 m. Chinese cassia is commercially grown for its aromatic bark which is used as a spice. Besides bark, cassia oleoresin, cassia oil and cassia buds are the important products, which are marketed commercially. Cassia cinnamon has a tremendous potential in the spice industry for flavouring food and beverages and in the manufacture of value added products. It has immense medicinal properties and is used by the pharmaceutical industry. It is also used by the perfume industry to a limited extent. Chinese cassia has originated in China and is cultivated commercially. China is the main producer and exporter of cassia cinnamon.

The Indian Institute of Spices Research (IISR), Calicut has conserved 408 accessions of *Cinnamomum* germplasm in the field repository, of which 25 accessions are of Chinese cassia. They were evaluated, for the bark oleoresin content, which ranged between 6 to 10.5 percent (Krishnamoorthy *et al.*, 1999). Cinnamon accession, IC370415 was identified as an elite accession with very high bark oleoresin content (10.5%). This accession was collected as seedling from Srikundra Estate, Valparai, Coimbatore District during 1990 and is maintained as C-1 (IC370415) at the IISR, Calicut. This accession could be commercially exploited for production of bark specie, which is used in food industry for flavouring food and confectionaries. Plant is 6 m tall, with an average of three main shoot and around 24 secondary shoots. The girth of main shoot one meter above ground is 18.2 cm. Leaves are large, lanceolate, young leaf light green, velvet, old dark green coriaceous, average length 27, breadth 7.8 cm with ratio of 3.46 and size index 2.1; length of petiole 1 cm brown and pungent. Bark, spicy, sweet and pungent, bark oleoresin 10.50 per cent, bark essential oil 3.45 per cent, leaf essential oil 0.5 per cent, cinnamaldehyde content in bark oil is 86.5 per cent and cinnamaldehyde content in leaf oil is 76.5 per cent.

S 288 (INGR No. 05030; IC522201), a Spontaneous Hybrid between *Coffea arabica* and *C. liberica*

Santa Ram, RL Narasimha Swamy, S Vishveshwara and D Ganesh
Division of Botany, Central Coffee Research Institute, Coffee Research Station, Post 577 117, Chikmagalur District, (Karnataka)

S. 288 was developed by pure line selection from S.26 (Thomas, 1960). This is a putative spontaneous interspecific hybrid between tetraploid *C. arabica* (2n=4x=44) and diploid *C. liberica* (2n=2x=22). This hybrid was spotted in 'Doobla Estate' in Chikmagalur District of Karnataka in 1928 and maintained at the Central Coffee Research Institute (Ramachandran and Srinivasan, 1979). This material is known for its wide adaptability. The bushes are tall, vigorous and spreading with a yield potential of 800–1000 kg/ha. It produces

References

Dixon, Anna R, McMillen, Heather, Etkin, L Nina (1999) Ferment This: The transformation of Noni, a traditional Polynesian medicine (*Morinda citrifolia*, Rubiaceae). *Economic Botany* **53(1)**: 51-68.

Nelson Scot C (2005) Species profiles for Pacific Island agroforestry "*Morinda citrifolia* (noni) Version 1.2 (www.traditionaltree.org).

Singh DR, RB Rai (2005) Effect of growth regulators in rooting of stem cuttings of *Morinda citrifolia* var. *citrifolia* in Bay islands. *Intl J Noni Res* **1(1)**: 17-22.

Singh, DR and RB Rai (2005) Influence of Gibberllic acid on seed germination in Noni (*Morinda citrifolia* Linn.) of Andamans. *Intl J Noni Res* **1(1)**: 31-35.

Acc. C 1 (INGR No. 05029; IC370415), Chinese Cassia or Cinnamon *(Cinnamomum cassia)* Germplasm with High Oleoresin Content

B Krishnamoorthy, J Rema and PA Mathew
Indian Institute of Spices Research, Kozhikode (Kerala)

Cinnamomum cassia Blume (Syn. *C. aromaticum* Nees), of family Lauraceae known as cassia cinnamon or Chinese cassia. It is a medium sized and straight trunked evergreen tree reaching a height of about 20 m. Chinese cassia is commercially grown for its aromatic bark which is used as a spice. Besides bark, cassia oleoresin, cassia oil and cassia buds are the important products, which are marketed commercially. Cassia cinnamon has a tremendous potential in the spice industry for flavouring food and beverages and in the manufacture of value added products. It has immense medicinal properties and is used by the pharmaceutical industry. It is also used by the perfume industry to a limited extent. Chinese cassia has originated in China and is cultivated commercially. China is the main producer and exporter of cassia cinnamon.

The Indian Institute of Spices Research (IISR), Calicut has conserved 408 accessions of *Cinnamomum* germplasm in the field repository, of which 25 accessions are of Chinese cassia. They were evaluated, for the bark oleoresin content, which ranged between 6 to 10.5 percent (Krishnamoorthy *et al.*, 1999). Cinnamon accession, IC370415 was identified as an elite accession with very high bark oleoresin content (10.5%). This accession was collected as seedling from Srikundra Estate, Valparai, Coimbatore District during 1990 and is maintained as C-1 (IC370415) at the IISR, Calicut. This accession could be commercially exploited for production of bark specie, which is used in food industry for flavouring food and confectionaries. Plant is 6 m tall, with an average of three main shoot and around 24 secondary shoots. The girth of main shoot one meter above ground is 18.2 cm. Leaves are large, lanceolate, young leaf light green, velvet, old dark green coriaceous, average length 27, breadth 7.8 cm with ratio of 3.46 and size index 2.1; length of petiole 1 cm brown and pungent. Bark, spicy, sweet and pungent, bark oleoresin 10.50 per cent, bark essential oil 3.45 per cent, leaf essential oil 0.5 per cent, cinnamaldehyde content in bark oil is 86.5 per cent and cinnamaldehyde content in leaf oil is 76.5 per cent.

S 288 (INGR No. 05030; IC522201), a Spontaneous Hybrid between *Coffea arabica* and *C. liberica*

Santa Ram, RL Narasimha Swamy, S Vishveshwara and D Ganesh
Division of Botany, Central Coffee Research Institute, Coffee Research Station, Post 577 117, Chikmagalur District, (Karnataka)

S. 288 was developed by pure line selection from S.26 (Thomas, 1960). This is a putative spontaneous interspecific hybrid between tetraploid *C. arabica* (2n=4x=44) and diploid *C. liberica* (2n=2x=22). This hybrid was spotted in 'Doobla Estate' in Chikmagalur District of Karnataka in 1928 and maintained at the Central Coffee Research Institute (Ramachandran and Srinivasan, 1979). This material is known for its wide adaptability. The bushes are tall, vigorous and spreading with a yield potential of 800–1000 kg/ha. It produces

References

Dixon, Anna R, McMillen, Heather, Etkin, L Nina (1999) Ferment This: The transformation of Noni, a traditional Polynesian medicine (*Morinda citrifolia*, Rubiaceae). *Economic Botany* **53(1)**: 51-68.

Nelson Scot C (2005) Species profiles for Pacific Island agroforestry "*Morinda citrifolia* (noni) Version 1.2 (www.traditionaltree.org).

Singh DR, RB Rai (2005) Effect of growth regulators in rooting of stem cuttings of *Morinda citrifolia* var. *citrifolia* in Bay islands. *Intl J Noni Res* **1(1)**: 17-22.

Singh, DR and RB Rai (2005) Influence of Gibberllic acid on seed germination in Noni (*Morinda citrifolia* Linn.) of Andamans. *Intl J Noni Res* **1(1)**: 31-35.

Acc. C 1 (INGR No. 05029; IC370415), Chinese Cassia or Cinnamon *(Cinnamomum cassia)* Germplasm with High Oleoresin Content

B Krishnamoorthy, J Rema and PA Mathew
Indian Institute of Spices Research, Kozhikode (Kerala)

Cinnamomum cassia Blume (Syn. *C. aromaticum* Nees), of family Lauraceae known as cassia cinnamon or Chinese cassia. It is a medium sized and straight trunked evergreen tree reaching a height of about 20 m. Chinese cassia is commercially grown for its aromatic bark which is used as a spice. Besides bark, cassia oleoresin, cassia oil and cassia buds are the important products, which are marketed commercially. Cassia cinnamon has a tremendous potential in the spice industry for flavouring food and beverages and in the manufacture of value added products. It has immense medicinal properties and is used by the pharmaceutical industry. It is also used by the perfume industry to a limited extent. Chinese cassia has originated in China and is cultivated commercially. China is the main producer and exporter of cassia cinnamon.

The Indian Institute of Spices Research (IISR), Calicut has conserved 408 accessions of *Cinnamomum* germplasm in the field repository, of which 25 accessions are of Chinese cassia. They were evaluated, for the bark oleoresin content, which ranged between 6 to 10.5 percent (Krishnamoorthy *et al.*, 1999). Cinnamon accession, IC370415 was identified as an elite accession with very high bark oleoresin content (10.5%). This accession was collected as seedling from Srikundra Estate, Valparai, Coimbatore District during 1990 and is maintained as C-1 (IC370415) at the IISR, Calicut. This accession could be commercially exploited for production of bark specie, which is used in food industry for flavouring food and confectionaries. Plant is 6 m tall, with an average of three main shoot and around 24 secondary shoots. The girth of main shoot one meter above ground is 18.2 cm. Leaves are large, lanceolate, young leaf light green, velvet, old dark green coriaceous, average length 27, breadth 7.8 cm with ratio of 3.46 and size index 2.1; length of petiole 1 cm brown and pungent. Bark, spicy, sweet and pungent, bark oleoresin 10.50 per cent, bark essential oil 3.45 per cent, leaf essential oil 0.5 per cent, cinnamaldehyde content in bark oil is 86.5 per cent and cinnamaldehyde content in leaf oil is 76.5 per cent.

S 288 (INGR No. 05030; IC522201), a Spontaneous Hybrid between *Coffea arabica* and *C. liberica*

Santa Ram, RL Narasimha Swamy, S Vishveshwara and D Ganesh
Division of Botany, Central Coffee Research Institute, Coffee Research Station, Post 577 117, Chikmagalur District, (Karnataka)

S. 288 was developed by pure line selection from S.26 (Thomas, 1960). This is a putative spontaneous interspecific hybrid between tetraploid *C. arabica* (2n=4x=44) and diploid *C. liberica* (2n=2x=22). This hybrid was spotted in 'Doobla Estate' in Chikmagalur District of Karnataka in 1928 and maintained at the Central Coffee Research Institute (Ramachandran and Srinivasan, 1979). This material is known for its wide adaptability. The bushes are tall, vigorous and spreading with a yield potential of 800–1000 kg/ha. It produces

large percentage of defective beans (20–30%) due to false poly-embryony (Anonymous, 1997). This material is reported to have S_H3 resistance gene introgressed from diploid species *C. liberica* (Prakash *et al.*, 2002) imparting resistance against races I and II of rust fungus *Hemileia vastatrix* (Srinivasan *et al.*, 2002). These races are the most prevalent in all coffee growing countries of the world. Thus S.288 is considered to be important source of S_H3 gene. It is reported that the virulence gene V_3 occurs at the lowest frequency in the populations of *H. vastatrix*, implying that the deployment of S_H3 in combination with S_H genes from Hibrido de Timor may prove to be very important in resistance breeding (Ram, 2005). Therefore, it has strategic as well as applied value.

It is a unique Indian coffee germplasm as source of genes for leaf rust resistance and drought in the context of Indian coffee breeding. S.288 donated the S_H3 gene (one of the resistance genes to coffee leaf rust) to the popular coffee selection S.795, the flagship coffee variety of India. S_H3 homozygous individual plants manifesting high resistance to leaf rust are being identified for use in maintenance breeding of S.795, as well as deployment of S_H3 in other breeding exercises like pyramiding resistance gene (Ram, 2001).

References

Anonymous (1997) Coffee Guide, Central Coffee Research Institute, Coffee Board Research Department. p.12.

Prakash NS, MC Combes, S Naveen and P Leshermes (2002) AFLP analysis of introgression of coffee cultivar (*Coffea arabica* L.) derived from a natural interspecific hybrid. *Euphytica* **124:** 265–271.

Ram AS (1995) New dimensions in understanding inheritance of coffee leaf rust resistance. A Mendelian perspective. *Proceedings of International Scientific Colloquium on Coffee Science*. Kyoto. p. 548-553.

Ram AS (2001) Breeding for rust resistance in coffee; the gene pyramiding model. *Journal of Plantation Crops* **29**:10-15

Ram AS (2005) Breeding coffee for leaf rust resistance–The Indian Experience. *Indian Coffee LXIX* **4**:10–13.

Ramachandran M and CS Srinivasan (1979) Four generation of selection for resistance to Race I of leaf rust (*H. vastatrix* B and Br.) in *Coffea arabica* cv.288 x Kent. *Indian Coffee XLIII* **5:** 59–160.

Srinivasan CS, M Ramachandran and SS Bhat (2002) Relative importance of resistance genes for management of leaf rust in coffee. *Journal of Coffee Research* **30:** 24-33.

Thomas KM (1960) Station selections. *Indian Coffee XXIV* **6:** 18-27.

S 2464 (Sln 11) (INGR No. 05031; IC522202), a Natural Self Compatible Tetraploid (*Coffea liberica x C. eugenoides)* Coffee

Santa Ram, RL Narasimha Swamy, S Vishveshwara, AGS Reddy and D Ganesh

Division of Botany, Central Coffee Research Institute, Coffee Research Station, Post 577 117, Chikmagalur District, (Karnataka)

S.2464 (Ligenioides) is a self-compatible allotetraploid of *C. liberica* x *C. eugenoides*. The plants are drought hardy and show high field tolerance to leaf rust disease (*Hemileia vastatrix*). S.2464 was born as a spontaneous tetraploid (2n=4x=44) by natural doubling of chromosomes in a single bud on a hybrid of *C. liberica* and *C. eugenioides* at the Central Coffee Research Institute, Chikmagalur and hence named as 'Ligenioides' (Reddy *et al.*, 1984). This shows characters intermediate between *C. liberica* and *C. eugenioides* and bear close resemblance to *C. arabica* (Narashimhaswamy and Vishveshwara, 1967). This hybrid evolved at central coffee research institute, India in 1955.

Ligenioides is characterized by profuse vegetative growth. The primary branches are 3–4 ft in length; internodes are short, ranging 5–6 cm; leaves are elliptical with sub-acute leaf tip, wavy margin sub-coriaceous. Tip leaves are green. Fruits are born in loose clusters and smaller than spontaneous *arabica* and other *arabica* selections. Plants are drought hardy and show high field tolerance to leaf rust disease and also observed to be least affected by white stem borer (*Xylotrechus quadripes*). The yield of this genotype is ranging from 750–1000 kg/ha under wide range of agro climatic conditions tested. It is drought hardy and is recommended for draught prone zones in the coffee growing tracts in traditional as well as in non-traditional areas in Andhra Pradesh and Orissa (Gopal, 1985 and Ganesh *et al.*, 2002). This is considered as a unique Indian coffee germplasm as it carries the genes of diploid species *C. liberica* and *C. eugenioides*, but resembles *C. arabica* in morphological features as well as beverage characteristics. It has proven

large percentage of defective beans (20–30%) due to false poly-embryony (Anonymous, 1997). This material is reported to have S_H3 resistance gene introgressed from diploid species *C. liberica* (Prakash *et al.*, 2002) imparting resistance against races I and II of rust fungus *Hemileia vastatrix* (Srinivasan *et al.*, 2002). These races are the most prevalent in all coffee growing countries of the world. Thus S.288 is considered to be important source of S_H3 gene. It is reported that the virulence gene V_3 occurs at the lowest frequency in the populations of *H. vastatrix*, implying that the deployment of S_H3 in combination with S_H genes from Hibrido de Timor may prove to be very important in resistance breeding (Ram, 2005). Therefore, it has strategic as well as applied value.

It is a unique Indian coffee germplasm as source of genes for leaf rust resistance and drought in the context of Indian coffee breeding. S.288 donated the S_H3 gene (one of the resistance genes to coffee leaf rust) to the popular coffee selection S.795, the flagship coffee variety of India. S_H3 homozygous individual plants manifesting high resistance to leaf rust are being identified for use in maintenance breeding of S.795, as well as deployment of S_H3 in other breeding exercises like pyramiding resistance gene (Ram, 2001).

References

Anonymous (1997) Coffee Guide, Central Coffee Research Institute, Coffee Board Research Department. p.12.

Prakash NS, MC Combes, S Naveen and P Leshermes (2002) AFLP analysis of introgression of coffee cultivar (*Coffea arabica* L.) derived from a natural interspecific hybrid. *Euphytica* **124:** 265–271.

Ram AS (1995) New dimensions in understanding inheritance of coffee leaf rust resistance. A Mendelian perspective. *Proceedings of International Scientific Colloquium on Coffee Science*. Kyoto. p. 548-553.

Ram AS (2001) Breeding for rust resistance in coffee; the gene pyramiding model. *Journal of Plantation Crops* **29**:10-15

Ram AS (2005) Breeding coffee for leaf rust resistance–The Indian Experience. *Indian Coffee LXIX* **4**:10–13.

Ramachandran M and CS Srinivasan (1979) Four generation of selection for resistance to Race I of leaf rust (*H. vastatrix* B and Br.) in *Coffea arabica* cv.288 x Kent. *Indian Coffee XLIII* **5:** 59–160.

Srinivasan CS, M Ramachandran and SS Bhat (2002) Relative importance of resistance genes for management of leaf rust in coffee. *Journal of Coffee Research* **30:** 24-33.

Thomas KM (1960) Station selections. *Indian Coffee XXIV* **6:** 18-27.

S 2464 (Sln 11) (INGR No. 05031; IC522202), a Natural Self Compatible Tetraploid (*Coffea liberica x C. eugenoides)* Coffee

Santa Ram, RL Narasimha Swamy, S Vishveshwara, AGS Reddy and D Ganesh

Division of Botany, Central Coffee Research Institute, Coffee Research Station, Post 577 117, Chikmagalur District, (Karnataka)

S.2464 (Ligenioides) is a self-compatible allotetraploid of *C. liberica* x *C. eugenoides*. The plants are drought hardy and show high field tolerance to leaf rust disease (*Hemileia vastatrix*). S.2464 was born as a spontaneous tetraploid (2n=4x=44) by natural doubling of chromosomes in a single bud on a hybrid of *C. liberica* and *C. eugenioides* at the Central Coffee Research Institute, Chikmagalur and hence named as 'Ligenioides' (Reddy *et al.*, 1984). This shows characters intermediate between *C. liberica* and *C. eugenioides* and bear close resemblance to *C. arabica* (Narashimhaswamy and Vishveshwara, 1967). This hybrid evolved at central coffee research institute, India in 1955.

Ligenioides is characterized by profuse vegetative growth. The primary branches are 3–4 ft in length; internodes are short, ranging 5–6 cm; leaves are elliptical with sub-acute leaf tip, wavy margin sub-coriaceous. Tip leaves are green. Fruits are born in loose clusters and smaller than spontaneous *arabica* and other *arabica* selections. Plants are drought hardy and show high field tolerance to leaf rust disease and also observed to be least affected by white stem borer (*Xylotrechus quadripes*). The yield of this genotype is ranging from 750–1000 kg/ha under wide range of agro climatic conditions tested. It is drought hardy and is recommended for draught prone zones in the coffee growing tracts in traditional as well as in non-traditional areas in Andhra Pradesh and Orissa (Gopal, 1985 and Ganesh *et al.*, 2002). This is considered as a unique Indian coffee germplasm as it carries the genes of diploid species *C. liberica* and *C. eugenioides*, but resembles *C. arabica* in morphological features as well as beverage characteristics. It has proven

itself to be a carrier of genes conditioning resistance against biotic adversaries like leaf rust (*Hemileia vastatrix*) and white stem borer (*Xylotrechus quadripes*) and abiotic stress (drought). This amphidiploid freely inter-crosses with a variety of *C. arabica* genotypes to yield fertile hybrids (Reddy *et al.*, 1981 and 1985) and thus constitutes an important source of new genes for breeding of *C. arabica* (Ram *et al.*, 2002 and 2004).

References

Ganesh D, AS Ram, NS Prakash, MK Mishra, Jamsheed Ahmed, M Jagadeesan, AGS Reddy and CS Srinivasan (2002) Evaluation *of Coffea liberica* x *Coffea eugenioides* and its progenies for yield, leaf rust tolerance and quality. *Proceedings of XV Plantation Crops Symposium on Plantation Crops*, Mysore, India. p. 72–77.

Gopal NH (1985) Performance of coffee cultivars of Andhra Pradesh region with reference to drought. *Journal of Coffee Research* **15**:58.

Narasimhaswamy RL and S Vishveshwara (1967) Progress report on hybrids between diploid species of *Coffea*. *Turrialba* **17(1)**: 11–17.

Ram AS, D Ganesh, AGS Reddy and CS Srinivasan (2004) Ligenioides- A source of new genes for Arabica coffee breeding. *Journal of Plantation Crops* **32(Suppl.)**: 5–11.

Reddy AGS, KVVS Raju and PS Dharmaraj (1981) Fruit set in coffee under different modes of pollination in Andhra Pradesh. *Proceedings of IV Plantation Crops Symposium on Plantation Crops*, Bangalore, India. p. 252–256.

Reddy AGS, KVVS Raju and PS Dharmaraj (1985) Breeding behavior of 'Ligenioides' A spontaneous amphidiploid between *Coffea liberica* and *Coffea eugenioides*. *Journal of Coffee Research* **15(1&2)**: 33–37.

Recombinant Inbred Lines of Wheat (*Triticum aestivum* L.) Combining Drought Resistance with High Yield

Renu Khanna-Chopra and Rajendra V Patil

Stress Physiology Laboratory, Water Technology Centre, Indian Agricultural Research Institute, New Delhi 110 012

With the objective of combining drought resistance with high yield, a well-known drought resistant wheat cultivar C306 (*Ne1ne2*) was crossed with a high yielding cultivar WL711 (*ne1Ne2*) at the Water Technology Centre, Indian Agricultural Research Institute, New Delhi. The resulting F_1 hybrid (*Ne1Ne2*) was necrotic and survived up to booting stage but died before seed formation. Hence, the F_1 ears enclosed in dead leaf sheath were excised and cultured in ear culture medium (Dalal *et al.*, 1999) to obtain F_2 seeds. In F_2 generation, segregation for necrosis was observed in ratio of 9 necrotic: 7 healthy plants and only surviving healthy F_2 plants were used to raise the subsequent generations (Khanna-Chopra and Patil, 2002). In early generations (F_2 to F_4), the large segregating plant material was evaluated for number of morphological and physiological traits and yield and yield components under fully irrigated and water deficit conditions. In advanced generations i.e. from F_5 to F_8, the selected lines along with their parents were evaluated for response to water variable environments under different irrigation regimes and also using line-source sprinkler system (Hanks *et al.*, 1976) in the fields of Water Technology Centre and in the rain-fed field of Division of Agronomy, IARI, New Delhi. The selected lines were characterized for crop growth rate, cell membrane stability, water relation parameters, canopy temperature depression, water use efficiency and yield and yield components (Patil, 2005). The selected lines were also evaluated for grain characteristics and chapati making quality. The necrosis gene (*Ne1* and *Ne2*) was identified by crossing the selected lines with both the parents and by growing F_1 generation under controlled conditions. The advanced generation lines were developed by pedigree selection. Following were found to be novel and distinct for the features described below.

33. WCF8-BL10 (INGR No. 05032; IC443618)

BL10 is of medium height (110 cm), erect in habit, high yielding (600 g m^{-2}) under normal condition and shows medium yield stability (bi = 1.20) across water variable environments. The phenology is intermediate of parents. It has higher cell membrane stability, lower canopy temperature and improved water use efficiency under drought conditions. It is a carrier for *Ne2* gene of necrosis as it produced necrotic F_1 hybrid when crossed with the parent C306 (*Ne1*).

33. WCF8-W12 (INGR No. 05033; IC443619)

W12 is medium height line (120 cm) with semi-spreading growth habit and shows higher early vigour under normal and water stress conditions. It yields intermediate of parents under normal condition (550 gm^{-2}) and shows higher yield stability (bi = 0.77) across water variable environments. It is slightly early in phenology than both the parents. It is characterized by longer coleoptile,

itself to be a carrier of genes conditioning resistance against biotic adversaries like leaf rust (*Hemileia vastatrix*) and white stem borer (*Xylotrechus quadripes*) and abiotic stress (drought). This amphidiploid freely inter-crosses with a variety of *C. arabica* genotypes to yield fertile hybrids (Reddy *et al.*, 1981 and 1985) and thus constitutes an important source of new genes for breeding of *C. arabica* (Ram *et al.*, 2002 and 2004).

References

Ganesh D, AS Ram, NS Prakash, MK Mishra, Jamsheed Ahmed, M Jagadeesan, AGS Reddy and CS Srinivasan (2002) Evaluation *of Coffea liberica* x *Coffea eugenioides* and its progenies for yield, leaf rust tolerance and quality. *Proceedings of XV Plantation Crops Symposium on Plantation Crops*, Mysore, India. p. 72–77.

Gopal NH (1985) Performance of coffee cultivars of Andhra Pradesh region with reference to drought. *Journal of Coffee Research* **15**:58.

Narasimhaswamy RL and S Vishveshwara (1967) Progress report on hybrids between diploid species of *Coffea*. *Turrialba* **17(1)**: 11–17.

Ram AS, D Ganesh, AGS Reddy and CS Srinivasan (2004) Ligenioides- A source of new genes for Arabica coffee breeding. *Journal of Plantation Crops* **32(Suppl.)**: 5–11.

Reddy AGS, KVVS Raju and PS Dharmaraj (1981) Fruit set in coffee under different modes of pollination in Andhra Pradesh. *Proceedings of IV Plantation Crops Symposium on Plantation Crops*, Bangalore, India. p. 252–256.

Reddy AGS, KVVS Raju and PS Dharmaraj (1985) Breeding behavior of 'Ligenioides' A spontaneous amphidiploid between *Coffea liberica* and *Coffea eugenioides*. *Journal of Coffee Research* **15(1&2)**: 33–37.

Recombinant Inbred Lines of Wheat (*Triticum aestivum* L.) Combining Drought Resistance with High Yield

Renu Khanna-Chopra and Rajendra V Patil

Stress Physiology Laboratory, Water Technology Centre, Indian Agricultural Research Institute, New Delhi 110 012

With the objective of combining drought resistance with high yield, a well-known drought resistant wheat cultivar C306 (*Ne1ne2*) was crossed with a high yielding cultivar WL711 (*ne1Ne2*) at the Water Technology Centre, Indian Agricultural Research Institute, New Delhi. The resulting F_1 hybrid (*Ne1Ne2*) was necrotic and survived up to booting stage but died before seed formation. Hence, the F_1 ears enclosed in dead leaf sheath were excised and cultured in ear culture medium (Dalal *et al.*, 1999) to obtain F_2 seeds. In F_2 generation, segregation for necrosis was observed in ratio of 9 necrotic: 7 healthy plants and only surviving healthy F_2 plants were used to raise the subsequent generations (Khanna-Chopra and Patil, 2002). In early generations (F_2 to F_4), the large segregating plant material was evaluated for number of morphological and physiological traits and yield and yield components under fully irrigated and water deficit conditions. In advanced generations i.e. from F_5 to F_8, the selected lines along with their parents were evaluated for response to water variable environments under different irrigation regimes and also using line-source sprinkler system (Hanks *et al.*, 1976) in the fields of Water Technology Centre and in the rain-fed field of Division of Agronomy, IARI, New Delhi. The selected lines were characterized for crop growth rate, cell membrane stability, water relation parameters, canopy temperature depression, water use efficiency and yield and yield components (Patil, 2005). The selected lines were also evaluated for grain characteristics and chapati making quality. The necrosis gene (*Ne1* and *Ne2*) was identified by crossing the selected lines with both the parents and by growing F_1 generation under controlled conditions. The advanced generation lines were developed by pedigree selection. Following were found to be novel and distinct for the features described below.

33. WCF8-BL10 (INGR No. 05032; IC443618)

BL10 is of medium height (110 cm), erect in habit, high yielding (600 g m^{-2}) under normal condition and shows medium yield stability (bi = 1.20) across water variable environments. The phenology is intermediate of parents. It has higher cell membrane stability, lower canopy temperature and improved water use efficiency under drought conditions. It is a carrier for *Ne2* gene of necrosis as it produced necrotic F_1 hybrid when crossed with the parent C306 (*Ne1*).

33. WCF8-W12 (INGR No. 05033; IC443619)

W12 is medium height line (120 cm) with semi-spreading growth habit and shows higher early vigour under normal and water stress conditions. It yields intermediate of parents under normal condition (550 gm^{-2}) and shows higher yield stability (bi = 0.77) across water variable environments. It is slightly early in phenology than both the parents. It is characterized by longer coleoptile,

higher cell membrane stability, lower canopy temperature and improved water use efficiency. It is a carrier for *Ne1* gene as it produced necrotic F_1 hybrid when crossed with WL711 (*Ne2*). It is characterized with grains bolder than both the parents and showed better chapati making characteristics when tested for quality traits.

34. WCF8-HT13 (INGR No. 05034; IC 443622)

HT13 is slightly taller (130 cm) than parent C306 and does not lodge, shows early semi-spreading habit and higher early vigour under normal and water stress condition. It is medium yielding (520 gm^{-2}) under normal condition and shows higher stability (0.67) across water variable environments. It is similar in phenology of parent C306 under both normal and water stress conditions. It is characterized with higher cell membrane stability, lower canopy temperature and higher water use efficiency under water stress conditions. It is carrier for *Ne2* gene as it produced necrotic F_1 hybrid when crossed with C306 (*Ne1*). It is also characterized with bolder grains than both the parents and possesses better chapati making qualities.

References

Dalal M, KVS Vijaya Lakshmi, R Khanna-Chopra and S Bharti (1999) Ear culture as a technique to overcome hybrid necrosis in wheat. *Plant Cell Tissue and Organ Culture* **59:** 151-154.

Hanks RJ, J Keller, VP Rasmussen and GO Wilson (1976) Line-source sprinkler for continuous variable irrigation-crop production studies. *Soil Sci Soc Am. J* **40:** 420-429.

Khanna-Chopra, R and RV Patil (2002) Successful hybridization between drought resistant cultivar C306 and high yielding varieties by overcoming hybrid necrosis leads to exposition of hidden genetic variability. ICAR New Delhi, p 1-30.

Patil RV (2005) Use of morpho-physiological traits as selection criteria for drought resistance in advanced generations of wheat (*Triticum aestivum* L.) crosses between drought resistant and high yielding cultivars. Ph.D. thesis, Devi Ahilya Vishwavidyalaya, Indore (Madhya Pradesh)

BOOK REVIEW

BP Singh and Umesh Srivastava 2004. Plant Genetic Resources in Indian Perspective: Theory and Practices. Hardback, Price Rs 400/-, ISBN 81-7164-017-6, 715 pages, Directorate of Information and Publications of Agriculture (DIPA), Indian Council of Agricultural Research, New Delhi

Existence of genetic diversity is fundamental for any crop improvement related efforts. The biological diversity among plants is often underutilized and undervalued resource. The local land races are not only numerous, fulfilling a variety of needs and adapted to different conditions, but are also genetically variable adverse biotic and abiotic stresses. These genetic resources would continue playing an important role in the development of new cultivars possessing unique characteristics. Unfortunately, these valuable resources are neither conserved nor documented and utilized properly in many developing countries. It is in this context that conservation of these resources has assumed increasing importance throughout the world. Globally, an awareness has grown to conserve these valuable resources both scientifically and systematically for the benefit of our society and for posterity. It is in right earnest that the ICAR has decided to publish a book, which emphasizes on the latest concepts, methodologies, approaches and practices in the field of plant genetic resources. In view of the growing global debate on aspects such as access, benefit sharing and conservation of genetic resources for food and agriculture, it is rather essential to have all relevant literature compiled documented and published

The contents of the book are dealt with in 13 chapters, which cover a wide range of topics. In the beginning ahead to the regular chapters, an overview was done on plant genetic resources activities in Indian perspective. The first two chapters provide information on general aspects such as Plant genetic resources –Global Scenario, Plant genetic resources–Conservation and Management. Chapters 3, 4, 5 and 6 deal with History of plant genetic resources activities in India and the domestication of crop plants, the centres/ regions of diversity and the richness of crop plant diversity and its distribution in the Indian subcontinent and wild relatives of crop plants. Chapters 7 to 12 elaborate mainly, on the concepts, theories/methodologies, approaches and practices followed namely, the principles of plant germplasm exchange and quarantine regulations and their role as a national service; the techniques, principles and practices of germplasm collecting; ethnobotany in relation to plant genetic resources, methods and techniques of ethnobotanical studies, relevance of indigenous knowledge (IK) with practical approach; the evaluation and utilization of plant genetic resources, core concept, genetic enhancement and genetic manipulations with the emphasis on techniques and procedures, practical considerations, wherever possible practical protocols also followed; documentation of PGR information; different approaches to plant genetic conservation, *ex situ* and *in situ* : *ex situ* through medium-term and long-term storage the gene bank and its management, the recent approaches such as tissue culture and cryo-preservation and role of recent tools i.e., biotechnology in PGR conservation, field gene banks, community gene banks, on-farm conservation, conservation in traditional farming systems etc., *in situ* conservation relating to management of biosphere reserves. The last chapter 13 deals with emerging PGR issues in relation to multi-level and multi-dimensional conflicts of ideas over the ownership/ control, access and sustainable utilization of biodiversity, which rightly led to the development of international legal mechanisms/ global PGR scenario–such as CBD, IUPGR, WTO, TRIPS, increased relevance of MoUs and MTA in PGR management, biosafety protocols, evaluation of transgenic plants, IPR, Farmers' Rights, Breeders' Rights, terminator technology and their applications and registration of plant germplasm.

The book 'Plant Genetic Resources in Indian Perspective : Theory and Practices", the first of its kind, is expected to stimulate interest in the field of plant genetic resources among scientists, researchers, users, curators and all those who are engaged and interested in safeguarding plant biodiversity to promote sustainable agriculture intensification for the benefit of humankind. It will also be useful to teachers and post graduate students of PG School of IARI, traditional and State Agricultural Universities and equally so, by the policy makers and conservationists advocating national and global concern on plant genetic resources conservation and management.

BM Singh, Former Principal Scientist, National Bureau of Plant Genetic Resources, New Delhi

Indian Journal of Plant Genetic Resources

ISSN 0971-8184
Vol. 18 No. 3 2005

CONTENTS

Published by the *General Secretary*, Indian Society of Plant Genetic Resources, NBPGR Campus, New Delhi 110 012 and printed at *Aakriti Graphics*.