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Evaluation of Paprika Genotypes in Kerala

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Paprika, is the term used by international spice traders for non-pungent red capsicum powder. Paprika is valued most for its colour and mildness of flavour. In India, paprika variety is not yet grown commercially. The work was initiated to study the feasibility of paprika cultivation in Kerala (humid tropical climate). Forty indigenous and exotic genotypes collected from various sources and were evaluated for three seasons. Morphological evaluation was done according to International Plant Genetic Resources Institute descriptor list. Variation was found in morphological and quantitative characters. Genotype Paprika King was found to be superior to other types in yield and colour value, followed by PBC 066, KT-pl-8 and KT-pl-20.

Key Words: Characterization, Evaluation, Paprika, Kerala

International spice traders use the term paprika for non-pungent red *Capsicum* powder. Paprika is the Hungarian word plants in the genus *Capsicum*. This mild powder can be made from any type of *Capsicum annuum* that is non-pungent and has brilliant red colour. Paprika is valued most for its colour and mildness of flavour. The market value of paprika depends largely on its red colour, both surface hue and extractable colour. Its flavour quality is of secondary importance. Oleoresin of paprika, extracted from the ground pods, is used to impart bright red color to meat, sausage products, sauces and to other processed foods, thus, making the product more acceptable.

The pigment content of paprika varies from 0.1-0.8%. The pigments comprise a mixture of closely related carotenoids such as capsorubin, capsanthin, β-carotene, zeaxanthin, violaxanthin and lutene. The most important pigments responsible for red colour are capsanthin and capsorubin. The paprika colours are not metabolised in human body and, hence, it is an ideal natural colour additive for food items. The colour value of paprika is expressed in (ASTA) units American Spice Trade Association. This is the extractable colour present in paprika. Common paprika ASTA colour values preferred in the industry are 85, 100, 120 and 150 (Tainter and Grenis, 1993). According to Govindarajan (1985), the group paprika contains less than 0.1% of capsaicinoids, the best grade of Spanish paprika having 0-0.0003% and for the pungent grades a maximum of 0.5%. Paprika of commerce comes from Hungary, Spain, Morocco, America, Yugoslavia, Czechoslovakia, Chile, Romania, Turkey, Greek and Portugal. Paprika has price advantage over chilli. The weekly International Prices at New York Market as on January, 2000, showed the price of Indian chilli to be 0.62 dollars/pound and that of Spanish paprika (120 ASTA) to be 1.30 dollars/pound (Anon, 2000). In India, as yet, there is no spice paprika variety grown commercially. The Byadagi chillies in Dharward district in Karnataka and Tomato chillies in Warangal district in Andhra Pradesh are near to qualities of paprika types grown in Spain or Hungary. A few selections were made from Byadagi chillies at the Indian Institute of Horticultural Research (IIHR), Bangalore and the selection was released as 'Arka Abir'. In the breeding programme at Indian Agricultural Research Institute (IARI), Regional Stations, Katrain, Kulu valley, Himachal Pradesh, germplasm from abroad were evaluated and a variety 'Kt-pl-19', having high oleoresin and high colour was released. The present study was initiated to study the feasibility of paprika cultivation under the humid conditions of Kerala.

Materials and Methods

Paprika lines were collected through survey and correspondence from centres of cultivation and genebanks like Asian Vegetable Research and Development Centre (AVRDC) Taiwan; Kerala Agricultural University (KAU), Trichur; IIHR, Bangalore IARI, Regional Station, Katrain, Himachal Pradesh; Institute of Plant Genetics and Crop Plant Research (IPGRI), Gaterslaben, Germany; Agricultural Research Station, Lumle, Nepal and Synthite, Kollenchery, Kerala. Field survey of 'Byadagi' chillies of the Dharward district in Karnataka was done. Samples were collected from farmer's field and practices of cultivation and post-harvest operations were studied. Details of genotypes used in this study are given in Table 1.

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Table 1. Sources of paprika genotypes evaluated for field performance

Sample Number	Genotype	Source
1.	PBC 436	Asian Vegetable Research and Development Centre, Taiwan
2.	PBC 554	Asian Vegetable Research and Development Centre, Taiwan
3.	PBC 1369	Asian Vegetable Research and Development Centre, Taiwan
4.	PBC 066	Asian Vegetable Research and Development Centre, Taiwan
5.	PBC 375	Asian Vegetable Research and Development Centre, Taiwan
6.	PBC 384	Asian Vegetable Research and Development Centre, Taiwan
7.	PBC 384	Asian Vegetable Research and Development Centre, Taiwan
8.	PBC 473	Asian Vegetable Research and Development Centre, Taiwan
9.	PBC 535	Asian Vegetable Research and Development Centre, Taiwan
10.	PBC 717	Asian Vegetable Research and Development Centre, Taiwan
11.	PBC 743	Asian Vegetable Research and Development Centre, Taiwan
12.	PBC 1347	Asian Vegetable Research and Development Centre, Taiwan
13.	PBC 1350	Asian Vegetable Research and Development Centre, Taiwan
14.	PBC 828	Asian Vegetable Research and Development Centre, Taiwan
15.	PBC 999	Asian Vegetable Research and Development Centre, Taiwan
16.	PBC 971	Asian Vegetable Research and Development Centre, Taiwan
17.	CAP 1088/35	Institute of Plant Genetics and Crop Research, Germany
18.	CAP 35/95	Institute of Plant Genetics and Crop Research, Germany
19.	CAP 1036/35	Institute of Plant Genetics and Crop Research, Germany
20.	CAP 1063/35	Institute of Plant Genetics and Crop Research, Germany
21.	Paprika King	Synthite Chemicals, Kollencherry, Cochin, Kerala, India
22.	Cluster chilly	Lumle Agricultural Research Station, Lumle, Nepal
23.	Kt-pl-18	Indian Agricultural Research Institute, Regional Station, Katrain, HP, India
24.	Kt-pl-8	Indian Agricultural Research Institute, Regional Station, Katrain, HP, India
25.	Kt-pl-19	Indian Agricultural Research Institute, Regional Station, Katrain, HP, India
26.	Kt-pl-20	Indian Agricultural Research Institute, Regional Station, Katrain, HP, India
27.	Kt-pl-22	Indian Agricultural Research Institute, Regional Station, Katrain, HP, India
28.	Kt-pl-23	Indian Agricultural Research Institute, Regional Station, Katrain, HP, India
29.	Kt-pl-24	Indian Agricultural Research Institute, Regional Station, Katrain, HP, India
30.	Kt-pl-25	Indian Agricultural Research Institute, Regional Station, Katrain, HP, India
31.	Kt-19	Indian Agricultural Research Institute, Regional Station, Katrain, HP, India
32.	Arka Abir	Indian Institute of Horticultural Research, Bangalore, India
33.	CA-219	Kerala Agricultural University, Thrissur, Kerala, India
34.	Modhpur	Kerala Agricultural University, Thrissur, Kerala, India
35.	Paprika type-1	Kerala Agricultural University, Thrissur, Kerala, India
36.	Round ornamental	Kerala Agricultural University, Thrissur, Kerala, India
37.	Small conical	Kerala Agricultural University, Thrissur, Kerala, India
38.	517-1	Kerala Agricultural University, Thrissur, Kerala, India
39.	Jwala	Kerala Agricultural University, Thrissur, Kerala, India
40.	Byadagi	Byadagi thaluk, Karnataka

Three seasons (January to June 1997, January to June 1998 and September 1998 to March 1999) were selected for evaluation of 40 genotypes. Seeds of all genotypes were sown in sterilized sand in plastics cups and transplanted to pots. The potting mixture had a composition of soil:sand:farmyard manure in the ratio of 1:1:1. The mixture was chemically sterilized using formalin. The solution was prepared by mixing formaldehyde with water in the ratio of 1:30. Three litres of solution was applied per m^2 of soil when the soil was moist. The mixture was covered for three days, stirred, covered again for three days and kept in open condition for 15 days.

Six plants were raised for each genotype and observations were recorded from five plants. One plant out of each genotype was kept for selfing to collect selfed seeds for the next generation. Selfing was done by covering the pot with a cage of mesh size 20 x 16 holes/2.5 cm^2 (Bosland, 1993) to prevent insect pollination. The plants were watered daily except during rains. Morphological evaluation of these lines was done according to the IPGRI descriptor list. Biochemical characters like extractable colour (ASTA method, Hort and Fischer, 1971) and percentage of capsaicin (ISO/ DIS 7543-1, 1988) were also studied. For estimation of colour, red ripe chillies were dried and the stalk and seeds were removed before powdering. Ground chilli powder (0.1 g) was transferred in to a 250 ml Erlenmeyer flask, and kept overnight at room temperature. The content were filtered through a Whatman No. 42 filter

paper, the first 10 ml was discarded and 25 ml of the filtrate was pipetted into a volumetric flask and diluted to the mark with isopropanol. The absorbance was recorded at 450 nm against isopropanol as blank.

For determination of capsaicin content, whole chillies were dried and powdered. Ten gram of the powder was quantitatively transferred to a soxhlet apparatus and extracted using 100 ml tetrahydrofuran for eight hours. The solvent was then evaporated to the maximum extent possible in the rotary vacuum evaporator under reduced pressure in a 250 ml round bottomed flask one water bath. 0.05 to 0.1g of carbon black was added to the extract so as to maintain a ratio of the order of 10 between the extract and carbon black. A volume of 90 ml of methanol was added to this and agitated in magnetic stirrer for 30 minutes. The solution was allowed to stand for 5 minutes and filtered through a membrane filter into a 100 ml volumetric flask and made up to the mark with methanol solution (70 parts methanol and 30 parts water). Using this filtrate, six dilutions were prepared for spectrophotometric measurements. Zero was adjusted with methanolic solution and absorbances measured at 248 nm and 296 nm.

Results and Discussion

The morphological characters of the paprika lines are given in Table 2. Quantitative characters of the paprika lines were recorded for three seasons and are presented in Tables 3-5. Plant height ranged from 32.3 cm to 92.0 cm (Table 3). Days to flowering ranged from 29.0-64.6 (Table 4). Kt-19 (64.60) and Dokomlasi 640 (55.6) were late flowering lines and the remaining lines showed intermediate days to flowering. Days to fruiting ranged from 42-80 (Table 4). Fruit length ranged from 1.65cm to 13.6cm (Table 5). Genotypes with short fruits were round ornamental (1.65 cm), PBC 1369, PBC 436, CAP 1086/35, PBC 743, PBC 717 and Paprika type-1 (4.10). Lines with long fruit were Paprika King (13.6 cm), PBC 828, PBC 999, Kt-pl-24, PBC 385, PBC 066, and PBC 375 (10.06). The remaining lines had fruits of intermediate length. Variation in fruit length is shown in Fig. 1. Fruit width ranged from 0.60 cm to 3.83cm (Table 5). Fruit width was high in PBC 1369 (3.83cm), PBC 436, PBC 066, Kt-pl-19, Kt-pl-24, Kt-pl-23, PBC 828, PBC 999 and Paprika King (2.26 cm). PBC 743 (0.60 cm), PBC 717 and Jwala (0.77) were narrow fruited lines. Colour value ranged from 70.3 to 268 ASTA (Table 7). Percentage of capsaicin ranged from 0.05 to 0.63 (Table 8). Capsaicin content was high in 517-1 (0.63%), CAP 1086/35(0.60%) and Jwala (0.52%) and low in PBC 436 (0.05%), PBC 1369 (0.106%), Kt-pl-18 (0.14%) and Kt-pl-25 (0.16%).

Evaluation of morphological characters showed that there was significant difference among the lines in several characters (Table 2). There was significant difference among the lines in plant growth habit. The growth habit ranged from erect, intermediate to compact. The genotypes varied in stem pubescence also. Most of the lines had no pubescence at all. CAP 1086/35 has dense stem pubescence. Significant difference was also found in other morphological characters like leaf colour (varying from light green to dark green), leaf shape, number of flowers/axil, flower position, corolla colour, anther colour, stigma exertion, fruit colour at mature and intermediate stage, fruit shape, fruit shape at blossom end fruit surface. Variation in growth habit, stem pubescence, stem colour, leaf pubescence, flower position, fruit shape and fruit length were reported by Mohammed (1994) and variation in morphological characters like plant height, number of branches and number of leaves among sweet pepper varieties was reported by Aliyu and Olerawaju (1994). Variation in quantitative characters was also found among the genotypes (Tables 3 -8). There was significant variation among the lines for characters like plant height, days to flower and days to fruit. Lines Kt-19 and Dokomlasi 640 were the latest to flower. They were also late to fruit. Significant difference was found in fruit length among the lines. A few lines had fruits ten times as long as some other lines. Round ornamental, had small cherry like fruit, PBC 1369 and PBC 436 had round blocky fruits. PBC 743 and PBC 717 had narrow small fruits. Paprika king had the longest fruit. There was also considerable variation in fruit width among the lines. PBC 743 and PBC 717 had narrow fruit width whereas, PBC 1369 and PBC 436 had broad fruits. Fresh fruit weight is an important character in determining the amount of paprika powder obtained because paprika powder is made from dried powdered fruit wall. Fruit weight was highest in CAP 1088/35 (18.2 g). Low yield being the limiting factor in paprika production (Bosland *et al.,* 1991), yield/plant is also a crucial character in paprika breeding. Among the 40 lines evaluated, Paprika King had the highest yield (255.6 g), followed by PBC 066 (227.3 g) and Kt-pl-8 (190.3 g). Seed size and seed number also varied among the lines. Paprika types with fleshy fruits generally had large seeds and highly pungent types had small seeds.

Table 2. Morphological characters of 40 paprika genotypes

Character	Expression	Genotypes
Stem shape	Cylindrical	All
Stem pubescence	Dense	CAP 1086/35
	Intermediate	PBC 385, PBC 473, PBC 535, Byadagi.
	Sparse/nil	CA 219, PBC 066, PBC 1369, PBC 375, PBC 384, PBC 554, PBC 436, Small conical, Round ornamental, Arka Abir, Modhpur, CAP 1088/35, Kt-pl-19, CAP 1063/35, PBC 1350, PBC 1347, PBC 743, PBC 717, Paprika type-1, Dokomlasi 640, Kt-19, Cluster chilli, 517-1, PBC 828, PBC 971, Kt-pl-22, Kt-pl-24, Kt-pl-25, Kt-pl-18, Kt-pl-23, Kt-pl-8, Kt-pl-20, PBC 999, Jwala, Paprika king.
Plant growth habit	Erect	PBC 385, PBC 473, PBC 535, Byadagi, CA 219, PBC 1347, PBC 743, Paprika type – 1, Dokomlasi 640, Kt-19, PBC 828, PBC 999, Jwala, Paprika king, Arka Abir.
	Intermediate	CAP 1086/35, PBC 066, PBC 1369, PBC 375, PBC 384, PBC 554, Kt-pl-19, PBC 1350, PBC 717, 517-1, Kt-pl-22, Kt-pl-25, Kt-pl-18, Kt-pl-23, Kt-pl-8, Kt-pl-20, PBC 971, Modhpur.
	Compact	PBC 436, Small Concial, Round Ornamental, CAP 1088/35,AP 1063/35, Cluster chilli, Kt-pt-l24.
Branching habit	High	Cluster chilli
	Intermediate	PBC 385, PBC 473, PBC 1347, PBC 743, Paprika type–1, Dokomlasi 640, PBC 828, PBC 999, Jwala, CAP 1086/35, PBC 066, PBC 1369, PBC 375, PBC 384, PBC544, Kt-pl-19, PBC 1350, PBC 717, 517-1, Kt-pl-22, Kt-pl-25, Kt-pl-23, Kt-pl-8, PBC 436, Small conical, CAP 1088/35, CAP 1063/35, Kt-pl-24, PBC 971, PBC 535, Modhpur, Arka Abir.
	Sparse	Byadagi, CA 291, Kt-19, Paprika king, Kt-pl-18, Kt-pl-20, Round ornamental
Leaf colour	Light green	Jwala, Byadagi.
	Green	PBC 385, PBC 473, PBC 1347, Paprika type–1, Dokomlasi 640, PBC 066, PBC 1369, PBC 384, PBC 554, Kt-pl-19, PBC 1350, PBC 717, 517-1, Kt-pl-22, Kt-pl-25, Kt-pl-23, Kt-pl-8, PBC 436, Smallconical, CAP 1063/35, Kt-pl-24, CA 219, Paprika king, Kt-pl-18, Kt-pl-20, Round ornamental, PBC 971, PBC 535, PBC 743, Arka Abir, Modhpur.
	Dark green	Cluster chilli, PBC 828, PBC 999, CAP 1086/35, PBC 375, CAP 1088/35, Kt-19.
Leaf shape	Ovate	Jwala, Byadagi, PBC 385, PBC 473, PBC 1347, Paprika type –1, Dokomlasi 640, PBC 066, PBC 1369, PBC 384, PBC 554, Kt-pl-19, PBC 1350, PBC 717, Kt-pl-22, Kt-pl-25, Kt-pl-23, Kt-pl-8, PBC 436, Small conical, CAP 1063/35, Kt-pl-24, CA 219, Paprika king, Kt-pl-18, Kt-pl-20, Round ornamental, Cluster chilli, PBC 828, PBC 999, CAP 1086/35, PBC 375, Kt-19, PBC 535, Arka Abir, Modhpur, PBC 743.
	Lanceolate	517-1, CAP 1088/35, PBC 971.
No. of flowers/axil	1	Jwala, Byadagi, PBC 385, PBC 473, Paprika type–1, PBC 1347, Dokomlasi 640, PBC 066, Kt-pl-19, PBC 1350, Kt-pl-22, Kt-pl-25, Kt-pl-23, Kt-pl-8, PBC 436, Small conical, Kt-pl-24, Paprika king, Kt-pl-18, Kt-pl-20, Round ornamental, PBC 828, PBC 999, PBC 375, Kt-19, 517-1, CAP 1088/35, PBC 971, PBC 535, Arka Abir, Modhpur, PBC 743.
	>2	PBC 1369, PBC 384, PBC 554, PBC 717, CAP 1063/35, CA 291, Cluster chilli, CAP 1086/35.
Flower position	Pendent	Byadagi, PBC 385, PBC 473, PBC 1347, Dokomlasi 640, PBC 066, Kt-pl-19, PBC 1350, Kt-pl-22, Kt-pl-25, Kt-pl-24, Paprika king, Kt-pl-18, Kt-pl-20, PBC 828, PBC 999, PBC 375, Kt-19, 517-1, CAP 1088/35, PBC 971, PBC 535, Modhpur, PBC 1369.
	Intermediate	Jwala, Kt-pl-23, Kt-pl-8, PBC 436, Arka Abir, PBC 554.
	Erect	Paprika type–1, Small conical, Round Ornamental, PBC 743, PBC 384, CAP 1063/35, CA 219, Cluster chilli, CAP 1086/35, PBC 717.
Corolla colour	White	Byadagi, PBC 385, PBC 473, PBC 1347, Dokomlasi 640, PBC 066, Kt-pl-19, Kt-pl-22, Kt-pl-25, Kt-pl-23, Kt-pl-24, Kt-pl-18, Kt-pl-20, PBC 828, PBC 999, PBC 375, Kt-19, 517-1, CAP 1088/35, PBC 971, PBC 535, Modhpur, Jwala, PBC 436, Arka Abir, Paprika type–1, Round ornamental, PBC 384, CA 219, Cluster chilli, CAP 1086/35, PBC 717.
	Light yellow	PBC 1350, Paprika king, PBC 1369, Kt-pl-8, PBC 554, Small conical, PBC 743, CAP 1063/35.
Anther colour	Blue	Byadagi, PBC 473, Kt-pl-22, Kt-pl-25, Kt-pl-20, PBC 828, 517-1, PBC 971, Modhpur, Jwala, Arka Abir, Round ornamental, Paprika king, Small conical, PBC 743, CAP 1063/35.
	Purple	PBC 385, PBC 1347, Dokomlasi 640, PBC 066, Kt-pl-19, Kt-pl-24, Kt-pl-18, PBC 999, PBC 375, Kt-19, CAP 1088/35, PBC 535, PBC 436, Paprika type–1, PBC 384, CA 219, Cluster chilli, CAP 1086/35, PBC 717, PBC 1350, PBC 1350, PBC 1369, Kt-pl-8, PBC 554.
Fruit shape	Elongate	PBC 554, PBC 473, PBC 535, PBC 717, PBC 1347, PBC 1350, PBC 971, PBC 384, CAP 1063/35, Arka Abir, CA-219, Byadagi, Kt-pl-22, Kt-pl-23, PBC 385, PBC 743, 517-1, Dokomlasi 640, Kt-19, Modhpur, Jwala, PBC 066, Paprika King, Kt-pl-18, Kt-pl-20, PBC 375, Kt-pl-24.
	Triangular	PBC 999, PBC 828, CAP 1086/35, CAP 1088/35, Paprika type–1, Small conical, Kt-pl-8, Kt-pl-25, Cluster chilli, Kt-pl-19
	Round	Round ornamental
	Blocky	PBC 1369, PBC 436.
Fruit shape at blossom end	Pointed	PBC 473, PBC 535, PBC 717, PbC 1347, PBC 971, PBC 384, CAP 1063/35, CA-219, Byadagi, Arka Abir, PBC 385, 517-1, PBC 743, Dokomlasi 640, Kt-19, Modhpur, Jwala, PBC 066, Paprika King, Kt-pl-18, Kt-pl-20, PBC 375, Kt-pl-24, PBC 999, CAP 1086/35, CAP 1088/35, Kt-pl-8, Cluster chilli.
	Blunt	PBC 554, PBC 1350, Kt-pl-22, Kt-pl-23, PBC 828, Paprika type–1, Small conical, Kt-pl-19.
	Sunken	Round ornamental PBC 1369, PBC 436.
	Sunken and Pointed	Kt-pl-25.

Contd.

Character	Expression	Genotypes
Fruit blossom end appendage	Absent	PBC 473, PBC 535, PBC 717, PBC 1347, PBC 971, PBC, 384, CAP 1063/35, CA–219, Byadagi, Arka Abir, PBC 385, PBC 535, PBC 743, Dokomlasi 640, Kt-19, Modhpur, Jwala, PBC 066, Paprika King, Kt-pl-18, Kt-pl-20. PBC 375, Kt-pl-24, PBC 999, CAP 1086/35, CAP 1088/35, Kt-pl-8 Cluster chilli, PBC 554, PBC 1350, Kt-pl-22, Kt-pl-23, PBC 828, Paprika type–1, Kt-pl-19, Round ornamental PBC 1369, Kt-pl-25, 517-1.
	Present	Small conical, PBC 436
Fruit surface	Smooth	PBC 535, PBC 717, PBC 971, PBC 384, CAP 1063/35, CA-219, Arka Abir, Modhpur, Jwala, Paprika King, Kt-pl-20, PBC 375, Kt-pl-24, PBC 999, CAP 1086/35, CAP 1088/35, Cluster chilli, PBC 554, PBC 1350, Kt-pl-22, Kt-pl-23, PBC 828, Paprika type–1, Kt-pl-19, Round ornamental, PBC 1369, Kt-pl-25, PBC 436, PBC 1347, Small conical, 517-1.
	Semi-wrinkled	PBC 473, PBC 385, PBC 743, Kt-19, PBC 066, Kt-pl-18, Kt-pl-8, Dokomlasi 640, Kt-19
	Wrinkled	Byadagi
Placenta length	>1/2	All genotypes
Seed colour	Straw	All genotypes

Table 3. Variability of paprika genotypes in plant height, days to flower, days to fruit, fruit length and fruit width

S. No.	Accession No.	Plant height	Days to flower	Days to fruit	Fruit length (cm)	Fruit width (cm)
1.	PBC 436	32.3	43.6	56.6	4.5	3.8
2.	PBC 385	65.3	39.6	52.6	8.73	1.5
3.	PBC 384	68.6	41.3	54.6	10.5	2.1
4.	PBC 375	59.3	40.3	53.0	10.6	1.86
5.	PBC 1369	44.6	35.6	47.7	3.56	3.83
6.	PBC 066	58.3	36.0	49.3	11.03	3.16
7.	CA 219	62.0	37.0	49.6	6.0	1.6
8.	PBC 473	52.0	41.3	53.6	9.76	1.96
9.	PBC 535	48.6	42.3	55.0	9.5	1.96
10.	PBC 554	41.3	44.3	56.3	9.6	1.83
11.	Kt-pl-18	44.0	31.6	43.0	7.5	1.66
12.	Cluster chilly	45.0	52.6	64.6	5.53	1.80
13.	Small conical	45.3	.45.6	57.3	4.90	1.93
14.	Round ornamental	45.6	46.6	60.3	1.65	1.90
15.	Arka Abir	82.6	45.0	57.6	8.5	1.87
16.	Byadagi	92.0	48.0	63.0	9.32	1.64
17.	Modhpur	49.0	44.0	57.3	7.86	1.63
18.	CAP 1088/35	43.6	41.3	56.0	7.53	1.36
19	CAP 1086/35	55.0	41.0	53.6	3.04	1.13
20.	Kt-pl-19	50.3	40.6	54.0	6.33	2.56
21.	CAP 1063/35	47.7	38.6	50.6	5.8	2.0
22.	PBC 1350	51.0	41.0	54.3	5.96	2.2
23.	PBC 1347	45.6	43.0	55.6	8.03	1.66
24.	PBC 743	70.6	43.6	56.0	5.2	0.60
25.	PBC 717	84.0	45.0	57.3	5.06	0.89
26.	Paprika type–1	68.0	43.0	56.6	4.10	2.43
27.	Dokomlasi–640	43.3	55.6	68.3	7.23	1.46
28.	Kt-pl-22	53.0	36.3	50.3	9.13	2.1
29.	Kt-19	86.0	64.6	80.0	9.6	1.36
30.	Kt-pl-24	36.6	34.3	48.3	10.26	1.56
31.	Kt-pl-25	49.0	33.6	46.3	8.0	1.96
32.	Kt-pl-23	47.3	31.6	42.0	8.05	2.96
33.	Kt-pl-8	44.6	34.6	46.6	7.1	2.36
34.	Kt-pl-20	44.6	29.0	42.0	9.43	2.10
35.	PBC 828	68.0	34.6	46.6	10.0	3.10
36.	PBC 971	66.6	41.6	53.6	12.4	1.76
37.	PBC 999	61.6	41.3	54.6	13.23	3.30
38.	Jwala	44.6	32.0	44.0	7.5	0.77
39.	517–1	71.3	31.0	45.0	3.63	1.30
40.	Paprika King	68.3	32.0	47.3	13.6	2.26
	Mean	55.45	40.5	53.5	7.8	1.98
	SD	14.12	6.88	7.29	2.94	0.72
	CV%	25.4	16.9	13.6	37.6	36.3

Table 4. Variability of paprika genotypes in fruit weight, yield/plant, seed size and seed number

S. No.	Accession no.	Fruit weight	Yield/ plant	Seed size(cm)	Seed number
1.	PBC 436	13.3	60.3	0.44	76
2.	PBC 385	2.13	125.3	0.28	119
3.	PBC 384	2.90	155.3	0.33	92.6
4.	PBC 375	2.30	169.6	0.31	122.3
5.	PBC 1369	16.6	53.3	0.48	77
6.	PBC 066	11.4	227.3	0.38	101
7.	CA 219	1.11	92.3	0.30	114
8.	PBC 473	2.28	110.3	0.31	114
9.	PBC 535	1.83	128.0	0.34	129.6
10.	PBC 554	4.20	113.6	0.45	86.3
11.	Kt-pl-18	3.60	157.3	0.46	86.0
12.	Cluster Chilli	3.40	95.0	0.32	140.6
13.	Small Conical	4.70	123.3	0.30	132.0
14.	Round oranmental	1.80	174.3	0.32	79.3
15.	Arka Abir	2.12	117.0	0.42	100.3
16.	Byadagi	2.63	115.0	0.41	104.0
17.	Modhpur	2.13	113.6	0.32	110.3
18.	CAP 1088/35	18.2	141.6	0.44	67.0
19.	CAP 1086/35	0.57	56.0	0.27	89.3
20.	Kt-pl-19	8.53	120.3	0.45	76.3
21.	CAP 1063/35	0.68	71.3	0.24	62
22.	PBC 1350	3.03	162.6	0.35	108
23.	PBC 1347	2.26	173.3	0.35	135.0
24.	PBC 743	0.16	62.0	0.26	109.3
25.	PBC 717	0.53	75.6	0.24	90.6
26.	Paprika type-1	1.85	101.3	0.34	98.3
27.	Dokomlasi-640	2.02	99.66	0.33	99.6
28.	Kt-pl-22	5.99	135.0	0.38	90.0
29.	Kt-19	1.79	93.33	0.29	100.6
30.	Kt-pl-24	5.2	113.3	0.38	100.3
31.	Kt-pl-25	8.1	167.0	0.46	70.6
32.	Kt-pl-23	4.73	144.3	0.47	95.0
33.	Kt-pl-8	7.40	190.3	0.45	85.6
34.	Kt-pl-20	13.16	155.0	0.46	90.6
35.	PBC 828	5.56	108.6	0.40	89.6
36.	PBC 971	8.50	107.3.	0.42	96.0
37.	PBC 999	7.63	103.5	0.50	90.6
38.	Jwala	1.56	78.3	0.35	104.6
39.	517-1	1.20	119.6	0.32	105.0
40.	Paprika King	16.9	255.6	0.45	61.0
	Mean	5.1	124.1	0.36	96.5
	SD	4.85	44.4	0.07	19.2
	CV%	95	35.8	19.4	19.8

Table 5. Variability of paprika genotypes in colour value and capsaicin content

S. No.	Accession No.	Colour value (ASTA)	Capsaicin (%)
1.	PBC 436	121	0.05
2.	PBC 385	172	0.47
3.	PBC 384	143.8	0.53
4.	PBC 375	100.6	0.37
5.	PBC 1369	70.3	0.106
6.	PBC 066	128.6	0.226
7.	CA 219	116.6	0.526
8.	PBC 473	112.3	0.47
9.	PBC 535	86.3	0.22
10.	PBC 554	132.6	0.41
11.	Kt-pl-18	133.6	0.14
12.	Cluster Chilly	137.0	0.57
13.	Small Conical	106.3	0.50
14.	Round Ornamental	105.0	0.39
15.	Arka Abir	173.3	0.28
16.	Byadagi	216.0	0.286
17.	Modhpur	110.3	0.42
18.	CAP 1088/35	93.0	0.31
19.	CAP 1086/35	89.3	0.60
20.	Kt-pl-19	225.0	0.21
21.	CAP 1063/35	188	0.30
22.	PBC 1350	105.6	0.263
23.	PBC 1347	120.0	0.426
24.	PBC 743	88.66	0.403
25.	PBC 717	94.0	0.426
26.	Paprika type-1	115.6	0.26
27.	Dokomlasi-640	104	0.316
28.	Kt-pl-22	107	0.293
29.	Kt-19	140.6	0.383
30.	Kt-pl-24	148.3	0.063
31.	Kt-pl-25	223.0	0.16
32.	Kt-pl-23	158.6	0.30
33.	Kt-pl-8	102	0.283
34.	Kt-pl-20	137	0.386
35.	PBC 828	258	0.253
36.	PBC 971	118.9	0.24
37.	PBC 999	114.0	0.226
38.	Jwala	78.86	0.52
39.	517-1	134.3	0.63
40.	Paprika King	268.3	0.36
	Mean	136.5	0.34
	S.D	49.1	0.14
	CV%	35.9	41.1

Paprika is valued most for its colour and mildness of flavour. Hence, biochemical analysis for colour and pungency were done for all the lines. Genotypes with ASTA colour values in the range of 101-105 are classified under high colour groups those with 70-100 ASTA units under medium colour group and those below 70 ASTA units under low colour groups. Among the 40 geno-types, Paprika King has the highest colour value (268 ASTA), followed by PBC 828 (258 ASTA) and Kt-pl-19 (225 ASTA). There were quite a few genotypes under the high colour group. Paprika as a group entertains a pungency value less than 0.1%. Among the lines studied, PBC 436 had the lowest capsaicin percentage (0.05) and the highest was in 517-1 (0.63%).

It was found that Paprika King had high fresh fruit weight (16.9 g), high yield (225 g), high colour value (268 ASTA) and low capsaicin percentage (0.34). PBC 066 also had high fruit weight (11.4 g), yield (227 g), high colour value (128.6 ASTA) and low capsaicin (0.23%). PBC 1347 gave good yield (173.3 g) and high colour value (120 ASTA), but had high percentage of capsaicin (0.42). Round ornamental also

gave high yield (174.3g) and high colour value (105 ASTA), but the percentage of capsaicin was high. With the technology to separate colour and pungency compounds already available using super critical CO_2 as solvent (Skerget, 1998), the high capsaicin lines can also be used to prepare paprika oleoresin with low pungency. Byadagi, a well-known paprika type from Dharwad, Karnataka, was low yielding (115 g) under Calicut (North Kerala) conditions. Kt-pl-19 was low yielding (120.3 g), but Kt-pl-8 was high yielding (190.3 g) and has high colour value (102 ASTA) and capsaicin (0.28%). Kt-pl-20 was moderate in yield (155 g), but had high colour value (137 ASTA) and capsaicin content of 0.38%. Seasonal variation in the expression of both quantitative and qualitative characters was also found in the present study. It could be due to the difference in adaptability and response to changes in the environment. Future line of work includes the evaluation of the promising lines like Paprika King, PBC 066, Kt-pl-8 and Kt-pl-20 for several seasons at several locations, to release a paprika cultivar suitable for Kerala.

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References

Aliyu L and JD Olarewaju (1994) Variation in morphological and agronomic characters in sweet pepper (*Capsicum annuum* L.) *Capsicum Eggplant Newslet.* **13:** 52-53.

Anon (2000) Weekly international prices at New York market as on 21st January 2000. VCH Publishers, New York, 45p.

Bosland PW (1993) An effective plant field cage to increase the production of genetically pure chilly (*Capsicum* spp.) seed. *Hort. Sci.* **28:** 1053.

Govindarajan VS (1985) Capsicum – production, technology, chemistry and quality Part I: History, botany, cultivation and primary processing. *Critical Rev. Food Sci. Nutr.* **22:** 109-176.

Hort AM and JH Fisher (1971) ASTA method of analysis of colour in chillies. Modern Food analysis. Springer Verlag, New York, pp 338-39.

International Organization for Standardization (1988) Determination of total capsaicinoid content – spectrophotometric method. Budapest, Hungary ISO: 7543-1.

IPGRI Descriptors (1995) Descriptors for Capsicum (*Capsicum* spp.) IPGRI, AVRDC & TAIE.

Mohammed ETI (1994) Collection and characterization of hot pepper germplasm in Sudan. *Capsicum and Eggplant Newslet* **13:** 36-39.

Skerget M, Z Knez Z Novak and D Bauman (1998) Separation of paprika components using dense CO_2. *Acta Alimentaria* **27:** 149-160.

Tainter DR and AT Grenis (1993) Spices and Seasonings – A Food Technology Hand Book. VCH Publishers, New York, 45p.

Screening of Rice Genotypes for Leaf Folder, *Cnaphalocrocis medinalis* (Guenee) and Bacterial Leaf Blight, *Xanthomonas oryzae* pv. *oryzae* (Ishiyama) Dye

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Seventy-four genotypes of different maturity groups of rice were evaluated for identification of resistant sources against rice leaf folder, *Cnaphalocrocis medinalis* (Guenee) under field and screenhouse conditions during 1999. Forty-seven genotypes in 1998 and 57 genotypes in 1999 were also assessed for resistance against bacterial leaf blight, *Xanthomonas oryzae* pv. *oryzae* (Ishiyama) Dye through clip inoculation technique. Only 4 genotypes, namely, HKR 95-130, PAU 2023-80-1-3, PAU 1920-100-2-1-3-3 and PAU 1973-121-1-2-2-1 were found consistently promising in different situations and better than resistant donors against leaf folder whereas 10 genotypes *viz.*, Ajaya, PAU 1920-100-2-1-3-3, PAU 1061-19-2-2, PAU 1973-121-1-2-1-1, PAU 2212-25-1-2, CR 837, HKR 95-131, HKR 95-128, HKR 95-129 and PAU 1966-77-22-1 exhibited resistance to bacterial leaf blight during both the years. However, only two genotypes *viz.*, PAU 1920-100-2-1-3-3 and PAU 1973-121-1-2-1-1 can be used as promising sources of multiple resistance against rice leaf folder and bacterial leaf blight in rice protection breeding programmes.

Key Words: Bacterial Leaf Blight, Rice Germplasm, Rice Leaf Folder

The rice leaf folder, *Cnaphalocrocis medinalis* (Guenee) (Lepidoptera: Pyralidae) is distributed in humid tropical to temperate countries of Asia, Oceania and Africa and now it has become widespread throughout the rice growing regions of Asia (Khan *et al.*, 1988; Islam and Karim, 1997). Similarly, bacterial leaf blight caused by *Xanthomonas oryzae* pv. oryzae (Ishiyama) Dye, has become a major constraint of rice production in South-east Asia (Leach *et al.*, 1995; Raina *et al.*, 1999).

In early 1980s, effective insecticides were identified to control leaf folder (Heinrichs and Valencia, 1980). But insecticides besides being increasingly costly, were often applied too late to prevent severe leaf folder damage and also caused resurgence of *Nilaparvata lugens* (Stal) (Reissig *et al.*, 1982) and even leaf folder (Panda and Shi, 1989; Dakshayani *et al.*, 1983). So far, there is no successful chemical control for bacterial leaf blight (Raina *et al.*, 1999). Hence, host plant resistance is the best alternative to combat these pests. The studies on search for resistance to leaf folder (Velusamy *et al.*, 1973; Heinrichs, 1986; Ramachandran and Khan, 1991; Singh *et al.*, 1993; Mandal *et al.*, 1997) and bacterial leaf blight (Panwar *et al.*, 1988; Saini *et al.*, 1992; Sing and Dodan, 1995; Raina *et al.*, 1999) were conducted but little success has been reported on multiple resistance against these pests. Therefore, present investigations were aimed to identify sources of resistance against leaf folder under field as well as screenhouse conditions. Some promising genotypes were also assessed against bacterial leaf blight.

Materials and Methods

Plant Material

A wide range of rice germplasm was obtained from the Directorate of Rice Research, Rajendranagar, Hyderabad, India. Seventy-four genotypes of rice comprising different maturity groups (Table 2) were evaluated at CCS Haryana Agricultural University, Rice Research Station, Kaul (29°51'N latitude, 76°41'E longitude, elevation 241msl) both under field (natural pest infestation) and screenhouse (artificial infestation) conditions during 1998 and 1999.

Field Screening against Leaf Folder

Thirty-day-old seedlings of each entry were transplanted in two rows of 1m length at 10×10 cm spacing in July, 1999. After every 10 test entries, two resistant donors (TKM 6 and Ptb 33) and two susceptible checks (HKR 120 and IR 36) were transplanted. Recommended agronomic practices were followed to raise the crop except the application of pesticides. The observations on total and leaves damaged by leaf folder were recorded from 10 randomly selected hills of each genotypes in the month of October. Percent damaged leaves and damage rating were worked out for each genotype (IRRI, 1988). The adjusted damage rating (D) was calculated, as given below and the genotypes were compared on the basis of 0-9 scale (IRRI, 1988).

Mass Screening against Leaf Folder in Screenhouse

Initially, the insect was mass reared in screenhouse as suggested by Waldbauer and Marciano (1979). Earthen pots of 3 kg capacity (20 cm height and 17 cm diameter) were filled with soil and saturated with water two days before sowing the seeds. Twenty seeds of each entry were sown in individual pots and fertilizer was applied on soil test basis in 3 split doses *i.e.* before sowing, subsequently at 20 days interval. The thinning of seedlings was done twice *i.e.* 10 and 12 days after sowing to retain 5 plants in each pot for screening. Tillers were removed to retain only one tiller/plant. Pots were arranged in 3 sections randomly and each section was caged separately with nylon net (190x60x70 cm). In each cage liquid diet (10% sugar solution) soaked in cotton swabs was provided by hanging on bamboo sticks in each corner for feeding of adult moths. Four pairs of 3-day-old adults were released on 17-day-old seedlings in each cage to oviposit on the test plants. After 7 days, cotton swabs and nylon net were removed to provide adequate light to the plants. The test genotypes were evaluated for leaf damage at 21 days after infestation following Heinrichs *et al.* (1985a) and the standard evaluation system for rice (IRRI, 1988).

Retesting of Entries Found Promising in Mass Screenhouse Screening

The entries with a damage rating scale of 0-5 in mass screening along with resistant donors (TKM 6, Ptb 33, ASD 7, ARC 11128 and Darukasail) and susceptible checks (HKR 120 and IR 36) were re-assessed in a completely randomized design (CRD) with five replications, each pot represented one replication. In each replication additional tillers were removed and only 5 seedlings/ pot were maintained at the time of infestation. At 21 days after sowing each tiller was infested with two first-instar larvae. The pots were covered with nylon net. Seventeen days after larval infestation, the plants were evaluated on the basis of mean leaf damage rating (Heinrichs *et al.*, 1985a).

Screening against Bacterial Leaf Blight

The screening of 47 genotypes in 1998 and 57 genotypes in 1999 was carried out under artificial conditions. Thirty-day-old seedlings of each test entry were transplanted in two rows of 4 m long each. The plants were clip inoculated 45 days after transplanting with the bacterial suspension prepared by soaking pieces of infected leaves of TN-1 in water for 20 min (Jennings *et al.*, 1979) and the observations for disease incidence were recorded 14 days after inoculation (IRRI, 1988) The entries showing a disease score of 0-3, 5 and 7-9 were categorized as resistant, moderately resistant and susceptible, respectively. To measure overall severity of disease under test conditions, location severity index (L.S.I) was calculated as per the method of IRRI (1988).

$$\text{L.S.I.} = \frac{0(\text{NG})+1(\text{NG})+3(\text{NG})+5(\text{NG})+7(\text{NG})+9(\text{NG})}{\text{Total number of genotypes evaluated}}$$

Where 0-9: Disease score

NG: No. of genotypes under respective score

The L.S.I. was 6.4 and 6.3 during 1998 and 1999, respectively, indicating screening was carried under high disease incidence for identification of disease resistant genotypes.

Results and Discussion

Field Screening against Leaf Folder

Out of 71 genotypes evaluated under natural conditions against leaf folder, 14 exhibited less than 39.75 % damage rating and were considered as resistant with a damage score of 3 (Table 1). These included two previously identified resistant donors *viz.*, TKM 6 and Ptb 33. The minimum damage rating was recorded on IR 48725-B-B-103-2-3 followed by resistant check Ptb 33 and HKR 95-492. The range of damage rating in resistant genotypes varied from 23.42 to 39.75 %. Earlier workers (Nadarajan and Nair, 1983; Valusamy and Chelliah, 1985; Sundrababu and Rajendran, 1986) also assigned 3 damage score to TKM 6 and Ptb 33 under field conditions. However, Garg (1984) rated TKM 6 as moderately resistant with a score of 5.

But the extent of susceptibility increased when the genotypes were assessed under screenhouse conditions (Table 2). Among 74 genotypes evaluated only four *viz.*, HKR 95-130, PAU 2023-80-1-3, PAU 1920-100-2-1-3-3 and PAU 1973-121-1-2-1 could be designated as moderately resistant (score 5) and the rest were susceptible to highly susceptible. There was no genotype in the category of highly resistant or resistant group.

TKM 6, Ptb 33, ASD 7, ARC 11128 and Darukasail identified as resistant donors against leaf folder however, by earlier workers (Heinrichs *et al.*, 1985b; Joshi *et al.*, 1985; Rajendran *et al.*, 1986), these were found susceptible in screenhouse studies with a damage score of 7 to 9. This indicated the breakdown of resistance under no choice conditions. Besides, other plant factors and

Table 1. Evaluation of rice genotypes against rice leaf folder, *Cnaphalocrocis medinalis* (Guenee) in field during 1999

Damage score* (0-9)	Damage rating (D)	Resistance rating	Genotype
0-1	-	HR	Nil
3	23.42-39.75	R	Early duration (100-110 days): BR 51-282-8-HR-45. Medium duration (130-140 days): PAU 2061-20-2-1, BRC 16-127-4-1, IR 48725-B-B=103-2-3 Long duration (140-150 days): HKR 95-401, HKR 95-407, HKR 95-412, HKR 95-479, HKR 95-492, HKR 95-499, Pusa Basmati-1, Haryana Basmati-1, TKM 6, Ptb 33.
5	41.32-58-64	MR	Medium duration (130-140 days): HKR 95-222, HKRH 1059, HKR 126, HKR 95-138, PAU 1920-100-2-1-3-3, PAU 1973-121-1-2-1-1. Medium early duration (115-125 days): HKR 95-131, HKR 95-130, PAU 2023-80-1-3, PAU 1966-77-22-1, PAU 2338-151-1. Long duration (140-150 days): Taraori Basmati.
7	62.62-79.90	S	Early duration (100-110 days): HKR 97-1, PAU 2017-56-1-3. Medium duration (130-140 days): HKR 95-173, IR 60821-34-1-2, HKR 95-72, HKR 95-20, PR 114, Tox 3133-59-1-2-4-1, HKR 95-123, HKR 95-124, PAU 1061-19-2-2, CR 837, HKR 120. Medium early duration (115-125 days): HKR 95-139, HKR 95-157, HKR 95-188, HKR 95-218, HKR 95-219, HKR-46, HKR-95-128 Long duration (140-150 days): HKR 95-410.
9	82.79-133.94	HS	Early duration (100-110 days): UPR 1230-9-2, AS 89044, PAU 2017-58-1-3, RP 2829-32546-1875, HKR 97-14, HKR 97-41, HKRH 1002, Govind, IR 36. Medium duration (130-140 days): PR 113, PAU 2338-151-1, HKR 95-239, Aaya, PAU 2212-25-1-2. Medium early duration (115-125 days): HKR 93-3, HKR 95-192, CT 9153-4-1-12-6-1, PK 2557-24-2-1, HKR 95-191, IR 64, HKR 95-129, HKR 95-66, MTU 11335. Long duration (140-150 days): HKR 95-465.

* Standard Evaluation System for Rice; HR = Highly resistant; R = Resistant; MR = Moderately resistant; S = Susceptible; HS = Highly susceptible

Table 2. Evaluation of rice genotypes against rice leaf folder, *Cnaphalocrocis medinalis* (Guenee) in screen house

Damage score* (0-9)	Damage rating (D)	Resistance rating	Genotype
0-1	-	HR	Nil
3	-	R	Nil
5	39.04-43.68	MR	Medium duration (130-140 days): PAU 1920-100-2-1-3-3, PAU 1973-121-1-2-1-1. Medium early duration (115-125 days): HKR 95-130, PAU 2023-80-1-3.
7	50.98-73.32	S	Medium duration (130-140 days): PAU 1061-19-2-2, PAU 2016-20-2-1, IR 48725-B-B-103-2-3 Medium early duration (115-125 days): HKR 95-129, MTU 11335, PAU 1966-77-22-1. Long duration (140-150 days): Ptb 33.
9	81.72-100.00	HS	Early duration (100-110 days): UPR 1230-9-2, AS 89044, PAU 2017-58-1-3, RP 2829-32546-1875, HKR 97-1, HKR 97-14, HKR 97-41, HKRH 1002, Govind, PAU 2017-56-1-3, BR 51-282-8-HR-45, IR 36. Medium duration (130-140 days): PR 113, HKR 95-173, IR 60821-34-1-2, PAU 2338-151-1, HKR 95-72, HKR 95-20, HKR 95-222, PR 114, Tox 3133-59-1-2-4-1, HKR 95-239, HKR 95-123, HKR 95-124, HKRH 1059, HKR 126, Aaya, HKR 95-138, PAU 2212-25-1-2, CR 837, BRC 16-127-4-1, HRR 120. Medium early duration (115-125 days): HKR 93-3, HKR 95-131, HKR 95-192, CT9153-4-1-12-6-1, PK 2557-24-2-1, HKR 95-139, HKR 95-157, HKR 95-188, HKR 95-191, HKR 95-218, HKR 95-219, HKR 46, IR 64, HKR 95-128, HKR 95-66, PAU 2338-151-1 Long duration (140-150 days): HKR 93-401, HKR 95-407, HKR 95-410, HKR 95-412, HKR 95-465, HKR 95-479, HKR 95-492, HKR 95-499, Pusa Basmati-1, Haryana Basmati-I, Taraori Basmati, TKM 6, ASD 7, ARC 11128, Darukasail

* Standard Evaluation System for Rice; HR = Highly resistant; R = Resistant; MR = Moderately resistant; S = Susceptible; HS = Highly susceptible

environmental factors may also influence the behaviour of ovipositing females (Rajendran *et al.*, 1986). For confirmation, four promising genotypes selected from initial mass screening along with resistant donors were re-tested with two first instar larvae/tiller (Table 3). All the four genotypes that were found moderately resistant (5 damage score) in initial mass screening were found susceptible to leaf folder under no-choice conditions with a damage score of 7. Therefore, it may be concluded that rice genotypes respond differently when exposed to natural infestation conditions are artificial exposure to ovipositing females and larval stages. However, expression of resistance is further altered by prevailing environmental conditions (Rajendran *et al.*,

Table 3. Evaluation of rice genotypes (selected from initial mass screening) against *Cnaphalocrocis medinalis* (Guenee) in screen house**

Damage score* (0-9)	Damage rating (D)	Resistance rating	Genotype
0-1	-	HR	Nil
3	-	R	Nil
5	-	MR	Nil
7	51.65-71.23	S	Medium early duration (115-125 days): HKR 95-130, PAU 2023-80-1-3. Medium duration (130-140 days): PAU 1920-100-2-1-3-3-, PAU 1973-121-1-2-1-1 Resistant donors: Ptb 33, ASD 7, ARC 11128, TKM 6, Darukasail.
9	81.90-100.00	HS	Early duration (100-110 days): IR 36 Medium duration (130-140 days): HKR 120

* Standard Evaluation System for Rice

** Genotypes under re-testing infested with two Ist-instar larvae per tiller

1986). Stable sources of resistance will be those genotypes which perform better under different experimental situations. From the present studies, four genotypes *viz.*, PAU 2023-80-1-3, PAU 1920-100-2-1-3-3, PAU 1973-121-1-2-1-1 and HKR 95-130 were found consistently better than others and can be further used as sources of resistance against leaf folder.

Forty-seven genotypes in 1998 and 58 genotypes in 1999 were evaluated through inoculation against bacterial leaf blight (Table 4). Ten genotypes *viz.*, Ajaya,

Table 4. Evaluation of rice genotypes against bacterial leaf blight during 1998* and 1999**

Damage score* (0-9)	Resistance rating	Genotypes	
		1998	1999
0-1	HR	–	–
3	R	Medium duration (130-140 days): Ajaya, PAU 1920-100-2-1-3-3, PAU 1061-19-2-2, PAU 2061-20-2-1, PAU 1973-121-12-1-1, PAU 2212-25-1-2, CR 837	Medium duration (130-140 days): PR 114, Ajaa, PAU 1920-100-2-1-3-3, PAU 1061-19-2-2, PAU 1973-121-1-2-1-1, PAU 2212-25-1-2, CR 837
		Medium early duration (115-125 days): HKR 95-131, HKR 95-128, HKR 95-129, HKR 95-130, PAU 2023-80-1-3, PAU 1966-77-22-1	Medium early duration (115-125 days): HKR 95-131, HKR 95-128, HKR 95-129, PAU 1966-77-22-1
5	MR	Long duration (140-150 days): HKR 95-492.	Early duration (100-110 days): PAU 2017-58-1-3
			Medium duration (130-140 days): HKR 95-239, HKR 95-124, PAU 2061-20-2-1.
			Medium early duration (115-125 days): HKR 95-130, PAU 2023-8-0-1-3
7	S	Early duration (100-110 days): UPR 1230-9-2, Govind	Early duration (100-110 days): UPR 1230-9-2, AS 89044, RP 2829-32546-1875, HKR 97-14, HKR 97-41, HKRH 1002, Govind.
		Medium duration (130-140 days): PR 113, HKR 95-173, IR 60821-34-1-2, PAU 2338-151-1, HKR 95-20, HKR 95-123, HKR 95-124, HKR 126, HKR 95-138, HKR 120.	Medium duration (130-140 days): PR 113, HKR 95-173, IR 60821-34-1-2, PAU 2338-151-2, HKR 95-72, HKR 95-20, HKR 95-123, HKRH 1059, HKR 126, HKR 95-138, HKR 120.
		Medium early duration: (115-125 days) HKR 95-188, HKR 95-191, HKR 95-218, HKR 95-219, PAU 2338-151-1	Medium early duration (115-125 days): HKR 93-3, HKR 95-192, PK 2557-24-2-1, HKR 95-157, HKR 95-188, HKR 95-191, HKR 46, IR 64, PAU 2338-151-1.
		Long duration (140-150 days): HKR 95-407, HKR 95-465, Taraori Basmati	Long duration (140-150 days): HKR 95-407, HKR 95-410, HKR 95-465, HKR 95-479, HKR 95-492, HKR 95-499, Haryana Basmati, Taraori Basmati
			Early duration (110-111 days): HKR 97-1
9	HS	Medium duration (130-140 days): HKR 95-72, HKR 95-222, HKRH 1059	Medium duration (130-140 days): HKR 95-222
		Medium early duration (115-125 days): HKR 93-3, HKR 95-192, PK 2557-24-2-1, HKR 46, IR 64, HKR 95-66	Medium early duration (115-125 days): HKR 95-218, HKR 95-219
		Long duration (140-150 days): HKR 95-410, HKR 95-479, Pusa Basmati-I, Haryana Basmati	Long duration (140-150 days): HKR 93-401, Pusa Basmati-II

* Forty-seven genotypes were evaluated in 1998 from the list given in Table 1.

** Fifty-eight genotypes were evaluated during 1999 from the list given in Table 1.

PAU 1920-100-2-1-3-3, PAU 1061-19-2-2, PAU 1973-121-1-2-1-1, PAU 2212-25-1-2, CR 837, HKR 95-131, HKR 95-128, HKR 95-129 and PAU 1966-77-22-1 exhibited resistance with damage score of 3 in both the years. Partial resistance in rice genotypes against bacterial leaf blight has also been reported earlier (Saini *et al.*, 1992; Singh and Dodan, 1995; Raina *et al.*, 1999). It is worth mentioning that two genotypes *viz.*, PAU 1973-121-1-2-1-1 and PAU 1920-100-2-1-3-3 were found consistently resistant against both leaf folder and bacterial leaf blight and thus can prove as a good source for multiple resistance and fit in present day integrated pest management programme of rice.

References

Dakshayani K, JS Bentur and MB Kalode (1993) Nature of resistance in rice varieties against leaf folder, *Cnaphalocrocis medinalis* (Guenee). *Insect. Sci. Applic.* **14:** 107-114.

Garg DK (1984) Field resistance to rice leaf folder. *Intl. Rice Res. Newslet.* **9:** 9-10.

Heinrichs EA (1986) Perspectives and directions for the continued development of insect-resistant varieties. *Agric. Ecosystems Environ.* **18:** 9-36.

Heinrichs EA and SL Valencia (1980) Evaluation of insecticides applied as foliar sprays for rice leaf folder control. *Insecticide, Acaricide Tests* **5:** 145-146.

Heinrichs EA, FG Medrano and HR Rapusas (1985a) Genetic evaluation for insect resistance in rice. International Rice Research Institute, Los Baños, Laguna, Philippines, 356p.

Heinrichs EA, E Camang and A Romena (1985b) Evaluation of rice cultivars for resistance to *Cnaphalocrocis medinalis* (Guenee) (Lepidoptera: Pyralidae). *J. Econ. Ent.* **78:** 274-278.

Islam Z and ANMR Karim (1997) Leaf folding behaviour of *Cnaphalocrocis medinalis* (Guenee) and *Marasmia patnalis* Bradley, and the influence of rice leaf morphology on damage incidence. *Crop Prot.* **16:** 215-220.

IRRI (1998) Standard Evaluation System for Rice, International Rice Research Institute, Los Banos, Philippines, 55p.

Jennings PR, WR Coffman and HE Kauffman (1979) Rice Improvement, International Rice Research Institute, Los Baños, Laguna, Philippines, 39p.

Joshi RC, E Medina and EA Heinrichs (1985) Reaction to *Marasmia patnalis* Bradley of varieties resistant to *Cnaphalocrocis medinalis* Guenee. *Inte. Rice Res. Newslet.* **10:** 5.

Khan ZR, AT Barrion, JA Litringer, NP Castilla and RC Joshi (1988) A bibliography of rice leaf folders (Lepidoptera: Pyralidae). *Insect Sci. Applic.* **9:** 129-174.

Leach JE, H Leung, RJ Nelson and TW Mew (1995) Population biology of *Xanthomonas oryzae* pv. *oryzae* and approaches to its control. *Curr. Opinion in Biotech.* **6:** 298-304.

Mandal SMA, BC Das and AK Patra (1997) Field response of rice genotypes to leaf folder and grasshoppers. *Environ. Ecol.* **15:** 810-811.

Nadarajan L and NR Nair (1983) Screening for leaf folder resistance. *Inte. Rice Res. Newslet.* **8:** 5.

Panda SK and IL Shi (1989) Carbofuran induced rice leaf folder resurgence. *Inte. Rice Res. Newslet.* **14:** 30.

Panwar DVS, R Singh and H Chand (1988) Stable resistance to bacterial leaf blight and stem rot in rice. *Oryza* **25:** 94-96.

Raina GL, JS Sidhu, TS Bhardwaj, RK Gautam and Omvir (1999) Multiple disease resistance in rice. *Crop Improv.* **26:** 63-65.

Rajendran R, B Rajendran and PC Sundrababu (1986) Varietal resistance of rice to leaf folder *Cnaphalocrocis medinalis. Inte. Rice Res. Newslet.* **11:** 17-18.

Ramachandran R and ZR Khan (1991) Feeding site selection of first-instar larvae of *Cnaphalocrocis medinalis* on susceptible and resistant plants. *Entomol. Exp. Applic.* **60:** 43-49.

Reissig WH, EA Heinrichs and SL Valencia (1982) Effects of insecticides on *Nilaparvata lugens* and its predators: spiders *Microvelia atrolineata* and *Cyrtorhinus lividipennis. Environ. Ent.* **11:** 193-199.

Saini RS, SC Sharma and RG Saini (1992) Evaluation of some basmati rice genotypes against Indian pathotypes of *Xanthomonas campestris* pv. *Oryzae. Plant Dis. Res.* **7:** 268-270.

Singh R and DS Dodan (1995) Reactions of rice genotypes to bacterial leaf blight, stem rot and sheath blight in Haryana. *Indian J. Mycol. Plant Pathol.* **25:** 224-227.

Singh J, GS Dhaliwal and GS Sidhu (1993) Advances in insect resistance in rice. In: Dhaliwal, GS and VK Dilwari (eds) *Advances in Host Plant Resistance to Insect*, Kalyani Publishers, New Delhi, pp 31-38.

Sundrababu PC and R Rajendran (1986) Screening rice varieties for resistance to brown plant hopper and leaf folder. *Madras Agric. J.* **73:** 297-298.

Velusamy R and S Chelliah (1985) Field screening for resistance to leaf folder (LF). *Inte. Rice Res. Newslet.* **10:** 9.

Velusamy R, IP Janaki and TR Subramanian (1973) Varietal susceptibility of rice to rice leaf roller, *Cnaphalocrocis medinalis* Guenee. *Madras Agric. J.* **60:** 1806-1808.

Waldbauer GP and AP Marciano (1079) Rice leaf folder mass rearing and a proposal for screening for varietal resistance in the greenhouse. *IRRI Res. Paper Ser.* **27:** 17.

Assessment of Groundnut Genotypes for Genetic Variation, Disease Resistance and its Inter-relationship with Yield and its Component Characters

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Information on genetic variability, heritability and genetic advance was derived from data on 14 characters in 81 genotypes of groundnut. PCV and GCV estimates were relatively high for number of branches, leaf spot severity, rust severity and bud necrosis incidence. High heritability coupled with high genetic advance was recorded for test weight, pod yield, leaf spot and rust and bud necrosis incidences. Correlation co-efficient of three diseases with yield and its component characters revealed highly significant positive correlation of leaf spot severity with rust severity and oil content but significantly negative with days to 50% flowering, days to maturity and test weight. Rust severity showed highly significant negative association with days to maturity and plant height. Bud necrosis incidence showed significant negative association with plant height. Screening of genotypes for disease resistance revealed that sources of resistance to leaf spot, rust and bud necrosis diseases are available in groundnut. Six genotypes showed higher yields combined with high resistance to leaf spot and rust over checks.

Key Words: Disease Resistance, Groundnut, Inter-relationship, Variability

The success of any crop improvement programme depends on the magnitude of genetic variability and the extent of heritable portion of desirable traits. Hence, knowledge on these lines is a pre-requisite for planning an effective breeding programme. Groundnut (*Arachis hypogaea* L.) is the most important oilseed crop of India, but its productivity is one of the lowest. Pod yield being a complex character, its expression is influenced by the interaction of various component traits, each controlled by a different set of hereditary factors. Since the effectiveness of the selection depends on the extent of genetic variability, an attempt has been made to evaluate groundnut genotypes for various characters.

Low productivity in groundnut is mainly attributed to the wide occurrence of major diseases like leaf spot, rust and bud necrosis. Hence, the genotypes were also screened for resistance against these diseases as well as their correlation with yield and its component characters was analyzed.

Material and Methods

The material selected for the present study comprised 81 genotypes of groundnut grown at GKVK farm, UAS, Bangalore, The field experiment was laid out in 9 x 9 simple lattice design with two replications. A spacing of 30 x 10 cm was maintained. All along the border, susceptible check (JL-24) for leaf spot and rust was planted. Observations were recorded on five randomly chosen plants for 14 quantitative characters, viz., day to 50% flowering, days to maturity, plant height, number of branches, number of pods, pod yield, kernel yield/ plant, shelling percentage, test weight, oil content, oil yield, leaf spot and rust severity and bud necrosis incidence. Analysis of variance was computed and the genetic parameters were calculated as suggested by Burton and Devane (1953). Heritability in broad sense was worked out as per the formulae suggested by Hanson *et al.* (1956) and genetic advance as suggested by Johnson *et al.* (1955). Correlation of diseases severity with other characters was estimated by using the procedure suggested by Al-Jibouri *et al.* (1958). Disease incidence was studied under field conditions by recording their severity at 50% pod filling stage. For leaf spot and rust, the per cent leaf area affected was computed and expressed as per cent leaf area affected in a given accession. For bud necrosis, number of infected plants and total number of plants in a genotype were counted and expressed as per cent incidence.

Results and Discussion

Analysis of variance revealed that the genotypes differed significantly for all the characters studied. The estimates of variability parameters are given in Table 1. Wide range of variation was observed for test weight, number of pods, plant height, oil content, shelling per cent, pod yield, kernel yield as well as for leaf spot, rust and bud necrosis diseases. Wide range of variation for these characters was also reported by Reddy and Gupta (1992), Khurram *et al.* (1998) and Salara and Gowda (1998).

Table 1. Estimates of range, mean, phenotypic and genotypic co-efficients of variability, heritability and genetic advance for 81 genotypes in groundnut

Characters	Range		Mean	Co-efficient of variability		Heritability (%)	Genetic advance as % of mean
	Min.	Max.		PCV(%)	GCV(%)		
Days to 50% flowering	34.00	44.00	37.00	07.71	06.61	86.50	12.67
Days to maturity	108.00	125.00	113.00	04.41	04.26	93.60	08.50
Plant height	26.59	45.99	36.30	12.07	10.52	76.00	18.88
No. of branches/plant	05.00	12.00	08.00	22.79	15.75	47.70	22.44
No. of pods/plants	15.00	28.00	21.00	17.13	10.51	37.60	13.26
Pod yield/plant	14.18	30.39	21.20	17.67	13.78	60.80	22.13
Kernel yield/plant	10.38	23.67	16.20	16.21	11.86	53.50	17.88
Shelling per cent	64.94	85.25	76.94	04.99	04.49	80.90	08.30
Test weight	27.59	66.97	44.99	17.69	17.38	96.60	35.18
Oil content	33.65	52.52	43.40	09.67	09.05	87.50	17.44
Oil yield/plant	04.75	09.29	06.98	15.90	12.00	56.40	18.49
Leaf spot severity	06.94	34.73	24.58	32.10	30.54	90.50	59.88
Rust severity	02.19	22.38	13.27	35.16	33.46	90.60	65.56
Bud necrosis incidence	00.69	27.51	13.47	50.77	47.54	87.70	91.68

The variability estimates in general revealed that the PCV was higher than the corresponding GCV for different characters, though the extent of difference between the two was relatively low. This narrow difference between PCV and GCV imply low sensitivity to environmental effects. The PCV and GCV estimates were relatively high for number of branches, number of pods, leaf spot, rust and bud necrosis incidences. High PCV and GCV estimate for number of pods were in accordance with Khurram *et al.* (1998). Moderate PCV and GCV estimates were observed for plant height, pod yield, kernel yield, test weight and oil yield, which were reported to be high by Uddin *et al.* (1995), Kumar *et al.* (1998) and Naik *et al.* (2000).

High heritability coupled with high genetic advance was observed for pod yield, test weight, leaf spot, rust and bud necrosis. Selection for these traits is likely to accumulate more additive genes leading to further improvement in their performance and hence, may be used as selection criteria. High heritability with moderate genetic advance was observed for days to 50% flowering, plant height and oil content. Moderate heritability with moderate genetic advance was observed for number of pod, kernel yield and oil yield indicating considerable influence of environment, so that simple selection will not be effective because of non-additive gene action. These results are in accordance with Udin *et al.* (1995), Naik *et al.* (2000) and Salara and Gowda (1998).

Since groundnut is most susceptible to major diseases (leaf spot, rust and bud necrosis), one of the major objective of groundnut breeding programme is to develop disease resistant cultivars with acceptable agronomic characters. For this, it is important to know the association of characters with the diseases. Correlation coefficient analysis (Table 2) indicated highly significant and negative correlation of leaf spot severity with days to 50% flowering, days to maturity and test weight indicating

Table 2. Estimates of phenotypic correlation co-efficients of 13 characters and two diseases

Characters	Leaf spot	Rust incidence	Bud necrosis
Days to 50% flowering	-0.540**	- 0.200	- 0.132
Days to maturity	- 0.706**	- 0.438**	- 0.190
Plant height	0.037	- 0.229*	- 0.349**
No. of branches/plant	- 0.038	0.086	0.068
No. of pegs/plant	0.158	0.131	0.190
No. of mature pods/plants	0.075	0.041	0.172
No. of immature pods/plant	0.153	0.125	0.109
Pod yield/plant	-0.180	0.083	- 0.001
Kernel yield/plant	- 0.144	0.113	0.050
Shelling per cent	0.190	0.130	0.083
Test weight	- 0.459**	0.091	0.140
Oil content	0.338**	- 0.034	- 0.039
Oil yield/plant	0.055	0.090	- 0.089
Leaf spot	–	0.393	0.124
Rust incidence	–	0.186	

*Significant at 5% level; **Significant at 1% level

Table 3. Number of genotypes categorized into different infection classes in groundnut

Disease incidence (%)	Category	Number of entries		
		Leaf spot	Rust	Bud Necrosis
0-5	Highly resistant	11	15	37
5.0 - 10	Resistant	7	59	30
10.1 - 25	Moderately resistant	35	11	14
25.1 - 50	Susceptible	28	-	-
50% and above	Highly susceptible	-	-	-

less susceptibility of late flowering/maturing types for the disease. Its association was positive and significant with oil content and rust severity. Rust severity showed significant negative association with days to maturity and plant height. Bud necrosis incidence showed significant negative association with plant height. The inter-correlations estimate indicate the simultaneous improvement of these traits by selection.

The entries were also screened for resistance against three major diseases. Of the 81 entries screened, 11 entries were highly resistant to leaf spot, 15 to rust and 37 to bud necrosis incidence (Table 3). Six genotypes *viz.*, JSSP-13, VG-9711, VG-9516, CSMG-919, Dh-992 and TNAU-281 had combined resistance to all the three diseases. These six genotypes were found to be late flowering and late maturing with moderate levels of pod yield, shelling percentage, test weight and oil content. Hence, they offer a promising source of resistance to be used in further resistant breeding programme. Buiel *et al.* (1993), Vasanthi and Naidu (1998) and Mukund *et al.* (1999) have also reported on varietal screening for resistance to these diseases.

The genotypes were compared with the checks (JL-24, TMV-2, VRI-2, K-134) for pod yield and disease resistance (Table 4). Six genotypes, *viz.*, JSSP-18, CSMG-919, M-13, JCGV-86532, JSSP-16 and VG-9516 showed higher yields combined with high resistance to leaf spot and rust over the checks indicating that simultaneous improvement for high yield and resistance to diseases is possible in groundnut. These genotypes can be recommended for further traits to examine their consistent performance.

Table 4. Genotypes having significantly higher yield along with higher disease resistance than checks in groundnut

Genotype	Pod yield	Leaf spot severity (%)	Rust severity (%)
Entries			
JSSP-18	31.00	15.00	5.0
M-13	30.50	11.00	7.0
ICGV 86352	27.10	17.00	1.0
CSMG 919	26.95	3.50	1.0
JSSP 16	26.80	11.00	5.0
J-38	26.30	20.00	7.0
VG 9516	25.35	2.00	4.0
Checks			
JL-24	23.65	25.00	5.0
TMV 2	23.15	24.00	5.0
VRI 2	23.30	19.00	6.0
K-134	19.25	30.00	9.0

References

Al-Jibouri HA, PA Miller and HE Robinson (1958) Genotypic and environmental variances in upland cotton of inter-specific origin. *Agron. J.* **50:** 633-637.

Buiel AAM, T Jacobs and JE Parlevliet (1993) Resistance in groundnut to peanut bud necrosis virus. Durability of disease resistance 207-210. *Current Plant Science and Biotechnology in Agriculture* **18:** 207-210.

Burton GW and GM Devane (1953) Estimating heritability in tall Fescue (*Festuca arundinaceae*) from replicated clonal material *Agron. J.* **45:** 478-481.

Hanson GH, HF Robinson and RE Comstock (1956) Biometrical studies and yield in segregating populations of Korea Tes Pedeza *Agron. J.* **48:** 267-282.

Johnson RW, HF Robinson and RE Comstock (1955) Estimates of genetic and environment variability in soybeans. *Agron. J.* **47:** 314-318.

Khurram B, A Naazar and SN Malik (1998) Estimation of variability and heritability for quantitative traits in groundnut *Sarhad. J. Agric.* **14:** 575-579.

Kumar R, J Ghosh and JN Sah (1998) Variability and correlation studies in mutant cultures. *J. Appl. Biol.* **8**: 20-23.

Mukund S Kulkarni, KH Anahosur and K Giriraj (1999) Screening Groundnut Entries against bud necrosis virus in Karnataka. *J. Oilseeds Res.* **16:** 159-160.

Naik KSS, PN Reddy and CDR Reddy (2000) Variability studies in F_2 populations of some sub specific crosses in groundnut *National Seminar on Oilseeds and Oils, Research and Development Needs in the Millennium* **2-4:** 93.

Reddy KR and RVS Gupta (1992) Variability and inter-relationship of yield and its component characters in groundnut. *J. Maharashtra Agric. Univ.* **17:** 224-226.

Salara BS and MVC Gowda (1998) Variability and correlation studies on segregating generation of inter sub specific crosses of groundnut (*Arachis hypogaea*) *Crop Improv.* **25:** 122-123.

Uddin MJ, MAZ Choudhury, MK Sultan and BN Mitra (1995) Genetic variability, correlation and path analysis in groundnut (*Arachis hypogaea* L.). *Bangladesh J. Sci. Industrial Res.* **30:** 235-241.

Vasanthi RP and PH Naidu (1998) Evaluation of advanced groundnut lines for resistance to late leaf spot. *Int. Arachis Newslet.* No. **18:** 14-16.

Electrophoretic Study on Seed Storage Proteins of Groundnut (*Arachis hypogaea* L.) Cultivars of India

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Electrophoretic separation of seed storage protein of 70 Indian released groundnut cultivars was studied on SDS-PAGE to find distinction in banding pattern and to explore the possibility to use the traits to meet DUS (Distinction, Uniformity and Stability) testing. Buffer soluble proteins from seeds were extracted using Tris-HCI buffer and subjected to SDS-PAGE. Thirty-six distinct bands with molecular weight ranging from 7 to 128 kD were resolved and polymorphism was observed for the banding pattern. The cluster analysis based on cosine coefficient of association showed distinction of individual cultivars, indicating that seed storage protein trait can be supplemented to the morphological traits for DUS testing in groundnut.

Key Words: Cultivars, DUS Testing, Groundnut, Proteins, SDS-PAGE

Groundnut (*Arachis hypogaea* L.) is one of the important oilseed crops of India, being the second largest producer in the world. More than one hundred improved cultivars have been released for cultivation in India. As the countries are introducing Plant Breeders Rights, it is indispensable for the cultivars to be distinct, uniform and stable in the manifestation of various traits (Cooke, 1989). Based on the guidelines of the International Union for the Protection of New Varieties of Plants detailed morphological characterization was done by Rajgopal *et al.* (2000) and suggested that supplementation of biochemical/molecular characterization data may be useful in distinguishing the groundnut varieties. The importance of electrophoretic analysis of proteins and/or enzymes has been widely discussed for seed testing, production and certification (Cooke, 1988). Eletrophoretic studies have more advantages in autogamous species especially where distinctions through morphological traits is difficult to meet the requirement of DUS testing. Electrophoresis of seed storage proteins is one of the potential methods to assess polymorphism as it is coded genetically at more than one locus and in the genus *Arachis* the polymorphism was reported by Cherry (1975), Klozova *et al.* (1983) Krishna and Mitra (1988) and Lanham *et al.* (1994). Ladizinsky and Hymowitz (1979) and Singh *et al.* (1991) studied the phylogenetic relationship in the genus *Arachis* based on seed protein profile. However, intra-specific variation is not much studied in *A. hypogaea*. The present study is an extension of morphological characterization of Indian groundnut cultivars conducted by Rajgopal *et al.* (2000) to supplement the data on seed proteins banding pattern in distinction of different cultivars.

Materials and Methods

The seeds of uniform size and maturity were sampled from the freshly harvested and dried pods of 70 released cultivars grown in 1998 under good management conditions at National Research Centre for Groundnut, Junagadh, Gujarat, India (Table 1). Seeds were crushed in a mortar and de-fatted using hexane by changing the solvent 3 or 4 times till a fine powder is obtained. The de-fatted powder was extracted with 0.05 M Tris-HCI buffer (pH 7.5) by keeping overnight. The mixture was then centrifuged at 13,000 rpm in eppendorf tube and the supernatant collected was estimated for protein content using Bradford's method (Bradford, 1976). The extract was then mixed with sample buffer containing glycerol and bromophenol blue. Sample containing 100µg of proteins was loaded in each well of 15%T Polyacrylamide gel. The 70 samples were accommodated in four gels and in each gel, protein molecular weight markers (116,66,45 and 29kD) were also loaded in one well. All the gels were run simultaneously using a BIO-RAD Protean II electrophoresis system at constant current of 1.5 mA per well at 15°C. The run was continued till the dye front reached the bottom of the gel. The experiment was repeated three times to verify the stability. The gel was stained with coomassie brilliant blue and separated bands were scanned against the molecular weight markers using the gel scanner. The banding pattern was analyzed based on cosine coefficient of association.

Results

A maximum of 36 bands were resolved on gel with molecular weight ranging from 7kD to 128 kD across the cultivars and a maximum number of 26 bands were observed in ALR 1 and a minimum of 17 was observed

in J 11. The protein bands were classified in to five groups based on their molecular weight (above 100 kD, 76-100 kD, 51-75 kD, 26-50 kD, and below 25 kD) and the frequency of bands falling in each group for different cultivars are given in Table 1. Only a few bands were observed in high molecular weight protein and

Table 1. Frequency of bands in different categories based on molecular weight of proteins in groundnut cultivars

Cultivar		Pedigree	Frequency of bands				
	Virginia bunch		A	B	C	D	E
1	T 28	Selection from Bombay collection	1	5	4	7	3
2	ICGS 5	(Robut 33-1 X NCAc 316) F2	0	5	3	7	3
3	M 522	Punjab 1 X F 334-AB 14	0	6	3	6	3
4	TMV 10	Natural mutant from Argentina	0	6	3	9	4
5	T 64 (TG 64)	Selection from EC 1664	0	6	5	9	3
6	RSB 87	Selection from Brazilian culture	1	5	4	10	4
7	RS 138	Selection from Brazilian culture	0	6	4	7	5
8	M 145	A1-1 X D 3	0	5	3	7	5
9	Kadiri 3	Selection from Robut 33-1	1	5	3	9	3
10	ICGV 86325	ICGS 20 X G 201	1	4	3	12	3
11	ICGS 76	TMV 10 X Chico	0	6	3	9	4
12	HNG (HPS) 2	—	0	6	3	9	4
13	GG 20	GAUG 10 X Robut 33-1	0	6	3	9	4
14	BG 2	X ray mutant of 41-C	0	6	3	8	4
15	BAU 13	BAU 6 X M 13	0	5	4	10	3
16	B 95	M 13 X Shulamith	2	5	5	9	3
17	ALR 1	Pol 2 X PPG 4	2	5	4	10	5
	Virginia runner						
18	Somnath	Induced mutant of TG 18 A X M 13	1	2	3	9	3
19	RS 1	Selection from local collection	1	3	3	8	3
20	Punjab 1 (PG1)	Selection from Samrala local	1	3	4	8	4
21	M 37	A 1 X C 6-4-7-2	0	4	3	6	4
22	M 335	M 13 X F7	0	4	4	9	3
23	M 13	Selection from NC 13	0	4	4	8	5
24	Karad 4-11	Selection from local	0	5	4	8	4
25	GG 13	GAUG 10 X TMV 10	0	5	4	8	4
26	GG 12	Shulamith X GAUG 10	0	6	3	10	5
27	GG 11	M 13 X GAUG 10	0	5	5	9	3
28	GAUG 10	G 224-3 X GO 343	0	5	4	7	5
29	CSMG 84-1	Selection from MA 10	0	5	4	8	5
30	Chitra	Spanish 5B-1 X EC 1688	0	5	4	8	5
31	Chandra	Selection from AH 114	0	5	5	9	5
32	UF 70-103	Introduction from USA	0	5	5	10	2
33	M 197	C501 X U 4-7-2	1	5	5	10	3
34	Kaushal	Selection from T 28	1	4	5	10	2
	Spanish bunch						
35	Tirupati 1 (TPT-1)	Selection from EC 106983/3-1	0	4	3	6	4
36	Tirupati 2 (TPT-2)	GAUG 1 X NCAc FLA-14	0	4	5	7	4
37	TMV 7	Selection from Tenesse white	0	5	5	7	5
38	TMV 2	Selection from Gudhiatham bunch	0	4	4	8	5
39	TKG 19A	TG 17 X TG 1	1	3	4	8	4
40	TG 3	Mutant of Spanish improved	0	5	4	10	4
41	TG 26	BARCG 1 X TG 23	1	5	3	11	4
42	TG 22	—	0	5	3	11	2
43	TG 17	Dark green Mutant X TG 1	0	6	3	9	3
44	TAG 24	Selection from TGS 2	0	5	3	9	5
45	Spanish improved	Selection from Spanish peanut	0	5	4	9	5
46	SG 84	Selection from ICGS 1	0	5	3	10	5
47	SB XI	Ah 4213 X Ah 4354	0	5	3	11	5
48	RG 141	Robut 33-1 X NCAc 2821	0	5	3	10	4
49	MH-1	Selection from Faizpur1-5	0	5	4	11	5
50	JL 34	Kadiri 3 X JL 24	0	5	3	11	5
51	JL 24	Selection from EC 94943	0	5	4	11	3
52	AK 12-24	Selection from local	0	5	4	12	4
53	TMV 12	Selection from Ugandan culture	0	5	4	12	4

Contd.

Cultivar		Pedigree	Frequency of bands				
	Virginia bunch		A	B	C	D	E
54	J 11	Ah 4218 X Ah 4354	0	4	3	6	4
55	ICGV 86590	X 14-4-B-19-B X PI 259747	1	3	4	7	6
56	ICGS 44	Selection from Robut 33-1	0	3	4	10	6
57	ICGS 21	—	1	3	4	9	6
58	ICGS 11	Selection from Robut 33-1	1	3	4	10	5
59	ICGS 1	Selection from Robut 33-1	0	4	4	10	5
60	Girnar 1	X 14-4-B-19-B X NCAc 17090	0	4	4	9	5
61	GG 4	CGC 3 X Chico	0	4	4	8	5
62	GG 5	GAUG I X JL 24	0	4	5	8	5
63	GG 2	J 11 X EC 16659	0	4	4	9	5
64	Dh 8	Selection from RS 144	0	4	4	9	5
65	Dh 3-30	Spanish Improved X US 4	0	4	4	9	4
66	CO 1	Ah 6279 X TMV 3	0	4	5	8	5
67	ALR 2	Selection from ICGV 86011	0	4	3	10	4
	Valencia						
68	MH-4	—	0	4	3	9	5
69	MH-2	Selection from GDM	0	4	3	9	4
70	Gangapuri	Old groundnut strain	0	4	4	9	5

A = Very slow moving bands (> 100 kD); B = Slow moving bands (76-100 kD); C = medium fast moving bands (51-75 kD); D = Fast moving bands (26-50 kD); E = very fast moving band (<25 kD)

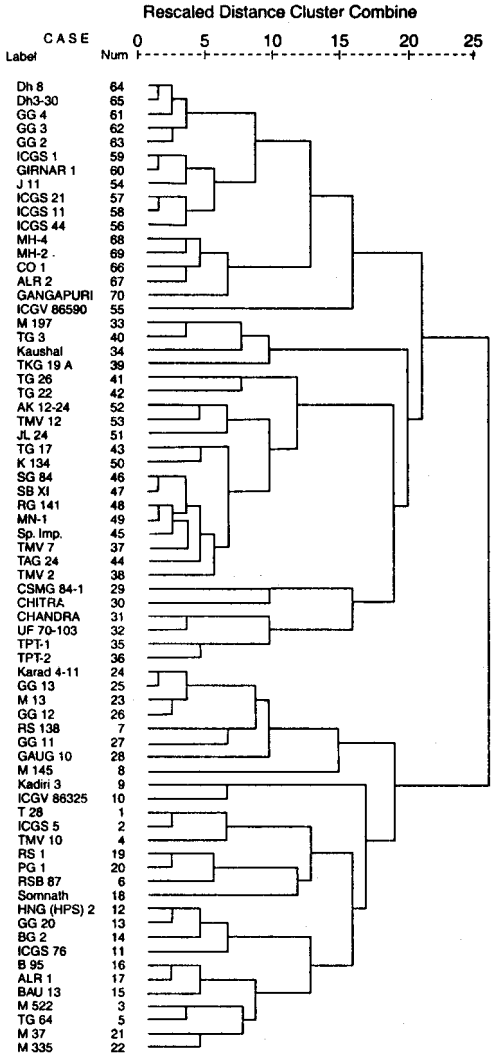

Fig. 1. Dendrogram based on banding pattern difference of seed proteins of 70 released cultivars

the maximum number of bands was observed in 26 to 50 kD range. The highest number of bands in this range shown by a cultivar was in ICGV 96325, AK 12-24 and TMV 12, and a minimum of 6 bands was expressed in Tirupati 1 and J 11. In proteins falling in between the molecular weight 51 to 75 kD, the range of variation was only 3 to 5. In general, the Spanish cultivars have more uniform distribution of bands compared to other habit types. In cluster analysis, based on cosine coefficient of association, distinction at cultivars level was worked out (Fig. 1). Two major groups were observed in the dendrogram; one group exclusively of virginia bunch cultivars and other with all spanish bunch cultivars, all valencia cultivars and six virginia bunch cultivars (M 197, Kaushal, CSMG 84-1, Chitra, Chandra and UF 70-103). The cultivar pairs, which showed maximum similarity in their banding pattern, were ICGS 1 and Girnar 1; ICGS 21 and ICGS 11; SG 84 and SB 11; RG 141 and MH 1; and Karad 4-11 and GG 13. Interestingly none of the cultivar pair's pedigree could be traced to common genotypes.

Discussion

Studies on intra-specific variation in seed protein banding pattern has not been explored in groundnut. Singh *et al.* (1991) reported 100% similarity between two *A. monticola* accessions. However, in this study only a maximum of 19 bands were resolved in electrophoresis. The level of polymorphism obtained in our study may be attributed to more number of bands (36) resolved in electrophoresis. Here, we used higher

percentage of polyacrylamide gel (15%) for electrophoretic separation. The reproducible banding pattern confirmed the results. Cooke (1989) suggests that the integration of electro-phoretic data and small number of highly discriminatory morphological characters would be more preferable in DUS testing. In groundnut, it will be useful as the morphological characterization alone could not distinguish the cultivars and many of the morphological characters are highly influenced by the environment.

References

Bradford M (1976) A rapid and sensitive method for the quantitation of microgram quantities of proteins utilizing the principle of protein dye binding. *Ann. Biochem.* **72:** 248.

Cherry JP (1975) Comparative studies of seed protein and enzyme of species and collections of *Arachis* by gel electrophoresis *Peanut Sci.* **2:** 57-65.

Cooke RJ (1988) Electrophoresis in plant testing and breeding. *Adv. Electrophoresis* **2:** 171-261.

Cook RJ (1989) The use of electrophoresis for the distinctness testing of varieties of autogamous species. *Plant Varieties Seeds* **2:** 3-13.

Klozova E, J Svachulova, J Smartt, E Hadac and V Turkova (1983) The comparison of seed protein patterns within genus *Arachis* by polyacrylamide gel electrophoresis. *Biol. Plant.* **25:** 266-273.

Krishna TG and R Mitra (1988) The probable genome donors to *Arachis hypogaea* L. based on Arachin seed storage protein. *Euphytica* **37:** 47-52.

Ladizinsky G and J Hymowitz (1979) Seed protein electrophoresis in taxonomic and evolutionary studies. *Theor. Appl. Genet.* **54:** 145-151.

Lanham PG, BP Forster, P McNicol, JP Moss and W Powell (1994) Seed storage protein variation in *Arachis* species. *Genome* **37:** 487-496.

Rajgopal K, K Chandran, A Bandyopadyay, HB Lalwani, NR Ghetia and PK Bhalodia (2000) Pattern of distribution of morphological traits among the released groundnut (*Arachis hypogaea* L.) cultivars *vis-a-vis* the DUS requirements. In: Extended Summeries, Proceedings of the National Seminar on Oilseeds and Oils - Research and development needs in the millennium. Indian Society of Oilseeds Research, Directorate of Oilseed Research, Hyderabad.

Singh AK, S Sivramakrishan, MH Mengesha and CD Ramaiah (1991) Phylogenetic relations in section *Arachis* based on seed protein profile. *Theor. Appl. Genet.* **82:** 593-597.

DNA Fingerprinting of Guava (*Psidium guajava* L.) Cultivars using RAPD Markers

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Guava (*Psidium guajava* L.) is one of the important tropical fruit crops of India. Detailed horticultural and systematic study of the species and cultivars is lacking. Molecular markers can complement morphological characterization of cultivars in identification and diversity analysis. RAPD analysis of some guava cultivars of North India is presented. Nine RAPD primers generated 133 amplicons discriminating all the 13 cultivars. Cultivar-specific bands were identified for five cultivars. Statistical analysis revealed moderate genetic diversity among the cultivars investigated. Present analysis demonstrates the feasibility of RAPD technique for DNA fingerprinting of guava cultivars.

Key words: DNA Fingerprinting, Guava, RAPD Analysis

Guava, known as apple of tropics, is one of the important fruit crops of India. Guava is more resistant to drought than any other fruit crop. Originated in tropical America, from Mexico to Peru, guava is in India since early 17th century (Mitra and Bose, 1985). Three species of *Psidium* are reported from India: *P. cattleyanum* Sabine. cultivated in gardens; *P. guineense* Sw. reported as growing wild in Tripura and *P. guajava* L. cultivated in gardens and orchards (Anonymous, 1965). For sustained success in guava improvement programmes, characterization and documentation of the available diversity is of prime importance. Though, medicinal uses of different plant parts of guava are well-documented (Blatter *et al.*, 1995), detailed horticultural and systematic study of the species and cultivars is lacking (Mitra and Bose, 1985). Molecular marker techniques such as RAPD, RFLP, AFLP, ISSR and STMS provide modern tools for plant systematics. They complement morphological characterization. In the era of sovereign rights over national resources and intellectual property protection of life forms, molecular profiles provide robust support to documentation.

Among the various molecular marker techniques developed over the past two decades, RAPD (Welsh and McClelland, 1990; Williams *et al.*, 1990) has been the most widely employed DNA technique because it is easy, quick, simple and economical. Despite questions about its reproducibility, its utility in diversity analysis, mapping and genotype identification has been exploited in many plant species (Harris, 1999; Weising *et al.*, 1995). Neither sequence information nor any prior genetic study is required for these analyses. Data analysis and interpretation can give reliable results if the limitations of RAPD such as low repeatability and non-specificity are internalised. Utility of molecular markers in diversity analysis of guava has been demonstrated (Prakash *et al.*, 2002). The present study attempts to demonstrate the feasibility of RAPD markers in the identification of selected guava cultivars from the northern region of India.

Materials and Methods

Young leaves of 13 cultivars were collected from Research Farm of Department of Horticulture, CCS Haryana Agricultural University, Hisar (Table 1). DNA was extracted based on cTAB method with minor modifications (Archak *et al.*, 2002) to suit guava leaf material. Essentially, the extraction buffer composition was 4% w/v cTAB, 1.4 M NaCl, 100 mM Tris-HCl (pH 8), 20 mM EDTA, 2% PVP w/v, and 0.2% 2-mercapto ethanol v/v. DNA was treated with bovine pancreatic RNase and extracted once with phenol: chloroform (1:1) and twice with chloroform: iso-amyl alcohol (24:1). After precipitation with iso-propanol, a 70% ethanol wash was given. DNA

Table 1. Important morphological features of guava cultivars used in the study

Cultivar	Tree Height (m)	Fruit weight (g)	Flesh colour
Lucknow-49	3.3	107	White
Allahabad Safeda	5.8	87	White
Hisar Safeda	5.6	92	White
Apple Colour	5.4	75	White
Chakaia Rahamnagar	6.1	63	White
Kothrud	6.3	58	Pink
Pear Shaped	7.1	105	White
Red Supreme	5.6	68	Pink
Nagpur Seedling	6.1	102	White
Sindh	6.2	90	White
Tehsidar	6.1	105	White
Nasik	6.1	70	White
Patilo	6.3	–	Pink

was dissolved to appropriate dilution in TE buffer and quantified in a fluorometer. Subsequent to screening of primers, nine random primers (Operon) were selected based on amplification pattern. Amplification reactions contained 2.5 mM $MgCl_2$; 50 µM KCl; 10 mM Tris-HCl (pH 9); 0.1% Triton X-100; 200 µM of each of dNTPs; 0.5 µM primer; 30 ng template DNA; and 1 unit Taq DNA polymerase (Bangalore Genei, Bangalore) in a reaction volume of 25 µl. After a pre-denaturation step of 4 min at 94°C, DNA amplification reactions were cycled 40 times at 94°C for 1 min, 35°C for 1 min and 72°C for 2 min in a Perkin Elmer 9600 thermocycler. A final extension was allowed for 5 min at 72°C. Upon completion of the amplification, reaction mixture was mixed with 6x loading dye containing 0.25% bromophenol blue, 0.25% xylene cyanol and 30% glycerol. Electrophoresis was carried out in a 1.2% agarose/1x Tris-Borate EDTA gel at 4 V/cm. Sizes of the identified bands were determined relative to a GeneRuler 100 bp DNA ladder (MBI Fermentas). Following ethidium bromide staining, amplified products were visualised on a UV trans-illuminator. Bands were scored as '1' for presence and '0' for absence to prepare the binary data matrix. Nei and Li (1979) coefficient was used to derive pair-wise relationships, and a dendrogram was developed based on neighbour-joining algorithm (Saitou and Nei, 1987). Once the profiles were generated, the probability of identical match by chance (Ramakrishna *et al.,* 1994) was calculated as: Pi = (Average similarity index)^n, where, n = average number of amplified products/ cultivar.

Results and Discussion

Nine primers produced 133 bands ranging from 300 bp to 3000 bp in size, of which 74.7% were polymorphic (Table 2). A typical amplification pattern is given in Fig. 1. All the bands generated by primers OPA-13 and OPE-13 were polymorphic. On the other hand, OPB-09 produced six bands of which only one was polymorphic.

Table 2. Primer-wise details of the amplification in guava cultivars

Primer	Number of Amplicons	Polymorphic amplicons
OPA-05	12	9
OPA-13	10	10
OPB-05	18	13
OPB-09	6	1
OPC-13	17	16
OPD-06	21	18
OPE-09	11	5
OPE-13	21	21
OPE-19	17	12

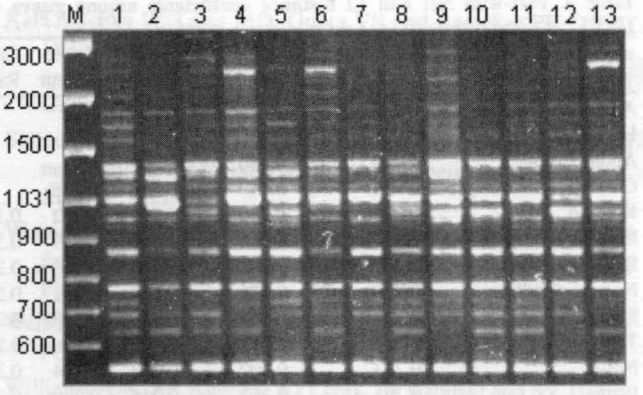

Fig. 1. RAPD profiles of 13 guava cultivars obtained using primer OPE-9. Lanes from 1-13 represent the cultivars Lucknow-49, Allahabad Safeda, Hisar Safeda, Apple Colour, Chakaia Rahamnagar, Kothrud, Pear Shaped, Red Supreme, Nagpur Seedling, Sindh, Tehsidar, Nasik and Patilo. M represents molecular weight marker; sizes of the bands are in base pairs.

Based on the total band profile all the cultivars could be discriminated from each other. However, cultivar specific markers could be identified for only five cultivars (Table 3). Inter-relationships between cultivars were

Table 3. Cultivar-specific amplicons generated by random primers in guava cultivars

Cultivar	Primer	Size of amplicon (base pairs)
Chakaia Rahamnagar	OPC-13	550
Kothrud	OPD-06	1100
Lucknow-49	OPA-05	600
	OPE-19	850 and 800
Pear Shaped	OPA-05	750
Red Supreme	OPD-06	950

revealed by computing pair-wise distance coefficient. Cultivars exhibited an average pair-wise distance of 0.242 (Table 4). Hisar Safeda and Allahabad Safeda were the closest pair of cultivars with a distance of 0.051 on a scale of zero to one. This was predictable since Allahabad Safeda is the female parent of Hisar Safeda, a hybrid cultivar. Cultivars Pear Shaped and Red Supreme were most distantly placed in relation to each other with a distance of 0.423. Average similarity index among 13 cultivars was 0.604 and on an average 81.85 bands were amplified/cultivar. Therefore, employing all the 9 primers, the probability of identical match by chance was 1.2×10^{-18} indicating a high degree of confidence in identification.

Dendrogram provided a clear picture of how the cultivars are placed in relation to each other (Fig. 2). Cultivars Kothrud and Pear Shaped formed a distinct cluster. Nasik, Patilo and Tehsildar were clustered together

Table 4. Pair-wise Nei and Li distance coefficients among guava cultivars

	Lucknow-49	Allahabad Safeda	Hisar Safeda	Apple Colour	Chakaia Rahamnagar	Kothrud	Pear Shaped	Red Suprme	Nagpur Seedling	Sindh	Tehsidar	Nasik
Allahabad Safeda	0.250											
Hisar Safeda	0.257	0.051										
Apple Colour	0.230	0.146	0.094									
Chakaia Rahamnagar	0.256	0.149	0.156	0.138								
Kothrud	0.225	0.200	0.207	0.202	0.157							
Pear Shaped	0.378	0.366	0.347	0.319	0.348	0.285						
Red Supreme	0.302	0.242	0.238	0.246	0.247	0.253	0.423					
Nagpur Seedling	0.259	0.178	0.162	0.191	0.227	0.221	0.388	0.152				
Sindh	0.293	0.161	0.156	0.198	0.200	0.229	0.376	0.202	0.091			
Tehsidar	0.244	0.218	0.202	0.246	0.247	0.241	0.376	0.236	0.182	0.176		
Nasik	0.293	0.300	0.283	0.294	0.346	0.289	0.386	0.268	0.222	0.256	0.154	
Patilo	0.291	0.262	0.246	0.280	0.305	0.275	0.422	0.233	0.200	0.232	0.171	0.107

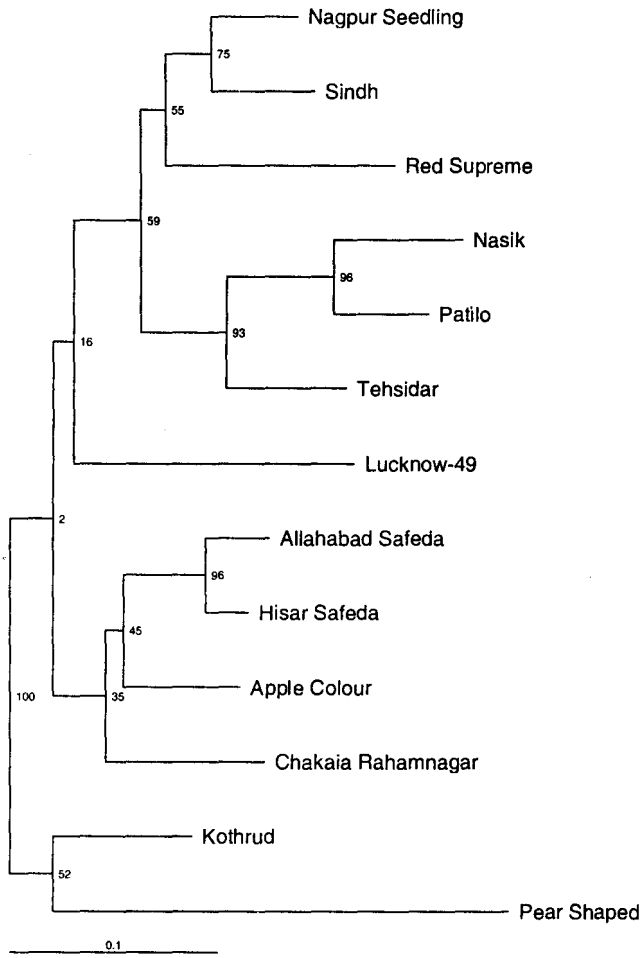

Fig. 2. Neighbour-joining tree of 13 guava cultivars. The bar represents Nei and Li coefficient

at a bootstrap probability of more than 93%. Hisar Safeda and Allahabad Safeda were grouped together with a bootstrap value of 96%. Rest of the groups did not have bootstrap probabilities high enough to be distinguished as clusters. The clustering pattern neither corresponded to the known attributes of the cultivars such as flesh colour or place of origin as reflected in their names. Guava is an allogamous tree crop, which is highly heterozygous. Correspondence between molecular markers and morphological traits may not be apparent. In the present experiment, the highest distance index was only 0.423, indicating high similarity among the cultivars analysed. This observation can be indicative only and cannot be conclusive. An accurate measure of molecular diversity in Indian guava cultivars may be obtained if a large number of them are screened using a higher number of markers. Nevertheless, the present report demonstrated that RAPD could be effectively used to identify cultivars. The utility of the specific RAPD markers can be increased by sequencing their termini and designing longer primers (SCARS) for specific amplification.

Acknowledgements

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References

Anonymous (1965) *Psidium.* In: *The Wealth of India – Raw materials*. Volume VIII: Publications and Information Directorate CSIR, New Delhi, pp 285-293.

Archak S, JL Karihaloo and A Jain (2002) RAPD markers reveal narrowing genetic base of Indian tomato cultivars. *Curr. Sci.* **82:** 1139-1149.

Blatter E, JF Caius and KS Mhaskar (1995) *Indian Medicinal Plants-II edition* Lalit Mohan Basu, Allahabad.

Harris SA (1999) RAPDs in systematics – a useful methodology? In: PM Hollingsworth, RM Bateman & RJ Gornall (eds) *Molecular Systematics and Plant Evolution.* Taylor and Francis London, UK, pp 211-228.

Mitra SK and TK Bose (1985) Guava. In: TK Bose (ed) *Fruits of India: Tropical and subtropical.* Naya Prokash, Calcutta, pp 277-297.

Nei M and Li WH (1979) Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proc. Natl. Acad. Sci.USA.* **76:** 5269-5273.

Prakash DP, Narayanaswamy P and Sondur SN (2002) Analysis of molecular diversity in guava using RAPD markers. *J. Hortic. Sci. Biotechnol.* **77:** 287-293.

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

Saitou N and Nei M (1987) The Neighbour-joining method: a new method for reconstructing phylogenetic trees. *Mol. Biol. Evol.* **4:** 406-425.

Weising K, H Nybom, K Wolff, and W Meyer (eds) (1995) *DNA fingerprinting in plants and fungi.* CRC Press, Boca Raton, Florida.

Welsh J and M McClelland (1990) Fingerprinting genomes using PCR arbitrary primers. *Nucleic Acids Res.* **18:** 7213-18.

Williams JGK, AR Kubelik, KJ Livak, JA Rafalski and SV Tingey (1990) DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. *Nucleic Acids Res.* **18:** 6531-35.

Characterization and Classification of HAU Male Sterile Lines of Pearl Millet (*Pennisetum glaucum* L.)

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Key Words: Characterization, Cytoplasmic Male Sterility, Pearl Millet

The real break through in hybrid development in pearl millet (*Pennisetum glaucum* L.) occurred with the discovery of CMS lines Tift 23A and Tift 18A in the USA (Burton 1965a,b). In India, Tift 23A was used in crossing programme at Punjab Agricultural University (PAU) Ludhiana and first single cross hybrid HB 1 (Tift 23A × BIL 3B) was developed and released in 1965 (Burton and Athwal, 1967). This increased the yield of pearl millet 3-5 folds. Since then the male sterile lines proved to be the back bone of hybrid breeding programme. This led to the development of new male sterile lines at different centres throughout India. The development of new CMS lines is of little value until these are evaluated and characterized. Characterization is an important aspect because it consists of recording those characters which are highly heritable, can be easily seen by the eye and those expressed in all environments.

Concerted efforts at CCS Haryana Agricultural University, Hisar (CCS HAU), were put in to develop new male sterile lines and their maintainers in early 1980s. The conventional back cross technique has been used to incorporate the sterility inducing cytoplasm (Allard, 1960, House 1980, Sharma 1980). Cytoplasmic male sterility was easily transferred to a given strain by using that strain as pollinator (recurrent parent) in successive generations of back crossing. The CCS HAU developed the first male sterile line HMA 1A in 1986. After 6-7 generations the nuclear genotype of the male sterile line would be almost identical to that of the pollinator strain. Likewise the line recovered from the cross DSA 134A × H 90/4-5 carry sterile cytoplasm and recessive gene 'ms' and, thus, became HMS 1A. Four to six back crosses may be adequate if the new B line and the cytoplasmic donor CMS line are closely related, whereas up to 8 back crosses may be needed for more diverse line (Hanna 1989). Our main criteria of development of new male sterile line is good productivity, highest level of morphological uniformity, stable male sterility in diverse environments, short/medium plant height, synchronous flowering, good open-pollinated seed set and disease resistance particularly downy mildew.

The cytoplasmic diversification encompass other sources of cytoplasm within A1 cytoplasm and search for new sources and their utilization in the development of elite hybrids will certainly the risk of single cytoplasm hybrids. Thus, an ambitious male sterility cytoplasmic diversification programme was launched at CCS HAU, Hisar in 1984. Thirty-seven male sterile lines involving diverse cytoplasm were developed during 1984-2002 and are being utilized in hybrid breeding programme. Out of these 37, 19 CMS lines are on A_1,

Table 1. Pedigree and origin of HAU male sterile lines of pearl millet

S. No.	MS Lines	Pedigree	CMS system	Year of development
1	HMS 1A	DSA x H77/90/4-5	DSA	1986
2	HMS 2A	DSA x H77/833-2	DSA	1988
3	HMS 3A	DSA x HC 715	DSA	1988
4	HMS 4A	DSA x HC 715	DSA	1988
5	HMS 5A	843A x H77/45-6-4	A_1	1990
6	HMS 6A	841A x 54	A_1	1990
7	HMS 7A	81A x 35	A_1	1990
8	HMS 8A	81A x 52	A_1	1990
9	HMS 9A	843A x 44	A_1	1990
10	HMS 10A	DSA x HC 715 (653 x 11)	DSA	1993
11	HMS 11A	DSA x HC 715(563 x 564/1)	DSA	1994
12	HMS 12A	81A x 75-211 (557x581)	A_1	1994
13	HMS 13A	81A x SPF8-16	A_1	1997
14	HMS 14A	862A x SPF8-23	A_1	1997
15	HMS 15A	862A x SPF8-41	A_1	1997
16	HMS 16A	HMS 7A x SPF8-35	A_1	1999
17	HMS 17A	HMS 8A x 869	A_1	1999
18	HMS 18A	HMS 5A x 854	A_1	1999
19	HMS 19A	MS88004A x PHT 79	A_1	1999
20	HMS 20A	Pb 302A2 x SPF8-32	A_2	1999
21	HMS 21A	Pb 302A2 x 1275	A_2	1999
22	HMS 22A	HMS 2A x H78/711	DSA	1999
23	HMS 23A	HMS 3A x H78/711	DSA	1999
24	HMS 24A	HMS 3A x INB 748	DSA	1999
25	HMS 25A	HMS 4A x G73-107	DSA	1999
26	HMS 26A	HMS 5A x HB98/39	A_1	2000
27	HMS 27A	HMS 5A x H77/122	A_1	2001
28	HMS 28A	81A4 x H78/711	A_4	2001
29	HMS 29A	81A5 x CSSC 46-2	A_5	2001
30	HMS 30A	81Aegp x ICR 161	A_{egp}	2001
31	HMS 31A	81A4 x HTP 31	A_4	2002
32	HMS 32A	95111A x 98/174	A_1	2002
33	HMS 33A	81A x 98/44	A_1	2002
34	HMS 34A	81A x 98/203	A_1	2002
35	HMS 35A	81A x 1275	A_1	2002
36	HMS 36A	81A4 x HB98/213	A_4	2002
37	HMS 37A	81A4 x (90/4-5x551/4)	A_4	2002

2 on A_2, 4 on A_4, 1 on A_5, 1 on A_{egp} and 10 on DSA system of sterility. The brief account of pedigree and origin of HAU male sterile lines is presented in Table 1.

Materials and Methods

All the package and practices were followed to raise these CMS lines. The data were recorded on five competitive plants selected in each genotype. The following traits were recorded: plant height (in cm from ground to the ear tip), effective tillers/plant (number of tillers contributing to yield), days to 50% flowering (days from sowing to the start of 50% plants flowering), nodal tillers (tillers emerged from nodes), number of nodes (total nodes from the base of the plant up to the peduncle), nodal hairs (hairs present on the nodes), nodal color, inter-node color (pigment present at node at dough stage), leaf length (measured in cm from the base to the tip of the leaf below the flag leaf), leaf width (cm), leaf color (observed at head emergence), sheath pigmentation, blade pigmentation, midrib color, sheath hair, blade hair, ligule hair, spike length (in cm from the base to the spike tip on the primary tillers), spike girth (thickness of the spike in cm), spike shape, spike density, spike exertion, bristles (pubescence present on the spike), tip sterility (empty tip of spike), peduncle length (measured in cm from the flag leaf ligule to the spike base), anther color, flag leaf angle, seed color, 1000-grain weight (weight of 1000 grains dried at room temperature), maturity (days), downy mildew, smut, over all plant aspect and lodging susceptibility.

The classification of 33 CMS lines was done on the basis of plant height and days to 50% flowering. On the basis of plant height all the CMS lines were grouped into 4 categories, *viz.*, double dwarf (<100 cm), dwarf (101-120 cm), medium tall (121-140 cm) and tall (>141 cm). Based on days to 50% flowering 3 categories were made, *viz.*, early (45 days), medium late (46-50 days) and late (>51 days). The characterization and classification of HAU male sterile lines were done as per the IBPGR descriptors (Anonymous, 1981). for 34 traits (Table 2).

Table 2. Chief descriptive, morphological and botanical characters of HAU male sterile lines of pearl millet

S.No.	Characters	HMS 1A	HMS 2A	HMS 3A	HMS 4A	HMS 6A	HMS 7A	HMS 8A	HMS 9A	HMS 10A
1	Plant heigh (cm)	120	110	124	125	121	108	120	103	121
2	Effective tillers (No.)	4.0	5.0	4.2	4.2	3.6	4.2	3.8	3.3	5.1
3	Days to 50% flowering	46.3	46.8	44.0	46.0	50.0	50.2	50.8	50.0	46.0
4	Nodal tillers	P	P	P	P	A	P	A	P	P
5	No. of nodes	7	8	7	7	6	7	9	8	6
6	Nodal hairs	P	P	P	P	A	A	A	A	P
7	Nodal color	Pigmented	Green	Green	Green	Green	Pigmented	Green	-	Green
8	Internode color	Green	Green	Green	Green	Dull white	Greenish white	Green	Green	Green
	Leaf									
9	Length (cm)	41	46	50	48	58	59	61	54	50
10	Width (cm)	2.5	2.5	3.0	3.5	4.0	3.0	3.0	3.5	3.0
11	Color	Green	Green	Green	Green	Dark green	Dark green	Green	Green	Green
12	Sheath pigmentation	A	A	A	A	A	A	A	A	A
13	Blade pigmentation	A	A	A	A	A	A	A	A	A
14	Midrib color	Dull white	Dull white	Dull white	Dull white	Dull white	Greenish white	Dull white	Dull white	Dull white
15	Sheath hair	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy	hairy	Non-hairy	hairy	Non-hairy
16	Blade hairs	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy	hairy	Non-hairy	hairy	Non-hairy
17	Ligule hair	Prominent	Non-hairy	Present	Present	Present	Prominent	Prominent	Present	Present
	Spike									
18	Length (cm)	17.4	11.5	21.9	23.3	21.8	17.0	23.8	23.2	17.1
19	Girth (cm)	7.0	6.0	6.0	6.0	6.5	7.5	6.5	7.5	5.0
20	Shape	Lanceolate	Thin lanceo candle	Lanceo candle	Cylindro candle	Candle	Lanceocandle	Candle	Candle	Candle
21	Density	Dense	Dense	Dense	M. dense	Dense	Dense	Dense	Dense	Dense
22	Exertion	Complete	Complete	Complete	Complete	Complete	Complete	Complete	Complete	Complete
23	Bristles	A	A	A	A	A	A	A	A	A
24	Tip sterility	A	A	A	A	P	P	A	A	A
25	Peduncle length (cm)	24	20	29	27	34	28	29	25	22
26	Flag leaf angle	Erect	Intermediate	Erect	Erect	Pendent	Erect	Erect	Erect	Intermediate
27	Seed color	Light brown	Yellowish brown	Grey	Grey	Light brownish	Brown	Light brownish	Brown	Brownish grey
28	Seed shape	Obovate	Obovate	Obovate	Globular	Globular	Obovate	Obovate	Globular	Obovate
29	1000-grain wt (g)		7.0	8.1	9.2	8.9	6.6	7.5	6.7	6.6
30	Maturity (days)	74	75	74	76	77	78	77	78	75
31	Downy mildew									
32	Smut	Yes	No	No	Yes	No	No	No	Yes	No
33	Overall plant aspect	Good	Good	Good	Good	V. Good	V. Good	V. Good	V. Good	No
34	Lodging susceptibility	R	R	R	R	R	R	R	R	R

Contd. Table 2

S. No.	Characters	HMS 13A	HMS 14A	HMS 16A	HMS 17A	HMS 18A	HMS 19A	HMS 20A	HMS 21A	HMS 22A
1	Plant height (cm)	140.2	125	140	115	130	130	110	150	1'70
2	Effective tillers (No.)	7.0	3.0	6.0	4.0	5.0	3.0	4.0	3.0	4.0
3	Days to 50% flowering	54.3	44.0	49.0	49.0	44.0	45.0	50.0	46.0	49.0
4	Nodal tillers	P	A	A	A	A	A	A	A	A
5	No. of nodes	7.0	7.3	7.7	8.3	8.0	7.7	7.7	8.3	9.3
6	Nodal hairs	A	A	A	A	P, dense	P	A	A	P, on upper
7	Nodal color	Green	Green	Green	Green	Green	Pigmented	Pigmented	Green	Green
8	Internode color	Green	Green	Green	Green	Green	Green	Green	Green	Green
	Leaf									
9	Length (cm)	58	53	60	48	54	57	44	53	56
10	Width (cm)	4.0	4.0	3.0	4.0	4.0	4.0	2.5	4.5	6.0
11	Color	Dark Green	Green	Green	Green	Green	Green	Green	-	Green
12	Sheath pigmentation	A	P	A	A	A	A	A	A	P
13	Blade pigmentation	A	A	A	A	P	A	A	A	A
14	Midrib color	Dull white	Dull white	Green	Dull white	White	White	White	White	White
15	Sheath hair	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy
16	Blade hairs	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Yes, dense	Non-hairy	Non-hairy	hairy	on upper side
17	Ligule hair	P	P	P	P	P	P	P	P	P
	Spike									
18	Length (cm)	20.4	33.0	16.0	24.0	27.0	21.0	22.0	23.0	23.0
19	Girth (cm)	7.0	8.0	7.0	8.0	4.5	8.0	8.5	6.5	6.5
20	Shape	Candle	Semi conical to candle	Lanceolate	Lanceolate	Cylindrical	Lanceolate	Candle	Candle	Candle
21	Density	M. dense	Loose	Dense	Dense	V. dense	Dense	M. Dense	Dense	Dense
22	Exertion	Complete	Complete	Complete	Complete	Complete	Complete	Complete	Complete	Complete
23	Bristles	A	A	A	A	A	A	A	A	A
24	Tip sterility	A	A	P	P	A	A	P	A	A
25	Flag leaf angle	Pendant	Intermediate	Drooping	Drooping	Drooping	Erect	Intermediate	Intermediate	Drooping
26	Peduncle length (cm)	37	31	31	32	35	25	30	27	24
27	Seed color	Brownish grey	Brown	Brownish grey	Grey	Deep brown	Yellowish grey	Light yellowish	Grey	Yellowish grey
28	Seed shape	Globular	Globular	Globular	Globular	Globular	Obovate	Globular	Globular	Obovate
29	1000-grain wt. (g)	9.0	8.8	8.9	8.0	5.0	5.0	6.0	8.0	4.3
30	Maturity (days)	80	72	76	76	70	75	74	75	80
32	Downy mildew	R	R	R	R	R	R	R	R	R
32	Smut	R	R	R	R	R	R	R	R	R
33	Overall plant aspect	V. good	Good	V. good	V. good	V. Good	Good	Good	Good	V. good
34	Lodging susceptibility	R	R	R	R	R	R	R	R	R

contd. Table 2

S. No.	Characters	HMS 23A	HMS 24A	HMS 25A	HMS 26A	HMS 27A	HMS 28A	HMS 29A	HMS 30A	HMS 31A
1	Plant height (cm)	140	220	145	140	145	150	140	155	150
2	Effective tillers (No.)	3	3	3	5	5	6	4	3	4
3	Days to 50% flowering	48	55	44	52	50	52	52	56	46
4	Nodal tillers	A	P	A	A	P	A	A	P	P
5	No. of nodes	7.7	10.0	8.0	6.0	8.0	8.0	8.0	11.0	8.0
6	Nodal hairs	A	P	P	A	A	A	A	P	P
7	Nodal color	Green	Green	Green	Green	Green	Green	Green	Green	Green
8	Internode color	Green	Green	Green	Green	Green	Green	Green	Green	Green
	Leaf									
9	Length (cm)	42	64	57	51	50	49	44	47	44
10	Width (cm)	4.0	5.0	4.0	4.0	3.0	3.0	3.5	4.5	2.5
11	Color	Green	Green	Green	Green	D. green	Green	Green	D. green	Green
12	Sheath pigmentation	A	A	A	A	A	A	A	A	A
13	Blade pigmentation	A	A	A	A	A	A	A	A	A
14	Midrib color	White	White	White	White	Green	Green	Green	Dull white	Dull white
15	Sheath hair	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy
16	Blade hairs	Non-hairy	Non-hairy	Non-hairy	Hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy
17	Ligule hair	P	P	P	P	P	P	P	P	P
	Spike									
18	Length (cm)	22	19	23	18	24	14	29	18	13
19	Girth (cm)	7.0	6.5	7.5	8.0	6.0	10.0	9.0	8.0	6.0
20	Shape	Candle	Cylindrical	Lanceolate	Cylindrical	Lanceolate	Candle	Spindle	Cylindrical	Candle
21	Density	Dense	Dense	Dense	Dense	Dense	Dense	V. dense	V. dense	Dense
22	Exertion	Complete	Complete	Complete	Complete	Complete	Complete	Complete	Complete	Complete
23	Bristles	A	A	A	A	P	A	A	A	A
24	Tip sterility	A	A	P	P	A	A	P	A	A
25	Flag leaf angle	Drooping	Drooping	Drooping	Drooping	Erect	Drooping	Drooping	Erect	Drooping
26	Peduncle length (cm)	21	23	29	25	20	27	21	26	26
27	Seed color	Yellowish grey	Grey	Browinsh Grey	Yellowish Grey	Grey	Grey	Yellowish grey	Light grey	
28	Seed shape	Hexagonal	Obovate	Hexagonal	Hexagonal	Globular	Hexagonal	Obovate	Hexagonal	
29	1000-grain wt (g)	6.45	5.4	6.2	6.0	7.0	5.0	4.0	4.6	

30	Maturity (days)	80	85	69	80	76	78	76	86	74
33	Downy mildew	R	R	R	R	R	R	R	R	R
32	Smut	R	R	R	R	R	R	R	R	R
33	Overall plant aspect	V. good	V. good	V. good	V. good	V. good	V. good	V. good	V. good	Good
34	Lodging susceptibility	R	R	R	R	R	R	R	R	R

contd. Table 2

S. No.	Characters	HMS 32A	HMS 33A	HMS 34A	HMS 35A	HMS 36A	HMS 37A
1	Plant height (cm)	125	105	105	155	95	150
2	Effective tillers (Nos.)	4.0	6.0	3.0	4.0	4.5	5.0
3	Days to 50% flowering	49	50	49	48	48	50
4	Nodal tillers	A	A	A	A	A	P
5	No. of nodes	7	6	7	8	6	10
6	Nodal hairs	A	A	A	A	A	A
7	Nodal color	Green	Green	Green	Green	Green	Green
8	Internode color	L. green	Green	Green	Green	Green	Green
	Leaf						
9	Length (cm)	49	42	47	47	42	46
10	Width (cm)	4	2.0	3.5	3.0	2.5	3.0
11	Color	Green	D.green	Green	D.green	Green	D.green
12	Sheath pigmentation	A	A	A	A	A	A
13	Blade pigmentation	A	A	A	A	A	A
14	Midrib color	Dull white	white	Green	White	Green	White
15	Sheath hair	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy	Non-hairy
16	Blade hairs	Non-hairy	hairy	Non-hairy	Hairy	Non-hairy	Non-hairy
17	Ligule hair	P	P	P	A	A	A
	Spike						
18	Length (cm)	20	15	20	22	17	20
19	Girth (cm)	9	6.5	10.0	7.0	8.0	8.5
20	Shape	Lanceolate	Candle	Candle	Cylindrical	Lanceocandle	Lanceocandle
21	Density	Dense	Dense	Dense	Dense	M. dense	Dense
22	Exertion	Complete	Complete	Complete	Complete	Complete	Complete
23	Bristles	A	A	A	A	A	A
24	Tip sterility	A	A	A	A	A	A
25	Flag leaf angle	Erect	V. erect	Drooping	Drooping	Erect	Erect
26	Peduncle length (cm)	30	21	31	25	23	17
27	Seed color	Yellowish brown	Globular	Globular	Obovate	Globular	Globular
28	Seed shape	Hexagonal	Grey	Grey	Grey	White	Grey
29	1000-grain wt. (g)	10.4	7.1	12.1	7.2	10.7	10.2
30	Maturity (days)	78	79	78	76	74	78
34	Downy mildew	R	R	R	R	R	R
32	Smut	R	R	R	R	R	R
33	Overall plant aspect	V. good	V. good	V. good	V. good	Good	Good
34	Lodging susceptibility	R	R	R	R	R	R

A = Absent, P = Present, R = Resistant, T = Tolerance, S = Susceptible

Results and Discussion

Characterization and Classification

Maximum variability was recorded for plant height (90-220 cms), days to 50% flowering (44-56 days), effective tillers per plant (3-7), spike length (11.5-33 cms) and spike girth (4.5-10 cms). Further, these lines are classified based on plant height and days to 50% flowering (Table 3). On the basis of plant height 10 CMS lines are tall, 13 medium tall, 9 dwarf and 1 double dwarf (D_2Dwarf). Based on days to 50% flowering 6 CMS lines are early, 20 medium late and 7 late. This classification of CMS lines into groups is on the basis of data recorded at Hisar location. So users can reclassify selections based on their local conditions. When accessions are grown away from their place of origin, morpho-agronomic characters may change as suggested by Appa Rao *et al.* (1985) in case of spike size in pearl millet.

Evaluation

Evaluation of CMS lines is an important aspect to assess their effectiveness in hybrid breeding programme. Preliminary evaluation consists of recording a limited number of additional agronomic traits though desirable by a consensus of users. Hence, all the CMS lines are being evaluated continuously every year in the field as well as in sick plot conditions. Stability of male sterility across seasons and locations is the most essential requirement of a commercially viable CMS system. There are several reports on the breakdown of A_1 system male sterility. A_1, A_4 and A_5 system is considered to be the most stable system in comparison to A_2 and A_3 (Rai *et al.*, 1999). These lines are being tested for percentage of pollen shedders, seed set under bag, downy mildew incidence and other morphological traits. Based on these data the defective lines are being rejected. Based on characterization planning can be done for the development of hybrid for a specific traits.

Table 3. Classification of HAU male sterile lines based on plant height and days to 50% flowering

Character	Group	Number	CMS system	CMS lines
Plant height	D_2Dwarf (<100 cm)	1	A_4	HMS 36A
	Dwarf (101-120 cm)	9	A_1	HMS 7A, HMS8A, HMS9A, HMS17A, HMS33A, HMS 34A
			A_2	HMS 20A
			DSA	HMS 1A, HMS 2A
	Medium Tall (121-140 cm)	13	A_1	HMS 6A, HMS 13A, HMS 14A, HMS 16A HMS 18A, HMS 19A, HMS 26A, HMS 32A
			A_5	HMS 29A
			DSA	HMS 3A, HMS 4A, HMS 10A, HMS 23A
	Tall (>140 cm)	10	A_1	HMS 27A, HMS 35A
			A_2	HMS 21A
			A_4	HMS 28A, HMS 31A, HMS 37A
			A_{cep}	HMS 30A
			DSA	HMS 22A, HMS 24A, HMS 25A
Days to 50% flowering	Early (<45 days)	6	A_1	HMS 14A, HMS 18A HMS 19A
			DSA	HMS 2A, HMS 3A, HMS 25A
	Mid-late (36-50 days)	20	A_1	HMS 6A, HMS 7A, HMS 9A, HMS 16A, HMS 17A, HMS 27A, HMS 32A, HMS 33A, HMS 34A, HMS 35A
			A_2	HMS 20A, HMS 21A
			A_4	HMS 31A, HMS 36A, HMS37A
			DSA	HMS 1A, HMS 4A, HMS 10A, HMS 22A, HMS 23A
	Late (>51 days)	7	A_1	HMS 8A, HMS 13A, HMS 26A
			A_4	HMS 28A
			A_5	HMS 29A
			A_{cep}	HMS 30A
			DSA	HMS 24A

Registration and Notification

Eight male sterile lines, namely, HMS 1A, HMS 2A, HMS 3A, HMS 4A, HMS 7A, HMS 8A, HMS 9A and HMS 6A have been registered with National Bureau of Plant Genetic Resources in 1999. These lines have been notified as INGR 98037 to INGR 98043 and INGR 99006, respectively, in Indian J. Genet. 1999. Vol. 53. Two male sterile lines HMS 10A and HMS 13A has been given National Identity Number IC 296897 and IC 296898, respectively.

Although, some of these CMS lines have been utilized in breeding superior grain hybrids, yet emphasis is further needed to exploit more CMS lines (on diverse sources) to widen the cytoplasmic base of hybrids and to minimize the risk of becoming vulnerable to existing or unforeseen diseases. The characterization and classification of CMS lines will help the breeders in formulating the programme for the development of hybrids for a specific trait.

References

Allard RW (1960) *Principles of Plant Breeding*. John Wiley, New York.

Anonymous (1981) *Descriptors for Pearl Millet*. International Board of Plant Genetic Resources, Rome, 34p.

Appa Rao S, MH Mengesha and DS Sharma (1985) Collection, evaluation of pearl millet (*Pennisetum americanum*) germplasm from Ghana. *Econ. Bot.* **39:** 25-38.

Burton GW (1965a) Pearl millet Tift 23A released. *Crops soils* **18:** 19.

Burton GW (1965b) Cytoplasmic male sterile pearl millet Tift 18A released. *Crops soils* **18:** 19.

Burton GW and DS Athwal (1967) Two additional sources of cytoplasmic male sterility in pearl millet and their relationship to Tift 23A. *Crop Sci.* **7:** 209-211.

Hanna WW (1989) Characteristics and stability of a new cytoplasmic nuclear male sterility sources in pearl millet. *Crop Sci.* **29:** 1457-1459.

House LR (1980) *A Guide to Sorghum Breeding*. ICRISAT, Hyderabad.

Rai KN, IS Khairwal and HP Yadav (1999) Pearl millet (*Pennisetum glaucum*) hybrid parents research and development. Advances in Agril. Res. in India **XI:** 1-18.

Sharma JR (1980) A note on conversion of new male sterile lines by limited back crossing in pearl millet (*Pennisetum typhoides* (Burm.) S & H). *Curr. Sci.* 413-514.

Genetic Association Analysis in Asiatic Radish (*Raphanus sativus* L.)

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Genotypic and phenotypic coefficient of variation, heritability, expected genetic advance and character association of root weight and its contributing characters were studied in 18 diverse genotypes of Asiatic radish (*Raphanus sativus* L.) at Indian Institute of Vegetable Research, Varanasi during spring/summer season 2000-2001. Wide range of genetic variability was observed in all the 18 genotypes of the radish for almost all characters. Relatively high genotypic and phenotypic coefficients of variation were recorded for leaf size, leaf weight/plant, leaf length, root size and leaf: root weight ratio. Leaf length, leaf size, leaf weight/plant, leaf: root length ratio and leaf: root weight ratio has high genetic advance as percent of mean alongwith high heritability. Correlation studied revealed that root weight should positively and significantly correlated with plant height, leaf length, leaf width, leaf size, leaf weight/plant, root length, root thickness, root size and leaf: root weight ratio, while negative and significant correlation were found with root shape at both phenotypic and genotypic levels. The characters *viz.* leaf weight, leaf length and root length showed strong positive direct effects while number of leaves/plant, root thickness and leaf size had less direct effects or root weight.

Key Words: Asiatic radish (*Raphanus sativus* L.), Correlation, GCV, Genetic Advance, Heritability, Path Analysis, PCV,

Asiatic radish (*Raphanus sativus* L.) is an important root vegetable grown for its enlarged fleshy roots and tender foliage. It is cultivated throughout the country and is consumed by all sections of people. Due to high yielding and early maturing nature, it can be easily fit in different cropping systems to get higher returns/unit area and time. A wide range of variability is available for root and shoot characters in radish, which may be utilized for its genetic improvement. Genetic improvement of crop is largely depending on the magnitude of genetic variability and the extent to which desirable traits are heritable. Lal and Srivastava (1975) reported high phenotypic and genotypic variability, heritability and genetic advance by utilizing few lines. Till now very little information is available on genetic association in this crop. Therefore, an attempt was made in the present investigation to estimate the extent of variability, heritability, genetic advance, correlation and path analysis by utilizing 18 divergent lines of Asiatic radish.

Materials and Methods

The experiment was carried out at the Research Farm, Indian Institute of Vegetable Research, Varanasi during spring/summer season 2000-2001. Eighteen divergent genotypes (lines) *viz.*, Moto Towai, IIVR-1, Sungro Chetki, IIVR-2, Hill Queen, IIVR-3, Hong Mong, Local-10, Pusa Chetki, Japanese White, Punjab Local, NIC-1569, C-2, NIC-7214, NIC-7215, Chinese Pink. Mooli Early and Mino Early were grown in randomized block design with three replications. Recommended cultural practices were adopted for proper growth and stand of the crop. The observations were recorded on five randomly selected plants on different characters *viz.*, plant height (cm), number of leaves/plant, leaf length (cm), leaf width (cm), leaf size (cm^2), leaf shape, leaf weight/plant (g), root length (cm), root thickness (cm), root size (cm^2), root shape, leaf: root length ratio, leaf: root weight ratio and root weight (g). The mean value obtained were used for determining phenotypic coefficient of variation and genotypic coefficient of variation (Burton and De Vane, 1953), heritability (Hanson *et al.*, 1956) and expected genetic advance (Johnson *et al.*, 1955). The correlation coefficients were calculated as per methods given by Al-Jibouri *et al.* (1958). The path analysis was performed according to the methods followed by Dewey and Lu (1959).

Results and Discussion

The analysis of variance revealed that all the characters were found statistically significant. The mean, range, genotypic and phenotypic coefficient of variation, heritability, genetic advance (GA) and GA as per cent of mean are given in Table 1. In the present study, the range of variation was high for leaf size followed by root weight, root size and leaf weight/plant. The genotypic and phenotypic variances were high for leaf size, leaf weight/plant, root size and root weight. Leaf size (27.78, 30.66 cm^2), leaf weight/plant (24.87, 27.60

Table 1. Estimates of range, mean, genotypic and phenotypic variance, (σg & σp), genotypic and phenotypic coefficient of variation (GCV, PCV), heritability, genetic advance and genetic advance as percent of mean for different characters in radish

Characters	Range		Mean	SE±	MSS	5%					Heritability	GA	GA% of
	Max.	Min.			Values		σg	σp	GCV	PCV	(b.s.)		mean
Plant height (cm)	75.17	51.72	59.17	2.60	141.14	2.60	43.65	53.85	11.17	12.40	81.06	12.25	20.71
Number of leaves/plant	14.97	11.93	13.87	0.73	2.86	0.73	0.69	1.48	5.99	8.77	46.62	1.17	8.42
Leaf length (cm)	44.85	23.93	31.56	1.49	103.60	1.49	33.42	36.79	18.32	19.22	90.84	11.35	35.96
Leaf width (cm)	8.83	6.00	7.57	0.58	2.41	0.58	0.64	1.14	10.57	14.11	56.14	1.24	16.38
Leaf size (cm^2)	391.53	160.63	239.36	26.95	13972.2	626.95	4294.42	5384.14	27.78	30.66	79.76	120.56	50.37
Leaf shape	5.18	3.19	4.11	0.26	0.96	0.26	0.29	0.38	13.10	15.20	76/32	0.97	23.58
Leaf wt./plant (g)	110.37	53.00	76.94	7.51	1183.03	7.15	366.12	450.82	24.87	27.60	81.21	35.52	46.17
Root length (cm)	32.77	25.20	28.19	1.89	16.27	1.89	3.63	9.02	6.76	10.65	40.24	2.49	8.83
Root thickness (cm)	4.50	2.97	3.67	0.30	0.97	0.30	0.28	0.42	14.42	17.66	66.67	0.89	24.25
Root size (cm^2)	141.38	78.44	101.86	11.69	1295.43	11.69	363.37	568.69	18.71	23.41	63.90	31.39	30.82
Root shape	9.82	6.07	7.87	0.89	4.40	0.89	1.07	2.26	13.14	19.10	46.35	1.47	18.63
L: R length ratio	1.48	0.82	1.15	0.08	0.11	0.08	0.034	0.043	16.03	18.03	79.07	0.34	29.37
L : R wt. Ratio	0.82	0.43	0.59	0.06	0.04	0.06	0.012	0.017	18.57	22.10	70.59	0.19	32.14
Root wt. (g)	149.33	117.67	128.67	5.38	277.12	5.38	77.87	121.38	6.86	8.56	64.15	14.56	11.32

*, ** Significant at 5% and 1% levels, respectively GA = Genetic Advance L = Leaf, R = Root G = genotypic
Wt. = Weight P = Phenotypic

g), root size (18.71, 23.41 cm^2), leaf: root weight ration (1857,22.10), leaf length (18.32, 19.22) and leaf: root length ratio (16.03, 18.03) had high genotypic and phenotypic coefficient of variation value indicating the nature of genetic variability for these characters. The characters possessing high genotypic coefficients of variation value have better scope of improvement through selection. The influence of the environment on each trait could be determined on the basis of difference between phenotypic and genotypic coefficient of variation. The high difference between phenotypic and genotypic coefficient of variation for characters such as leaf size, leaf weight/plant and root size has shown wider range of variability and high covariance, therefore, indicating ample scope for effective improvement in these characters through selection. Other characters with low coefficient of variation are indication of less scope of selection. Similar results were reported by Pandey *et al.* (1981) and Khan *et al.* (1983) Characters such as plant height, leaf length, root weight, leaf: root length ratio and leaf shape had nearly equal genotypic and phenotypic coefficient of variation values indicating least influence of the environment on their expression. In such situation, selection can be effective on the basis of the phenotype alone with equal probability of success.

On the basis of genotypic coefficient of variation alone, it is not possible to determine the amount of heritable variation. It can be find out with greater degree of accuracy when heritability in conjunction with genetic advance is studied (Dudley and Moll, 1969). In the present study, all the characters showed high to moderate heritability. The high heritability was recorded for leaf length (90.84) followed by leaf weight/ plant (81.21), plant height (81.06), leaf size (79.76), leaf: root length ratio (79.07) and leaf shape (76.32). The characters which exhibited high heritability, suggested that the selection will be more effective whereas the characters showing low heritability indicated that the selection will be difficult as the expression of genotypes will be affected by the environmental factors (Arumugam and Muthu Krishnan, 1975). The higher heritability value may be attributed to additive gene action (Majumdar *et al.*, 1969). The estimate of genetic advance expressed as percentage of mean showed a wide range from 8.42 for number of leaf/plant to 50.37 for leaf size. Thus, the highest genetic advance was expressed by number of leaves/ plant followed by leaf weight/plant, leaf length, leaf: root weight ratio and root size. High heritability estimates in conjunction with high genetic advance is more useful than heritability alone in predicting the results and for selecting the best individual. High heritability alongwith high genetic advance observed for leaf length, leaf size, leaf weight/plant, leaf : root length ratio and leaf : root weight ratio indicated greater scope for improvement for the characters in breeding programme (Sirohi and Kutty, 2000; Singh *et al.*, 2001).

Estimates of correlation coefficients among yield contributing characters in radish population at genotypic and phenotypic level are presented in Table 2. In present investigation, root weight was found to be significantly and positively associated with plant height, leaf length, leaf width, leaf size, leaf weight/plant, root length, root

Table 2. Phenotypic and genotypic correlation coefficients for different traits in radish

Characters	No. of leaves/ plant	Leaf length (cm)	Leaf width (cm)	Leaf size (cm2)	Leaf shape	Leaf wt/ plant (g)	Root length (cm)	Root thickness (cm)	Root size (cm2)	Root shape	L : R length ratio	L : R wt ratio	Root wt (g)
Plant height (cm)	**0.217**	**0.896****	**0.615****	**0.881****	**0.518****	**0.734****	**0.614****	**0.721****	**0.860****	**-0.288**	**0.547***	**0.657****	**0.508***
	0.314	0.954**	0.754**	0.968**	0.691**	0.850**	0.598**	0.830**	0.902**	-0.586*	0.780**	0.778**	0.797
No. of leaves/plant		**0.301**	**0.275**	**0.318**	**0.111**	**0.483***	**-0.073**	**-0.331**	**0.225**	**-0.331**	**0.312**	**0.540***	**0.134**
		0.340	0.375	0.390	0.152	0.569**	0.067	0.298	0.266	-0.213	0.317	0.624**	0.326
Leaf length (cm)			**0.602****	**0.933****	**0.683****	**0.785****	**0.233**	**0.779****	**0.732****	**-0.562***	**0.852****	**0.719****	**0.515***
			0.696**	0.971**	0.810**	0.847**	0.329	0.881**	0.844**	-0.767	0.933**	0.823**	0.647**
Leaf width (cm)				**0.840****	**-0.164**	**0.533***	**0.337**	**0.468***	**0.521***	**-0.179**	**0.407**	**0.500***	**0.332**
				0.848**	0.149	0.607**	0.569*	0.575*	0.669**	-0.230	0.525*	0.571*	0.528*
Leaf size (cm^2)					**0.381**	**0.758****	**0.322**	**0.737****	**0.736****	**-0.452****	**0.737****	**0.694****	**0.503***
					0.647**	0.829**	0.469*	0.834**	0.854**	-0.615**	0.849**	0.801**	0.660**
Leaf shape						**0.476***	**-0.069**	**0.509***	**0.385**	**-0.537***	**0.705****	**0.427**	**0.323**
						0.660**	-0.042	0.729**	0.594*	-0.865**	0.872**	0.664**	0.431
Leaf wt/plant (g)							**0.193**	**0.633****	**0.599****	**-0.484***	**0.658****	**0.946****	**0.615****
							0.384	0.701**	0.729**	-0.555*	0.742**	0.971**	0.806**
Root length (cm)								**0.226**	**0.640****	**0.376**	**-0.306**	**0.131**	**0.219**
								0.381	0.668	0.099	-0.302	0.229	0.701**
Root thickness (cm)									**0.889****	**-0.792****	**0.644****	**0.527***	**0.533***
									0.941**	-0.885**	0.795**	0.587*	0.777**
Root size (cm^2)										**-0.450**	**0.373**	**0483***	**0.535**
										-0.676**	0.644**	0.579**	0.777**
Root shape											**-0.753****	**-0.421**	**-0.379**
											-0.858**	-0.492*	-0.520*
L : R length ratio												**0.625****	**0.387**
												0.775**	0.421
L : R weight ratio													**0.332**
													0.642**

*, **, Significant at 5% and 1% levels, respectively L = Leaf, R = Root
Figures presented in bold are phenotypic values

thickness, root size and leaf : root weight ratio, while negative and significant correlation were found with root shape at genotypic and phenotypic levels. Therefore, these characters should be taken into consideration while making selection for improvement of root yield. Leaf: root weight ratio showed significant and positive correlations with all the characters except root length and root shape at both the levels. Muthu Krishan and Arumugam (1977) and Khan *et al.* (1983) were found significant positive association between yield and leaf length, root length and root weight and leaf weight.

Path coefficient at phenotypic level revealed that leaf weight/plant (2.988), leaf length (0.656), root length (0.152), leaf size (0.081), root thickness (0.049) and number of leaves/plant (0.046) had highest positive direct effect on root weight, indicating these are the main contributors to yield (Table 3). Leaf weight had high direct positive effects towards root weight whereas number of leaves/plant (0.049), root thickness (0.049) and leaf size (0.081) had less direct effects on root weight. High direct negative effects were observed for leaf: root weight ratio (-2.469), root size (-0.453), leaf:

Table 3. Direct (Diagonal) and indirect effect of leaf and root attribute on root weight (phenotypic level)

Characters	Plant height	No. of leaves	Leaf length	Leaf width	Leaf size	Leaf shape	Leaf weight	Root length	Root thickness	Root size	Root shape	L : R length	L : R wt ratio	Pheno corrl. with root wt
Plant height (cm)	-0.108	0.010	0.587	-0.103	0.071	-0.089	2.193	0.093	0.035	-0.390	0.071	-0.223	-1.640	0.508*
No. of leaves/plant	-0.0.23	0.046	0.197	-0.046	0.026	-0.019	1.444	-0.011	0.016	-0.102	0.082	-0.127	-1.348	0.134
Leaf length (cm)	-0.097	0.014	0.656	-0.101	0.076	-0.117	2.345	0.035	0.038	-0.332	0.139	-0.347	-1.795	0.515*
Leaf width (cm)	-0.067	0.013	0.395	-0.167	0.068	0.028	1.593	0.051	0.023	-0.236	0.014	-0.166	-1.248	0.332
Leaf size (cm^2)	-0.095	0.015	0.612	-0.141	0.081	-0.065	2.266	0.049	0.036	-0.334	0.112	-0.300	-1.732	0.503*
Leaf shape	-0.056	0.005	0.448	0.027	0.031	-0.171	1.421	-0.011	0.025	-0.175	0.133	-0.287	-1.067	0.323
Leaf weight (g)	-0.076	0.022	0.515	-0.089	0.061	-0.081	2.988	0.029	0.031	-0.272	0.120	-0.268	-2.362	0.615**
Root length (cm)	-0.066	-0.003	0.153	-0.56	0.026	0.012	0.577	0.152	0.011	-0.290	-0.093	0.125	-0.326	0.219
Root thickness (cm)	-0.078	0.015	0.511	-0.078	0.060	-0.087	1.891	0.034	0.049	-0.403	0.196	-0.262	-1.315	0.533*
Root size (cm^2)	-0.093	0.010	0.480	0.087	0.060	-0.066	1.790	0.097	0.043	-0.453	0.112	-0.152	-1.206	0.535*
Root shape	0.031	-0.015	-0.368	0.030	-0.037	0.092	-1.445	0.057	-0.039	0.204	-0.248	0.307	1.051	-0.379
L : R length ratio	-0.059	0.014	0.558	-0.068	0.060	-0.121	1.967	-0.047	0.031	-0.169	0.187	-0.407	-1.560	0.387
L : R wt Ratio	-0.071	0.025	0.471	-0.048	0.056	-0.073	2.827	0.020	0.026	-0.219	0.104	-0.225	-2.496	0.332

*, ** Significant at 5% and 1% levels, respectively. The residual effect (Phenotypic) = 0.0188

root length ratio (-0.43), root shape (-2.496), root size (-0.453), leaf: root length ratio (-0.43), root shape (-0.248), leaf shape (-0.17), leaf width (-0.16) and plant height (-0.108) at phenotypic levels.

Root size had positive and significant association with plant height, leaf length, leaf width, leaf size, leaf shape, leaf weight/plant, root length and root thickness. Thus, in selection programme, more emphasis should be given for these characters due to more direct and indirect effect on root weight. In this study, the residual effect was relatively low (0.0188) indicating that adequate characters were utilized for the study. It is also evident that root shape, leaf width, root size, leaf : root weight ratio, leaf : root length ratio, leaf shape and plant height had the negative direct and indirect effect on root weight, thus these characters should be rejected during selection programme.

References

Al-Jobour NA, PA Miller and HR Robinson (1958) Genotypic and environmental variances and co-variance in an upland cotton cross of interspecific origin. *Agron. J.* **50:** 633-636.

Arumugam R and CR Muthu Krishnan (1975) Genetic variability in some quantitative characters of radish. *Indian J. Hortic.* **32:** 179-181.

Burton GW and EW De Vane (1953) Estimating heritability in tall Fescus (*Festuca arundinaces)* from replicated clonal material. *Agron. J.* **45:** 478-481.

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

Dudley JW and RH Moll (1969) Interpretation and uses of estimates of heritability and genetic variance in plant breeding. *Crop Sci.* **9:** 257-262.

Hanson GH, HF Robinson and RE Comstock (1956) Biometerical studies on yield in segregating population of Korean lespedeza. *Agron. J.* **48:** 268-271.

Johnson HW, HF Robinson and RE Comstock (1955) Estimates of genetic and environmental variability in soyabean. *Agron. J.* **47:** 314-318.

Khan MA, BS Dhankhar and G Kalloo (1983) Variability and correlation studies in radish (*Raphanus sativus* L.) *Haryana J. Hortic. Sci.* **12:** 89-95.

Lal S and JP Srivastava (1975) Heritability and genetic advance for root and fruit characters in radish. *Indian J. Hortic.* **32:** 99-93.

Majumdar PK, Prakash Ram and HD Fazlul Haque (1969) Genotypic and phenotypic variability in quantitative characters in groundnut. *Indian J. Genet. Plant Breed.* **29:** 291-296.

Muthu Krishnan CR and R Arumugam (1977) Correlation and regression studies in radish. *Indian J. Hortic.* **34:** 163-164.

Pandey SC, ML Pandita and J Dixit (1981) Genetics of yield and yield contributing characters in radish. *Haryana Agric. Univ. J. Res.* **11:** 384-388.

Singh B, Pandey Sudhakar, G Kalloo and MK Banerjee (2001) Genetic variability in Asiatic radish. *Indian J. Plant Genet. Resour.* **14:** 76-77.

Sirohi PS and C Kutty Narayanan (2000) Genetic analysis of yield and its components in radish. *Veg. Sci.* **27:** 142-144.

Quality Evaluation of some Thailand and Vietnam Scented Rice

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Twenty-two scented rice varieties of Thailand and Vietnam were evaluated at Central Rice Research Institute, Cuttack, for their quality indices. The study revealed that Haw mki Xwai, TD-52, Xiang Gengli, Hsiang Nou-1 and Khao Jao Hawn from Thailand and Tam Thomthankhoa and TamQuthankhoa from Vietnam are good donors for major quality indices. These varieties can be exploited for hybridization programme to produce better quality scented rice.

Key Words: Germplasm, Quality Characters, Scented Rice

Scented rice varieties are very much popular for their grain quality and aroma. Aroma quality of scented rice is a major character which increases the value of rice in international market. The cooking quality are highly indexed by volume expansion, water uptake and linear elongation of kernel. For breeding programme it is essential to identify suitable donor parents to improve the quality status of existing scented rice. The scented rice varieties of Thailand and Vietnam are well known for their qualitative properties. Therefore, in the present study some scented rice germplasm from Thailand and Vietnam were evaluated for their quality performance to identify suitable donors for quality characters to improve the Indian scented rice varieties through hybridization.

Materials and Methods

Twenty-two scented rice varieties collected from Thailand and Vietnam through Directorate of Rice Research, Hyderabad, were evaluated at Central Rice Research Institute, Cuttack for their quality characteristics. Thirty-day-old seedlings were transplanted in a Randomised Block Design with three replications. Recommended package of practices were followed to raise the scented rice varieties. The quality characters were analysed for hulling, milling and head rice recovery percentage as described by Ghosh *et al.*, (1971), kernel length and breadth were measured by digital micrometer and length/breadth ratio was calculated. Alkali spreading value (Little *et al.*, 1958), water uptake and volume expansion (Beachell and Stansel 1963), cooked kernel length was recorded using graph paper, elongation ratio (Azeez and Shafi 1966) and amylose (Juliano 1971) content were measured.

Results and Discussion

The head rice recovery, kernel length and breadth mainly depends upon opaqueness in the endosperm in the grain causes loose packing of starch/protein. The low temperature after flowering is also responsible for grain length (Jennings *et al.*, 1979). The grain with long length and short breadth also affect the head rice recovery. Most of the varieties in the experiment exhibited head rice recovery more than 45% except Jawi Hitan, Khao Luang and Tamduaonghaiduaong (Table 1). RD-15, Xiang Gengli, Khao ManPet, Hawmkaikwai, TamQuthankhoa, Tam thomthankhoa showed higher hulling, milling and head rice recovery percentage. For kernel length and length/breadth ratio Khao Dwak Mali-105, Hsiang Nuo-1, Khao Jao Hawn, Khao Mali, Naipon No-1 and Hawmkikwai showed more than 7.0 mm and 4.0 mm for respective characters among the tested varieties (Table 1).

The alkali spreading value is a major quality parameter which is determined by the digestation of starch by 1.7% KOH in 23 hours. The intermediate digestation means intermediate alkali spreading value where the rice does not become very waxy or very hard. The intermediate alkali value rice are soft to consume. The high ambient temperature after flowering effects the alkali spreading value directly (Jennings *et al.*, 1979). The alkali spreading value ranged from 2.0 (TD 15, Khao Mali) to 7.0 (Patoon Tahni-60). TD 52, Siong Pelandok, Khao Luang, Tamthomthankhoa and Tamduonghaiduong showed intermediate (4.0 to 5.0) alkali spreading value (Table 1).

In basmati rice, water uptake and volume expansion are quality characters directly related with amylose content and these characters determine the cooking quality of rice. The water uptake for different scented rice varieties ranged from 190 (Tamduonghaidoung) to 352 (Patoon Tahni-60) and the volume expansion ranged from 3.5 (Patoon Tahni-60) to 4.81 (Kho Jao Hawn). Khao Manpet, Patoon Tahni-60, Jawi Hitan, Jasmine Scented, Thamthomnamdinh and Tamthomthankhoa

Table 1. Quality indicies in scented rice

Variety	Country	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel Length (mm)	Kernel length/ breadth ratio	Alkali spreading value	Water uptake	Cooked kernel length (mm)	Elongation ratio	Volume expansion	Amylose content %	Grain yield/ plant (g)
RD-15	Thailand	78.05	72.45	63.20	5.40	3.49	2.00	220.00	7.00	1.30	4.14	16.10	4.94
TD-52	Thailand	75.65	70.55	59.50	4.97	3.11	4.00	230.00	8.60	1.73	4.40	19.38	11.60
Khao Dwak Mali-105	Thailand	69.60	64.55	49.45	7.40	4.73	5.25	235.00	11.30	1.53	3.82	16.36	7.65
Hsiang Nuo-1	Thailand	69.20	63.85	48,65	8.33	4.82	2.50	210.00	12.40	1.49	4.62	19.86	4.10
Xiang Gengli	Thailand	80.50	75.30	57.30	6.40	4.14	2.25	230.00	10.90	1.70	4.36	21.92	1.60
Khao Jao Hawn	Thailand	75.85	70.45	51.80	7.82	4.30	6.75	245.00	12.25	1.57	4.81	16.53	4.78
Khao Mali	Thailand	70.40	63.60	50.20	7.22	4.36	2.00	225.00	10.70	1.48	4.23	20.58	7.32
Kaho Manpet	Thailand	78.40	68.10	55.65	6.76	3.70	6.25	347.50	10.25	1.51	4.40	17.08	5.61
Lon Yung	Thailand	63.05	58.20	46.55	6.45	3.90	6.50	250.00	10.20	1.58	4.22	16.35	4.20
Naipon No-1	Thailand	68.00	61.80	49.30	7.72	4.29	5.75	225.00	11.25	1.46	3.75	16.92	6.09
Hawmkikwai	Thailand	63.80	78.80	62.85	7.68	4.4	6.50	245.00	11.20	1.46	4.36	16.80	11.32
Patoon Tahni-60	Thailand	76.75	71.00	54.50	6.97	3.78	7.00	352.50	12.00	1.72	3.50	19.10	17.49
Jawi Hitan	Thailand	72.00	66.10	44.00	4.27	2.95	5.25	265.00	8.20	1.92	4.07	19.48	2.94
Siong Pelandok	Thailand	73.35	67.95	52.20	6.18	3.78	4.25	230.00	10.90	1.76	4.14	19.82	4.64
Jasmine Scented	Thailand	72.80	67.15	52.10	6.51	3.93	5.75	315.00	12.45	1.91	3.75	18.65	8.77
Khao Luang	Thailand	69.35	63.05	41.25	6.81	4.14	4.00	210.00	11.90	1.75	3.75	25.47	3.16
TamxoanHaiduang	Vietnam	71.80	65.80	53.25	5.94	3.55	2.50	192.00	9.10	1.53	3.94	24.29	8.80
TamQuthankhoa	Vietnam	77.85	72.00	59.95	5.39	3.44	2.75	222.50	8.70	1.62	3.94	23.63	6.21
Tamthomnamdinh	Vietnam	67.80	63.10	49.00	5.93	3.80	5.25	295.00	10.10	1.70	3.57	19.86	6.26
Tamthomthankhoa	Vietnam	77.05	72.00	59.70	6.84	4.15	4.25	295.00	9.45	1.38	3.72	19.30	5.81
TamthomNinhbinh	Vietnam	74.15	67.85	53.45	6.61	3.88	3.00	250.00	9.70	1.47	3.82	21.23	5.97
Tamduonghaiduong	Vietnam	59.55	55.05	42.75	6.11	3.59	4.25	190.00	8.80	1.44	3.82	19.86	7.24

for water uptake and TD-52, Hsiang Nuo-1, Xiang Gengli, Khao Jao Hawn, Khao Manpet and Hawmkikwai for volume expansion showed best performances among the varieties tested.

The cooked kernel length more than 12 mm and elongation ration greater than 1.7 are preferred in international market. Khaw Dwak Mali-105, Hsiang Nou-1, Khao Jao Hawn, Patoon Tahni-60, Jasmine Scented, Khao Luang for cooked kernel length and TD-52, Jawi Hitan, Siong Pelandok, Jasmine Scented and Khao Luang for elongation ratio are best among the varieties.

The quality performance of scented rice mainly depends upon the amylose content. RD-15 exhibited lowest amylose content (16.10%) where as KhaoLuang had highest amylose content (25.47%). Xiang Gengli, Khao Mali, Khao Luang, Tamxoanhaiduang, TamQuthankhoa, TamthomNinhbinh showed intermidiate amylose content (20-25%) which are preferred in international market. The varieties like TD-52, Hawmki kwai, Patoon Tahni-60, Jasmine Scented and Tamxaon Haiduang showed higher yield performance among the scented rice studied.

From the present experiment, it is deduced that Hawmkikwai, TD-52, Xiang Gengli, Hsiang Nuo-1 and Khao Jao Hawn from Thailand and Tamthomthankhoa and TamQuthankhoa from Vietnam are best quality performers among the scented genotypes studied for quality characters. These scented rice varieties can be used as donor parents for quality characters to improve

Table 2. Best donors for different quality characters

Character	Varieties
Hulling	RD-15, Xiang Gengli, Khao Manpet, Hawmkikwai, TamQuthankhoa, Tamthomthankhoa
Milling	RD-15, Xiang Gengli, Hawmkikwai, Patoon Tahni-60, TamQuthankhoa, Tamthomthankhoa
Head rice recovery	RD-15, TD-52, Xiang Gengli, Khao Manpet, Hawmkikwai, Tam Quthankhoa, Tamthomthankhoa
Kernel length	Khao Dwakmali-105, Hsiang Nuo-1, Khao Jao Hawn, Khao Mali, Naipon No-1, Hawmkikwai
Length/breadth ratio	Khao Dwakmali-105, Hsiang Nuo-1, Khao Jao Hawm, Naipon No-1, Hawmkikwai
Alkali spreading value	TD-52, Siong Pelandok, Khao Luang, Tamthomthankhoa, TamxounHaiduong
Water uptake	Khao Manpet, Patoon Tahni-60, Jawi Hitan, Jasmine Scented, Tamthomnamdinh, Tamthomthankhoa
Cooked kernel length	Khao DwakMali-105, Hsiang Nou-1, Khao Jao Hawn, Patoon Tahni-60, Jasmine Scented, Khao Luang
Elongation ratio	TD-52, Jawi Hitan, Siong Pelandok, Jasmine Scented, Kaho Lunag
Volume expansion	TD-52, Hsiang Nou-1, Xiang Gengli, Khao Jaw Hawn, Khao Manpet, Kawmkikwai
Amylose content	Xiang Gengli, Khao Mali, Khao Luang, Tamxoan Haiduang, TamQuthankhoa, TamthomNinhbinh
Grain yield/plant	TD-52, Hawmkikwai, Pantoon Tahni-60, Jasmine Scented, Tamxoan Haiduang

our Indian varieties by manupulating genes in hybridization programme. These varieties can be grown in coastal conditions and exported to earn foreign exchange.

References

Azeez MH and M Shafi (1966) Quality in rice. Technical Bulletin 13. Dept of Agric. Government of West Pakistan, Lahore, 50p.

Beachell HM and JW Stansel (1963) Selecting rice for specific cooking characteristics in a breeding programme. *International Rice Comm. Newsl.* **12:** 25-40.

Chauhan JS, VS Chauhan, SB Lodh and PK Sihna (1991) Quality indices of some traditional rainfed upland rice cultivars. *Oryza* **28:** 151-154.

Ghosh AK, BB Nanda, S Govindaswami and BB Nayak (1971) Influence of nitrogen on the physicochemical characteristics of rice grain. *Oryza* **8:** 87-93.

Jennings PR, WR Coffman and HE Kauffman (1979) Grain quality in rice improvement. International Rice Research Institute, Manila, Philippines, pp 101-120.

Juliano BO (1971) A simiplified assay for milled rice amylose. *Cereal Sci. Today* **16:** 334-340.

Little RR, GB Hilder and EG Dowson (1958) Differential effect of dilute alkali on 25 varieties of milled white rice. *Cereal Chem.* **35:** 111-126.

Genetics of Some Quantitative Traits in Six-Rowed Barley (*Hordeum vulgare* L.) over Three Environments

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Genetic component of variances were estimated for ten characters in a 10 x 10 diallel fashion over three environments. The findings reveled that both additive (D) and non-additive (H1 & H2) components of variation were important for all the characters. However, the relative magnitude of dominance component was higher than additive component i.e. prevalence of non-additive gane effects and over dominance suggested that on or the other form of biparental and/or recurrent selection procedures and diallel selective mating might give fruitful results for improving the grain yield in six rowed barley.

Key Works: Component Analysis, Genetic Component, Six-Rowed Barley

Research done on improvement of barley (*Hordeum vulgare* L.) in the recent past has revealed that grain yield is determined by component traits, is a highly complex and variable character and the genes for yield *per se* do not exist (Grafius, 1959). The present investigation was carried out to determine the genotype x environment interactions and suitable breeding methods for the genetic improvement in six-rowed barley and would provide clearer picture of relative importance of additive and dominance component in the control of characters.

Materials and Methods

Ten genetically diverse six-rowed barley (*Hordeum vulgare* L.) genotypes, *viz.*, RD-2035, RD-2052, RD-2503, RD-2508, RD-2552, RD-2585, RD-387 (Raj Kiran), BL-2, ISBYT-4 and ISBYT-17 were crossed in all possible combinations excluding reciprocals. The 45 F_1s, their F_2s and 10 parents were grown in a randomized block design with three replications under early (E_1), normal (E_2) and late (E_3) sowing at Agricultural Research Farm, Asalpur, Jobner. Each plot consisted of 2 m long double rows for non-segregating materials *i.e.* parents and F_1s and four rows for segregating materials *i.e.* F_2s. Row to row and plant to plant distance was kept at 30 cm, respectively under all the three environments. Recommended cultural practices were followed for raising the crop. Ten competitive plants from each parents and F_1s and 30 plants in F_2s were randomly selected for recording observations for grain yield and its 10 component characters (Table 1) under each environment separately. Pooled analysis of variance over the environments was done according to Panse and Sukhatame (1967). The variance component analysis was done as suggested by Hayman (1954).

Results and Discussion

The pooled analysis of variance over the environments for the experimental design (Table 1) showed highly significantly differences among genotypes for all the traits indicating that the material used had enough genetic diversity. Significant differences among environments (sowing dates) also indicated the differential influence of environment on the character expression. The genotypes × environment interaction were also found significant for all the traits, indicating existence of non-linear response of genotypes to the varying environments.

Significant deviation of 'b' from zero and the non-significant departure of regression coefficient from unity in respect of flag leaf area, spike length, grains/spike, 1000-grain weight and grain yield/plant indicated that the aforesaid diallel assumptions were valid for these traits (Table 2). However, rest of the traits showed partial failure of the assumptions but estimates of the population parameters for that traits were still possible (Hayman, 1954) through certainly the estimates for such a trait are less reliable than they would have been, if all assumptions had been fulfilled. With the fulfillment of most of the assumptions of the diallel analysis fully or partially in the present study, the conclusions drawn are expected to be valid and should from a guideline for improvement in the genetic material studied.

Table 1. Pooled analysis of variance over environments for yield and its components in barley

Source of variation	d.f.	Days to heading	Plant height	Tillers/ plant	Flag leaf area	Spike length	Spikelets/ spike	Grains/ spike	1000-grain weight	Harvest index	Grain yield
Enviornment (E)	2	2879.49**	1625.72**	2.86**	3.43**	0.81*	256.92**	215.73**	972.53**	104.70**	205.21**
Genotypes (G)	99	136.21**	561.55**	4.90**	2.26**	2.09**	139.47**	140.07**	53.26**	15.88**	86.28**
G x E	198	17.56**	15.86**	0.17**	0.42**	0.34**	20.42**	21.85**	4.40**	1.79**	4.26**
Error	596	6.28	6.61	0.09	0.17	0.29	8.30	5.87	1.68	1.40	1.05

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

Table 2. Estimation of genetic component of variation for yield and yield component pooled over three environments

Source of components	Days to heading	Plant height	Tillers per plant	Flag leaf area	Spike length	Spikelets per spike	Grains per spike	1000-grain weight	Harvest index	Grain yield
D	5.57*	8.52*	0.11**	0.12**	0.08**	7.44*	7.25*	1.95**	0.38*	2.07*
H_1	67.21**	151.94**	2.29**	2.56**	1.49**	98.59**	94.14**	29.08**	8.36**	47.41**
H_2	44.22*	125.89**	1.60**	1.72**	1.08**	83.75**	78.36**	20.53**	6.43**	35.77**
F	12.04	10.99	0.37*	0.61*	0.33*	11.34*	10.83*	6.87*	1.51*	9.00*
E	1.82*	6.91**	0.05**	0.05**	0.04**	1.46	1.25	0.49*	0.22**	0.37
h^2	4.10*	5.33	0.18**	0.08*	0.00	0.23	4.17	0.90	0.08	1.17
$(H_1/D)1/2$	3.47	4.22	4.56	4.62	4.31	3.64	3.60	3.86	4.69	4.78
$H_2/4H_1$	0.16	0.21	0.17	0.17	0.18	0.21	0.21	0.18	0.19	0.19
$(4DH_1)1/2 + F/(4DH_1)1/2 - F$	1.90	1.36	2.17	3.55	2.89	1.89	1.90	2.68	2.47	2.66
(b-0)/sb	1.54	1.04	0.97	2.56*	2.31*	2.76*	2.65*	3.73**	5.51**	2.60*
(1-b)/sb	1.51	4.36**	4.11**	1.23	0.32	6.37**	1.24	0.46	3.11*	0.51

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

The estimates of genetic components of variation (D, H_1, H_2, h^2 and F) and various ratios based on these components are presented in Table 2. The estimates of additive genetic variance (D) were significant for all the traits. The two measures of dominance H_1 (dominant effect) and H_2 (proportion of dominance due to positive and negative genes) were also highly significant for all the traits. However, the magnitude of H_1 component was higher than that of D for all the traits indicating the greater role of non-additive gene effects in the inheritance of these traits. These results are in agreement with Bhatnagar and Sharma (1995). EI-Seidy (1997), Singh *et. al.* (1999) and Bhatnagar *et. al.*, (2001).

The estimates of 'F' value which indicated the relative frequency of dominant and recessive alleles in parents were found to be positive and highly significant for tillers/plant, flag leaf area, spike length, spikelets/spike, grains/spike, 1000-grain weight, harvest index and grain yield/plant indicating an excess of dominant alleles. Positive but non-significant 'F' in days to heading and plant height gave some indications of the excess of dominant alleles in the parental lines. The environmental component (E) was significant for days to heading, plant height, tillers/plant, flag leaf area, spike length, 1000-grain weight and harvest index. The overall dominance effect (h^2) was significant for days to heading, tillers/plant and flag leaf area.

The average degree of dominance $(H_1/D)^{1/2}$ indicated over dominance for all the characters. The proportion of dominant genes with positive or negative effects in parents ($H_2/4H_1$) was less than the expected value 0.25, for all the traits which indicated asymmetrical distribution of positive and negative dominant genes in the parents. The ratio $(4DH_1)^{1/2} + F (4DH_1)^{1/2} - F$ indicates the proportion of total number of dominant and recessive genes among the parents was greater than unity indicating accumulation of dominant alleles.

The present study revealed that non-additive component of genetic variance was involved in governing the inheritance of yield and its components. In this situation biparental mating and/or diallel selective mating offers good prospects for increasing the frequency of genetic recombination and hastening the rate of genetic improvement in six-rowed barley.

References

Bhatanagar VK and SN Sharma (1995) Diallel analysis for combining ability for grain yield and its component in barley. *Indian J. Genet.* **55:** 3, 228-232.

Bhatanagar VK, SN Sharma and EVD Sastry (2001) Genetics of quantitative characters in six rowed barley over environments. *Indian J. Genet.* 61, **4:** 358-359.

El-Seidy ESH (1997) Inheritance of earliness and yield in some barley crosses. *Ann. Agril. Sci.* Moshtohor. **35:** 2, 715-730.

Grafius JE (1959) Heterosis in barley. *Agron. J.* **51:** 551-554.

Hayman BI (1954) The theary and analysis of diallel crosses. *Genetics.* **39:** 789-809.

Panse VG and PV Sukhatme (1967) *Statistical Methods for Agricultural Workers.* Ed 2: 145-156, ICAR, New Delhi.

Singh I, SL Dashora, SN Sharma, EVD Shastry and I Singh (1999) Inheritance of some quantitative characters in six-rowed barley. *Indian J. Genet.* **59:** 1, 99-101.

Co-Adapted Yield Components in Elite Genepool of Bread Wheat Developed in North-Western and North-Eastern Plains of India

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Wheat breeding programme for the Indo-Gangetic plains is proactive. Wheat breeders of the North-western and North-eastern plains contribute in this programme to release varieties in either of the zones. The study is focussed to pin point advantages or disadvantages tagged to the breeding material developed in either zone. The North-western zone wheat breeding programme is good in adding grain number per unit area with assured grain weight. The material developed in this zone has better adaptation and tolerance against temperature spurt during grain filling period. On the other hand, the materials developed in the North-eastern region have more height instead of grains/M2 and fast ripening. The traits showing uniformity in expression across the zones have been discussed in both types of materials. The finding will prove useful in planning selection procedure for the development of bread wheat genotypes for the entire Indo-Gangetic plains stretching from Punjab to West Bengal.

Key Words: Co-adapted Traits, Elite Genepool, Growth Rate, North Eastern Plains Zone, North Western Plains Zone, *Triticum aestivum*, Yield Components

Introduction

In the Indo-Gangetic plains, over 15 million ha area is under timely sown irrigated condition. To facilitate the varietal development efforts, the All India Co-ordinated Wheat and Barley Improvement Project (AICWBIP) has divided the whole Indo-Gangetic region into two, agro-ecological zones, namely, North-western Plains Zone (NWPZ) and North-eastern Plains Zone (NEPZ). The NWPZ comprises states of Punjab, Haryana, Delhi, parts of Rajasthan (Alwar, Bharatpur and Sriganganagar), Paonta valley and Una district of Himachal Pradesh, while the states of Bihar, Jharkand, eastern part of Uttar Pradesh, West Bengal, Orissa and Assam constitute NEPZ. Active wheat improvement centres located in both the zones enrol new bread wheat entries for wide scale initial evaluation at the national level. These trials have test materials which are pre-tested for yield by the concerned centre and important diseases by the AICWBIP. The yield evaluation is carried out only to realise the yield potential under varying environments so that best line can be identified as a released variety for specific zone. The material put to test in the national trials is developed by a thorough understanding of the core germplasm as well as strategizing about ways to incorporate new traits into the core gene pool and therefore, according to Rasmusson (1996) it can be termed as 'elite gene pool'. The trial structure under the AICWBIP provides opportunity to compose performance of the elite gene pool coming from two distinct agro-ecological regions under two different environments. This system has helped in release of two wheat varieties *i.e.* HD 2733 and PBW 443 for the NEPZ. The wheat breeders located in NWPZ have bred these two varieties. Besides, another variety developed and notified for the NWPZ *i.e.* PBW 343 has also been recommended for cultivation in the NWPZ. The present study is an investigation in realise whether the elite gene pool developed in either zone through breeding has certain trait specific advantages. Apparently, there are just a few differences between two zones in the breeding methodology, use of parent lines and selection criteria for yield and component traits. It may be possible through this analysis to spot out advantages that get attached to breeding wheat in a specific region/zone.

Materials and Methods

The initial material coming for yield evaluation under timely sown condition in NIVT 1A and NIVT IB were considered for the five years period *i.e.* 1996-97 to 2000-2001. These normal sown trails are conducted in both the zones under irrigated conditions in 7x7 lattice design. Both these trials are individually conducted at nine locations in the NWPZ and 5 or 6 locations in the NEPZ, every crop season. In both kind of trials, the wheat material bred by NWPZ centres *i.e.* New Delhi, Hisar, Ludhiana, Pantnagar, Durgapura and Karnal, was separated from the NEPZ materials bred at places like Kanpur, Faizabad, Pusa, Varanasi, Sabour, Ranchi etc. In five years period of this study, 265 genotypes developed in NWPZ and 177 developed in NEPZ were evaluated

in both the trails. Five years multilocation testing of such a large materials can give a fairly good indication of overall performance of an elite genepool for a particular trait in the targeted environment. Average performance of each category of materials was subjected to statistical analysis. The characteristics taken into account were phenological traits (vegetative, grain filling and total duration), grain yield and yield components like plant height, grains/m^2 and kernel weight. To analyse the yield contributing traits more critically, physiological efficiency of different materials was derived to measure the growth rate. This per day growth during grain filling period was expressed as grain fill rate *i.e.* per day grain growth and yield fill rate *i.e.* per day yield filling, were utilized as tools in examining the physiological efficiency.

Results and Discussion

Performance of wheat germplasm developed in two different environment was examined individually under two agro-ecologically different zones. Besides identifying genetic difference between these the two groups of wheat material, such an evaluation also permitted to identify traits that are easily influenced by environment. Phenology and yield attributes of these wheat materials were, therefore, examined as per genetic and environmental influences.

Environmental Effect

Before identifying the genetic differences between two categories of wheat material, it is interesting to first identify the impact of a particular environment which may have on overall expression of wheat crop. NWPZ is the most productive land for wheat cultivation in the country. Information generated by the AICW&BIP, and compute simulations on the attainable yield indicates the NWPZ has potential of 7.0 t/ha grain yield (Nagarajan, 1998). The results indicate that vegetative period (days to heading), total maturity period and plant height expressed in this zone always remain significantly higher than the adjoining NEPZ in both type of germplasm (Table 1). All these traits converge to phenology that acts as a crucial factor for higher biomass production in NWPZ. Role of phenological development and its manipulation for increasing wheat yield potential has been emphasised by many wheat workers (Reynolds *et al.*, 1996, Slafer *et al.*, 1996 and Richard 1996). There was no significant difference among two zones in grain yield and grain number unit area. The differences for grain fill period and per day growth in grain development and yield filling also cease to exist between these two zones. Even though the native material under NEPZ conditions showed an edge over NWPZ-material in kernel weight, the difference was statistically insignificant. It implies that the NEPZ- bred material could match the yield levels of the NWPZ-bred material mainly on account of better physiological efficiency during vegetative phase that helped to produce more biomass expressed through tall plant types with matching grain number per unit area.

Crop growth and yield are derived from photosynthesis and, therefore, depend on receipt and capture of solar radiation (Loomis and Amthor, 1996). It has been suggested that increasing radiation use efficiency may improve yield directly by increasing total productivity, as well as indirectly by generating higher potential kernel number and weight (Reynolds *et al.*, 1996). It seems that broadly, both types of wheat germplasm match each other in their ability to make use of radiation energy under different environments.

Even with significant difference in the maturity period, 70-71% period of the crop duration is spent on vegetative growth in both the materials in the NWPZ. In the corresponding NEPZ, only 65% period of the crop duration gets utilized up to heading, leaving proportionately higher grain filling phase in comparison to NWPZ. Even in the absence of statistical significance, the numerical advantage that the wheat crop has for grain number per unit area in NWPZ and grain size in the NEPZ can be attributed to this phenomenon of phenological significance that aids in sustaining grain yield in the Indo-gangetic region.

Genetic Differences

Overall performance of the elite genepool developed in NWPZ was compared with elite genepool of the NEPZ under both the environments. The common difference noticed among the germplasm of two different origin lied in grain filling period and plant height (Table 2). The NWPZ-bred material generally had an added advantage of longer grain fill period when compared to NEPZ-material in both the environments whereas the NEPZ-bred material has specially in excelling for height under all environmental conditions. Though significant, the grain fill period difference in the NEPZ was not all wide to show any bearing on the kernel weight. However, this difference in grain fill period

Table 1. Environment effect on elite genepools from different regions (From 1996-97 to 2000-01)

Characteristics	NWPZ-bred elite genepool		NEPZ-bred elite genepool	
	NWPZ	NEPZ	NWPZ	NEPZ
Grain yield (q/ha)	47.5	44.7	44.6	43.7
Days to heading	98.5**	78.7	99.3**	78.9
Grain fill period (days)	42.3	43.1	40.7	42.1
Total duration (days)	141**	122	140**	121
Plant height (c)	95.4**	87.4	99.8**	91.5
Grains/m2 ('000)	12.7	11.8	12.2	11.5
Kernal weight (mg)	37.4	38.0	36.6	38.0
Grain fill rate (mg)	0.89	0.89	0.90	0.91
Yield fill rate (kg/ha)	113	105	110	104

* significant at P = 0.05
** significant at P = 0.01

Table 2. Genetic differences in elite genepools from different regions (Period 1996-97 to 2000-01)

Characteristics	North-western Plains Zone		North-western Plains Zone	
	NWPZ-bred elite genepool	NEPZ-bred elite genepool	NWPZ-bred elite genepool	NEPZ-bred elite genepool
Grain yield (q/ha)	47.5**	44.6	44.7	43.7
Days to heading	98.5	99.3	78.8	78.9
Grain fill period (days)	42.3*	40.7	43.1	42.1
Total duration (days)	141	140	122*	121
Plant height (c)	95.4**	99.8	87.4**	91.5
Grains/m2 ('000)	12.7*	12.2	11.8	11.5
Kernal weight (mg)	37.4	36.6	38.0	38.0
Grain fill rate (mg)	0.89	0.90	0.89	0.91*
Yield fill rate (kg/ha)	113	115	105	104

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

became wider in the NWPZ and it also registered some impact on the grain size *i.e.* kernel weight. Quick maturity and small grain size in the NEPZ bred material under NWPZ condition indicates that this material tends to show lack of heat tolerance. Similarly, when the material that has genetic superiority for tallness *i.e.* NEPZ elite genepool, is exposed to an environment that is highly favourable for producing taller plants *i.e.* NWPZ, the compound effect resulting in excessive height proves detrimental as it caused yield lose due to lodging.

Genetic Similarities

Both types of materials were examined for genetic similarities and it was noted that days to heading, grain size and also the seed fill rate were some of the traits which showed no significant differences under different environments (Table 2). It revealed that photo-thermal response remained similar in either of the zones and as such environment was no factor in bringing to surface any difference in biomass production among the germplasm. Both types of materials has similar potential in development of the grain, the numerical disadvantage that existed in the NEPZ-bred material under NWPZ conditions was mainly due to few environmental restrictions imposed on the grain ripening period. Translocation of the assimilates for yield accumulation was also carried out at similar rate that again supports the idea that no genetic differences existed among the materials in physiological efficiency as far as grain yield in concerned.

G × E Interaction

Exploitation of G × E to make better use of the favourable environmental conditions is also an advantages that a breeder would always like to have in the developed material. Such an interaction for grain yield was not visible among the two categories of wheat germplasm under North-eastern conditions (Table 2). Overall yield in both the materials remained around 44 q/ha. It was mainly because both the materials looked alike as far as the key yield components like grain number/unit area and kernels weight were concerned. However, with change of environment, both the materials started registering differences for these important traits. Besides, grain yield and grains/m^2, another trait that registered G × E interaction was the grain fill rate. There was

no difference in the grain fill rate among two types of germplasm in NWPZ. However, the same set of materials showed significant differences for this trait in the NEPZ. Such an interaction in NEPZ helped the native material to match with the corresponding materials in kernel weight inspite of faster grain fill period. Grain weight in wheat is the product of rate and duration of grain filling (Nass and Reiser, 1975). Przulj and Mladenov (1997) found no strong relation between grain fill duration and grain fill rate which enables the combining of these two traits in the process of cultivar development. They have suggested that in regions with shorter growing season, the yield can be more easily raised by increasing grain fill rate while in the temperate regions different values of these parameters can be combined.

Interaction could also be noted for maturity period, as significant differences among two materials of different origin could only be noticed in the NEPZ. Even though, the difference was too small to have an impact on yield, it does have relevance under NEPZ conditions where late maturity of the NWPZ material is normally argued.

Material for NWPZ

Under NWPZ conditions, overall performance of the locally derived elite genepool was better than NEPZ-bred material. An additional 2.8 q/ha yield was added to the native materials due to its distinct superiority in grain number/m^2 (Table 2). The grain fill period in the native material was also longer than the NEPZ-bred material which may have contributed to better grain size. The real advantage that the NWPZ-bred material has in the native zone, therefore, comes basically from three factors *i.e.* more number of grains/m^2, longer grain filling duration in aid to better grain filling, and proper plant height. It appears that the NWPZ-bred material has a better combination of traits that helps in adaptation and realising high yield potential under diverse environments. As evident from the historical evidence, it is the grain number that has been consistently associated with increase in wheat yields (Slafer *et al.* 1994 and 1996; Villariel *et al.*, 1994, 1995). The elite genepool derived in this region comes largely from winter × spring genepool recombination. Besides the 1B/1R translocation, other agronomic characters, a higher number of grains through either higher number of heads/m^2 or through bigger heads contribute to high yield in winter × spring wheat derived genepool (Rajaram and van Ginkel, 1996).

The NEPZ-bred material could not exploit the favourable environment of NWPZ to a real yield advantage, mainly for two reasons. First being the faster vertical growth *i.e.* plant height (100 cm) that not only added extra height to an disadvantage through lodging but it also helped in restricting the horizontal growth *i.e.* tillering, consequently resulting in limitation to the source and grain number/unit area. The second factor was short grain filling period that resulted ultimately in lower kernel weight. With matching rate in yield and grain fillings, it was clear that physiologically both the genepools were equally efficient in translocating assimilated to the heads during grain filling period. The reduction in grain filling period, therefore, can not be regarded as quick maturing, it is rather a forced maturity resulting on account of poor tolerance under sudden increased temperature. It is a kind of abiotic stress to which the NEPZ breeding materials is not exposed in the native zone during the process of development.

Material for NEPZ

Under NEPZ conditions, there was not much to choose between two types of materials as they matched each other in yield and yield components like grain number/m^2 and grain size. Morphologically, the NEPZ material appeared distinct only in height but this much height (92 cm) does not result in lodging, rather it adds to the total biomass under NEPZ conditions. Another difference lied in the phasic development where grain fill period of the native material was shorter than the NWPZ-bred material. Reduction in the grain fill period of the native material was not forced as the grain fill rate in this elite genepool was even better than the material developed in NWPZ. This faster filling of grains in the locally developed elite genepool was instrumental in sustaining grain yield. It became quite clear that under any environment, there are two in-built characteristics in the NEPZ-bred material (i) taller height and (ii) quick grain filling.

There were also indications that the NWPZ material attains maturity slightly later when compared to the native material. Even though the magnitude of such a difference was quite small with no bearing on the overall yield, it does have a great relevance under NEPZ conditions where late maturity of the NWPZ material is normally argued. In the past three years, three varieties for normal sown conditions have been released for NEPZ out of which, two varieties *i.e.* HD 2733 and PBW 443 have been developed in the NWPZ. It has been noted that

in comparison to 118 days crop duration in case of native variety HUW 468, the NWPZ-bred varieties HD 2733 and PBW 443 took 123 and 121 days, respectively, to complete maturity under NEPZ conditions (AVT: NEPZ, 198-99 to 2000-10). PBW 343, another NWPZ-bred variety recommended for NEPZ conditions as well, matures six days later than HUW 468 (AVT: 2000-01). Slight delay in maturity can hinder prospects of a high yielding variety in the NEPZ as the production condition favours short duration wheat varieties in this region.

The breeders located in the NWPZ and NEPZ are conducting wheat improvement programme in the Indo-Gangetic plains in combination. The trails run by the AICW&BIP for timely-sown irrigated condition are also common for yield evaluation of the incoming materials. It is, therefore, necessary for the breeders of each zone to know the kind of general behaviour of their material are expected to give within and outside the zone. To exploit conditions best to the yield advantage, it is also necessary to know the traits that remain unaffected with changing of environment and the specific advantages different materials carry under different environments. There is always certain in-built advantage of the place where a particular material is developed or selected. Wheat material developed in harsh environment carry certain degree of tolerance against moisture stress and high temperature. So is the case when wheat breeding and selection is carried out in salt-affected soils, knowingly or unknowingly, the developed materials usually have added advantage of better adaptation under saline-alkaline conditions. Whether breeding in a particular region also influences yield traits, is the key issue addressed in this investigation. The NWPZ is not only the most favourable area for wheat production in India but it also leads in development of improved wheat varieties. Since 1970, one third of the total notified wheat varieties belong to this region and NEPZ is the next to follow. Per hectare yield of over 7 tonnes has been recorded in many entries including check PBW 343 the most popular wheat varieties bred in NWPZ are capable of competing native varieties of the adjoining NEPZ, too (Mohan and Jag Shoran, 1999). In a related study, the authors have earlier indicated that the NIVT-1A, a trial where majority of the incoming material hails from NWPZ, has shown better adaptation across these zones when compared with NIVT-1B, a trial mostly packed with NEPZ-bred materials (Mohan and Jag Shoran, 2000). This analysis has confirmed that such kind of wider adaptation and ability to exploit favourable conditions to yield advantage though higher number of grains/m^2 is an in-built advantage tagged to the elite wheat breeding developed in the North-western region. Although the elite genepool bred in the North-eastern region is able to maintain its yield under NWPZ conditions but it fails to draw advantage of this favourable climate on account of small grain size and extra height. Tolerance to sudden rise in temperature during grain filling period and ability to exploit cooler environmental conditions of NWPZ for producing extra tillers, are missed in the elite genepool of the eastern region. Partitioning of yield through height rather than tillers is also a co-adapted trait in the NEPZ-bred wheat materials under NWPZ conditions, derivatives of winter × spring programme might prove more useful in exploiting yield through increased grain number/unit area and tolerance against spurt during grain filling.

Present study clearly suggests that some important yield components in wheat co-adapt during the process of varietal development. It could be demonstrated that there lies advantage of better adaptation, high grain number/m^2 through better tillering and good grain size, better tolerance against abiotic stresses especially during grain filling period in the elite genepool developed under NWPZ conditions. Extra height and short grain filling period, two important attributes of the elite genepool developed under NEPZ conditions, have some utility only under NEPZ conditions where they effectively contribute in sustaining grain yield. It is perceived that winter × spring genepool combinations and shuttle-breeding approach can prove handy to the NEPZ breeders in developing competitive elite genepool for the adjoining areas.

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References

D Mohan and Jag Shoran (1999) A case study for realizing importance of zonal checks in initial promotion of test entries in the AICWIP. Indian Wheat Newslet. **5:** 2-3 Directorate of Wheat Research, Karnal.

D Mohan and Jag Shoran (2000) Assessment of timely sown bread wheat NIVT's in the north-western and north-eastern palin zones. *Indian Wheat Newslet.* **6:** 3 Directorate of Wheat Research, Karnal.

Loomis Rs and JS Amthor (1996) Limits of yield revisited. *In:* MP Reynolds, S Rajaram and A McNab (eds) *Increasing Yield Potential in Wheat* Mexico, D.F.: CIMMYT pp 176-89.

Nagarajan S (1998) Perspective of Wheat Demand and Research Needs. *In:* S Nagarajan, Gyanendra Singh and BS Tyagi (eds) *Wheat Research Needs Beyond 2000AD.* Narosa Publishing House, New Delhi, pp 29-34.

Nass HG and B Reiser (1975) Grain filling and grain yield relationships in spring wheat. *Can. J. Plant Sci.* **55:** 673-678.

Progress Reports (1996-97 to 2000-2001) Results of the All India Co-ordinated Wheat, Barley and Triticale Varietal Trials. Directorate of Wheat Research, Karnal.

Przulj N and N Mladenov (1999) Inheritance of grain filling rate in wheat. *Cereal Res. Comm.* **27:** 259-266.

Rajaram S and M van Ginkel (1996) Yield potential debate: Germplasm vs. Methodology. *In:* MP Reynolds, S Rajaram and A McNab (eds) *Increasing Yield Potential in Wheat,* Mexico, D.F. CIMMYT, pp 11-18.

Rasmusson DC (1996) Germplasm is a pramount *In:* MP Reynolds, S Rajaram and A McNab (eds) *Increasing Yield Potential in Wheat,* Mexico, D.F. CIMMYT pp 28-35.

Reynolds MP, J van Beem, M van and D Hoshington (1996) Breaking the yield barriers in wheat: A brief summary of the outcome of an international consultation. *In:* MP Reynolds, S Rajaram and A McNab (eds) *Increasing Yield Potential in Wheat,* Mexico, D.F., CIMMYT, pp 1-10.

Richard RA (1996) Increasing the yield potential of wheat *In:* MP Reynolds, S Rajaram and A McNab (eds). *Increasing Yield Potential in Wheat,* Mexico, D.F., CIMMYT, pp 11-18.

Slafer GA and HM Rawson (1994) Sensitivity of wheat phasic development to major environmental factors: a re-examination of some assumptions made by physiologists and modellers. *Aust. J. Plant Physiol.* **21:** 393-426.

Slafer GA, DF Calderini and DJ Miralles (1996) Yield components and compentation in wheat: Opportunities for further increasing yield potential. *In:* MP Reynolds, S Rajaram and A McNab (eds) *Increasing Yield Potential in Wheat,* Mexico, D.F., CIMMYT, pp 11-18.

Villareal RL, A Mujeeb-Kazi, E Del Toro, J Crossa and S Rajaram (1994) Associated effect of chromosome 1B/1R translocation on agronomic traits in hexaploid wheat. *Breed. Sci.* **44:** 7-11.

Villareal RL, E Del Toro, A Mujeeb-Kazi and S Rajaram (1995) The IBL/IRS chromosome translocation effect on yield characteristics in a *Triticum aestivum* L. cross. *Plant Breed.* **114:** 497-500.

Crop Improvement in *Musa* – Evaluation of Germplasm for Male and Female Fertility

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A total of 450 accessions of *Musa* (bananas and plantains) at National Research Centre for Banana, Tiruchirapalli, (NRCB) field genebank were screened for their male and female fertility. Male fertility was screened with respect to pollen production, pollen fertility and pollen germination. Apart from AA members, ABB genomes namely Pisang Awak, Monthan and Bluggoe were found to be better pollen parents, with the exception of Peyan subgroup. Screening for female fertility revealed that subgroups Mysore and Pome (AAB) and Pisang Awak and Bluggoe (ABB) were potential female parents of use in *Musa* improvement programme. Though seed characters varied greatly with respect to pollen and female parent combinations, variability was noticed with respect to number of seeds/fruit, seed distribution, colour, shape and weight.

Key Words: Banana, Crop Improvement, Germplasm, Female Fertility, Fertility, Male Fertility, *Musa*, Seed Fertility

India is the largest producer of banana in the world with 14 million tonnes of production annually. It contributes to 31.7% of total fruit production and ranks as the number one fruit crop in the country (Singh and Uma 1996). India is believed to be one of the major centres of *Musa* origin, exhibiting great diversity for bispecific clones like AB, AAB and ABB. Three major species *M. acuminata, M. balbisiana* and *M. schizocarpa* are thought to be the original species responsible for evolution of present day cultivars (Horry 1993). In India diversity is observed mainly in *acuminata* and *balbisiana.*

Banana cultivars are characterized by male and female sterility, with a range from moderate to absolute sterility and parthenocarpy. But parthenocarpic expression is dependent on various factors like cultivar and congenial pollen parents. Hence, in the present study, efforts were made to recognize potential pollen parents with desirable traits and cultivars of commerce requiring improvement with respect to one or two traits and 450 *Musa* accessions were evaluated for this purpose.

Material and Methods

A total of 450 *Musa* accessions belonging to various groups and subgroups (Table 1) were evaluated for male and female fertility during 1995-98. Male fertility was evaluated in terms of pollen production and pollen fertility. Anther sacs for each accession were scored in 3 replicates for pollen count. Each anther sac was cut into four equal pieces and each quadrant was squashed and observed under microscope. Numbers of pollen grains produced per quadrant were counted and total pollen grain produced per sac was estimated (Sathiamoorthy, 1973). According to the count, accessions were classified as nil, scanty (<1,000), medium (1,000-10,000) and polleniferous (>10,000). Pollen fertility was assessed by *in vitro* germination of the pollen grains in 0.5% sucrose medium for 30 min. The per cent of fertile pollen was estimated for accessions and rated as highly fertile with >90% pollen germinating, 40-50% germination was rated as fertile, 20-40% germination was rated as medium 5.0-20.0% was rated poor and <5% as very poor (Sathiamoorthy, 1973).

Female fertility was assessed by selecting polleniferous male parents and hand pollinating during early morning hours (6-8 am). Mature anthers were slit vertically using a needle and pollen grains were extracted. These were collected on a camel hair brush and pollinated on to the flowers opened on the same day. The accessions setting seeds even under open-pollinated conditions were also considered to be female fertile. Data on seed in terms of colour, shape, size, 100-seed weight, seed position in fruit and seed bearing hands in a bunch were also collected.

Results and Discussion

Pollen fertility studies are shown in Table 1 which revealed that most of the *acuminata* (diploids and tetraploids) and *balbisiana* clones were highly polleniferous along with Monthan and Bluggoe subgroups. Subgroups Peyan, members of Monthan, Bluggoe and Pisang Awak exhibited medium polleniferous nature. Pome, Mysore, Nendra Padathi, Cavendish and AB subgroups exhibited very

Table 1. Pollen fertility details in *Musa* accessions

Genomic Group (rating)	Subgroup	Pollen production (rating)	Pollen fertility (rating)	Pollen germination (%)
AA	–	Profuse	74.8	+++
AAA	Robusta	Nil-scanty	2.8	+
	Dwarf Cavendish Thella Chakkarakeli	Nil-scanty	0.0	+
AB	Kunnan	Nil		–
	Ney Poovan	Nil		–
AAB	Silk	Scanty	3.6	+
	Mysore	Nil-scanty	8.4	+
	Plantain	Non-polleniferous	–	–
	Pome	Nil-scanty	6.9	+
	Nendra Padathi	Nil-scanty	10.7	+
ABB	Pisang Awak	Medium	66.3	+++
	Peyan	Medium	24.5	+++
	Monthan	Medium-profuse	61.4	++
	Bluggoe	Medium-profuse	78.6	+++
BB/BBB	–	Profuse	72.4	+++
Tetraploids		Profuse	88.9	+++

scanty pollen, while plantains, selected members of Pome, Mysore and Nendra Padathi produced no pollen at all. Most of the members of Pome group exhibited degenerating pollen sacs with the development of female phase.

Study on female fertility revealed that 46 female fertile accessions belonging to various genomic groups and subgroups were female fertile with an average seed set ranging from 1-250 seeds/fruit (Table 2). *Balbisiana* clones recorded the highest seeds of 150-250 seeds/fruit followed by Pisang Awak subgroup of ABB genome. Results show that a lot of variability exists in the *Musa* germplasm with respect to number of hands with seeds, fruits with seeds, number of seeds/fruit. Seed exhibited variability with respect to size, shape, colour, wrinkleness of seed coat and germinability (Table 2).

Table 2. Variability among *Musa* accessions with respect to open-pollinated seed characters

Genomic group	Subgroup	Average no. of seeds/fruit	Position in the fruit	Seed colour	Seed shape	100-seed wt. (g)
AA		2-10	Terminal	Black	Spherical	46.2-48.5
AAA		–	–	–	–	–
AB		–	–	–	–	–
AAB	Mysore	3-12	Random	Black	Flattenned	62.5-88.9
	Pome	5-12	Random	Black	Flattenned	48.3-77.8
	Silk	–	–	–	–	–
	Plantain	1-2	Distal end	Black	Round	56.3-72.8
	Nendra Padathi	–	–	–	–	–
ABB	Pisang Awak	5-30	Terminal & through out Black	Black to Pitch	Angular	74.0-115.6
	Bluggoe	1-35	Random	Black	Irregular Round Angular	48.6-85.3
	Monthan	1-3	Distal end	Black	Round	65.3-85.3
	Peyan	2-4	Random	Brown Black	Irregular	40.9-62.3
BB/BBB	*Balbisiana* clones non seeded	10-15	Random	Black	Flattenned	60.2-68.3
	Seeded	125-250	Throughout	Brown Brown-Black Black	Round Angular Flattenned	51.2-92.3

The study also revealed the potential female parents under each genomic group and subgroup easily set seeds when grown along with polleniferous varieties. Cavendish among AAA genome, Neypoovan and Kunnan among bispecific AB origin, Silk, Nendra Padathi of AAB failed to set seeds even under artificial, protected pollination. Though, Mysore and Pome subgroups of AAB exhibited good seed setting efficiency, Poovan (Mysore) had seasonal restrictions, which set seeds only during September-February months. Among ABB genome, all the four subgroups exhibited female fertility and the highest with Bluggoe subgroup. Position of the seed varied from terminal, distal, random and throughout the fruit length. But most subgroups exhibited affinity for random seed set while only Plantain (AAB) and Monthan (ABB) favoured seed set at distal end. Some members of Pisang Awak subgroups like Chinia set 25-30 seeds distributed throughout the pulp uniformly.

Seed colour and surface had little variability with brown to black and smooth to rough. Different seed shapes and embryo in the genus *Musa* were studied and described by Humphrey (1986) and Chin (1995). In the present study among the cultivated varieties, seed shape varied from round, irregular to flattened. In general, size of all seeds ranged from 4-6 mm. Hundred seed weight ranged from 40.9 g in Peyan subgroups (ABB) to 115.6 g in Pisang Awak (ABB) subgroup (Table 2). Germination percentage varied with genome and subgroups. The highest was recorded in Pisang Awak (54.8%) after *balbisiana* clones (68.9%) and least recorded among plantains with 1.8%. The reasons for varied germination and congenial conditions for germination needs to be worked out for different genome groups.

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References

Chin HF (1995) Germination and storage of banana seeds In: EA Frison, JP Horry and D Dewaele (eds) *Proceedings of the International Symposium on New Frontiers in Resistance Breeding for Nematodes, Fusarium Wilt and Sigatoka.* INIBAP, pp 218-228.

Horry JP (1993) Taxonomy and genetic diversity of diploid bananas. In: J Ganry (ed) *Proceedings of the International Symposium on Genetic Improvement of Banana for Resistance to Disease and Pests,* pp 35-42.

Humphery JE (1986) The development of the seed in Scitaminae. *Ann. Bot.* **10:** 1-40.

Sathiamoorthy S (1973) Preliminary investigations on breeding potential of some banana clones, M.Sc. (Ag) dissertation, Tamil Nadu Agricultural University, India.

Simmonds NW (1995) Wild bananas in Malaya. *Malayan Nature J.* **10:** 1-8.

Singh HP and S Uma (1996) Current approaches and future opportunities for improvement of major *Musa* types present in Asia and Pacific regions – Silk and Pome (AAB-dessert types). In: EA Frision, JP Horry and D Dewaele (eds) *New Frontiers in Resistance Breeding for Nematodes, Fusarium Wilt and Sigatoka,* INIBAP, pp 146-163.

Diversity Pattern, Elucidating Choice of Parents for Hybridization from Exotic Tomato (*Lycopersicon esculentum* Mill) Genepool

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An evaluation trial of 75 lines of exotic germplasm of tomato was conducted to identify suitable parents for high yield, biotic and abiotic stresses at Central Horticultural Experiment Station, Ranchi in the year 1999-2000. The analysis of variance showed high and significant differences for all the characters studied. Data were subjected through Mahalanobis D^2 multivariate analysis and subsequently genotypes were grouped into 10 clusters. The heat tolerant tomato lines EC-238508 and EC-238308 from cluster V and VII were selected for utilization in the breeding program. The exotic line EC-238308 not only possessed heat tolerance but also resistance to early blight. The bacterial wilt resistant lines EC-326142, EC-180188, EC-164672, EC-241147, EC-251677-1 and EC-368785 were identified from clusters II, IV, VI and VII. The tomato lines possessing high TSS, high fruit firmness belonged to cluster I (EC-2511579) and cluster II (EC-241147, EC-320571 and EC-321425-C). The tomato lines possessing marker characters like potato leaf marker (EC-164665, EC-165665, EC-164336 and EC-326142-B) belonged to cluster IV, VI and VII. Similarly, lines with stem pigmentation and hairiness appeared in cluster III and VI. Tomato lines possessing long-styled flowers for natural cross pollination studies (EC-251518 and EC-164336) belonged to VII.

Key words: Diversity, Exotic, Genepool, *Lycopersicon esculentum*, Tomato, Transgressive

A wide genetic base, with high level of productivity and combining ability to yield superior segregants is an essential requisite for selection of parents in any hybridization programme. However, in the absence of information on the relationship between different lines with similar performance, there is a possibility of related lines being chosen in a hybridization programme. This results in limited or no advance under selection to known material. In the past National Bureau of Plant Genetic Resources (NBPGR) New Delhi, has procured several exotic tomato germplasm which have been utilized in development of present day tomato varieties. Thus exotic tomato germplasm was obtained from NBPGR and work initiated with an objective to develop high yielding, bacterial wilt and early blight resistant varieties/hybrids suitable to eastern part of India. All the germplasm lines were evaluated, characterized and descriptors were prepared and lines were maintained through regular seed production for the use of breeders. In order to identify suitable parents for high yield, disease resistance, lines suitable for natural cross-pollination and lines with marker-aided characters, an evaluation trial was conducted and results are presented in this paper.

Materials and Methods

Seventy-five exotic tomato lines were obtained from NBPGR New Delhi, and evaluated in a randomized block design with two replications at Plandu farm of Central Horticultural Experiment Station (CHES), Ranchi during the rainy *(Kharif)* season1999-2000. In each line, the plants were raised in 2 rows, 3m long with inter- and intra-row spacing of 60 x 50 cm. Observations were recorded on five randomly selected plants for plot yield, plant height, fruit weight, fruit length, fruit firmness, total soluble solids (TSS) number of locules and pulp thickness. The mean data were analyzed for analysis of variance . A total of 2,415 D^2 values corresponding to all the 75 possible pairs of entries were computed. Divergence between any two populations was obtained as sum of squares of difference in the transformed values of the corresponding varieties (Mahalanobis, 1936). Co-variance between character pairs were computed as per the method described by Rao (1952). For generalized distance, correlated linear functions of the original value were obtained by transforming the original correlated un-standardized character means by the method of Pivotal condensation, a criterion suggested by cannonical approach described by Rao (1952). For determining group constellations, a relatively simple criterion suggested by Tocher (Rao, 1952) was adopted.

Results and Discussion

High and significant variation was found among the 75 tomato exotic lines (Table 1) for all the attributes studied. The D^2 values (2,415) obtained between 75 tomato lines showed considerable range indicating the existence of appreciable genetic divergence in the genotypes tested. All the lines were grouped into 10 clusters. Composition of different clusters are presented

in Table 2. Among these, cluster-IV (14), cluster-V (14), cluster-VI (14) consist of maximum number of genotypes followed by cluster-VII (11), cluster-III (8), cluster-VIII (7), cluster-II (3) and cluster-IX (2), whereas, cluster-I and X had one exotic line each. The material under study included all exotic tomato collections from different countries and clustering pattern of lines indicates that geographical isolation has not contributed much to the genetic divergence. The observed genetic divergence, therefore, seems to be possible due to differences in genotypes. In situations where the role of the geographic isolation is negligible, genetic drift and selection in different environment could lead to greater diversity. In the present study the clustering pattern revealed that high yielding, bacterial wilt resistance lines i.e., EC-241147, EC-326142, EC-180138, EC-164672, EC-251672 and EC-368785 belonged cluster-II, IV, VI and VII respectively. Similarly, high temperature tolerant lines i.e., EC-320578 (hairiness) and EC-251518 (hairiness and long style) were in Cluster-VII. On the other hand, lines with potato leaf marker i.e., EC-164165, EC-164336, and EC-326142 were in cluster-VI, VII and II respectively.

Table 1. Analysis of variance for 9 traits in 75 exotic tomato germplasm lines

Source	DF	Plot yield	Plant height	Fruit weight	Fruit length	Fruit breadth	Fruit firmness	TSS	No. of locules	Pulp thickness
Replication	1	4.16	1142.87	31.15	0.00	0.23	0.73	0.41	0.56	0.00
Treatment	74	1491.24	244810.10	112918.5	75.86	167.93	100.59	47.26	271.26	1.58
Error	74	273.18	70101.13	6693.46	4.41	13.48	25.35	15.58	57.36	0.17

Table 2. Distribution of 75 exotic tomato germplasm in various clusters

Cluster number	No. of genotypes in each cluster	Genotypes
I	1	EC-251579
II	3	EC-241147, EC-320571, and EC-321425-C
III	8	EC-168283, EC-310303, EC-277691, EC-315476, EC-320578, EC-321425-A, EC-357841-A, EC-321425
IV	14	EC-241148, EC-246028, EC-163606, EC-320581, EC-257751, EC-272496, EC-326142-B, EC-272982, EC-326145, EC-326142-A, EC-321425-D, EC-321425-B, EC-326144 and EC-339062
V	14	EC-162520, EC-168290, EC-1264653, EC-2585, EC-238508, EC-338725, EC-251578, EC-320583, EC-373966, EC-31761, EC-257751-A, EC-357841, EC-326142, and EC-362959
VI	14	EC-180188, EC-164665, EC-241446, EC-164660, EC-164672, EC-320565, EC-339059, EC-362940, EC-368757, EC-368785, EC-357846, EC-368832-1, EC-368833, and EC-368890
VII	11	EC-238308, EC-164336, EC-164336-B, EC-211672-1, EC-251566, EC-2920, EC-339060, EC-339060-1, EC-362949, EC-357840, and EC-368800
VIII	7	EC-164336, EC-339061, EC-251518, EC-320576, EC-339074, EC-361671, and EC-368707
IX	2	EC-361671 and EC-357846-1
X	1	EC-368863

Table 3 gives the inter- and- intra-cluster distances for all the ten clusters. The inter-cluster distance was maximum between cluster-I and X (D=21.56) comprising 2 genotypes *i.e.,* EC-251579 and EC-368863 followed by cluster-II and X (D = 20.86) and cluster-III and X (D=19.52). 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 height, maturity, and disease resistance. Therefore, measures based on genetic criteria quantifying diversity have become important in classifying the material for use by the breeders. Among them, assessment of divergence for a set of characters utilizing multivariate analysis like distance analysis, cannonical analysis, factor analysis and cluster analysis has been attempted and effectively utilized in a number of crop plants including vegetable crops with diverse breeding system (Murthy, 1979).

The characters contributing towards genetic divergence are presented in Table 4, which shows that maximum genetic divergence was observed in fruit weight (21.59%) followed by fruit length (18.41%) and fruit firmness (15.10%). The least contribution towards divergence was observed in TSS (2.55%) and pulp thickness.

The cluster means (Table 5) for plot yield was maximum in case of cluster-VIII (9.76 kg) followed by cluster-II (9.64 kg) which had lines for high temperature tolerance, early blight resistance, bacterial wilt resistance and the lines possessing long-styled flowers. Further, it is interesting to note that the germplasm lines possessing resistant genes fell in different clusters. It is generally believed that genetically divergent parents tend to give rise to heterotic hybrids on crossing. The divergent parent

Table 3. Average inter- and intra-cluster distances among 10 clusters

	I	II	III	IV	V	VI	VII	VIII	IX	X
I	0.00	30.31	35.53	54.67	76.53	97.02	107.97	177.96	237.24	464.90
	(0.00)	(5.50)	(5.79)	(7.39)	(8.74)	(9.85)	(10.39)	(13.34)	(15.40)	(21.56)
II		30.64	22.47	34.53	56.84	75.16	78.54	140.89	189.87	435.54
		(5.53)	(4.74)	(5.87)	(7.53)	(8.67)	(.8.86)	(11.87)	(13.77)	(20.86)
III			20.71	29.12	109.48	58.02	362.21	112.98	169.18	381.20
			(4.55)	(5.39)	(10.46)	(7.61)	(19.04)	(10.62)	(13.00)	(19.52)
IV				61.86	37.31	73.28	80.09	93.91	128.30	373.64
				(7.86)	(6.10)	(8.56)	(8.94)	(9.61)	(11.32)	(19.32)
V					30.32	38.02	48.59	68.74	100.51	324.05
					(5.50)	(6.16)	(6.97)	(8.29)	(10.02)	(18.490)
VI						51.25	35.75	119.04	88.10	30.909
						(7.15)	(5.97)	(10.91)	(9.38)	(17.58)
VII							28.99	49.87	77.91	277.52
							(5.38)	(7.06)	(8.82)	(16.65)
VIII								56.20	51.33	230.14
								(7.49)	(7.16)	(15.17)
IX									21.57	233.48
									(4.64)	(15.28)
X										0.00
										0.00)

Table 4. Contribution of different attributes towards genetic divergence

Character	Number of times appearing in first rank	Percent contribution towards divegence
Plot yield	194	6.99
Plant height	197	7.10
Fruit weight	599	21.59
Fruit length	511	18.41
Fruit breadth	242	8.72
Fruit firmness	419	15.10
TSS	79	2.85
No of locules	353	12.72
Pulp thickness	181	6.52

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Table 5. Cluster means for 9 traits of exotic tomato germplasm lines

Cluster number	Plot yield	Plant height	Fruit weight	Fruit length	Fruit breadth	Fruit firmness	TSS	No. of locules	Pulp thickness
1	3.67	145.75	12.5	2.13	2.79	3.50	4.00	3.30	0.30
2	3.96	153.08	9.83	2.61	2.58	2.18	4.08	2.10	0.25
3	4.75	139.71	18.62	2.72	3.12	2.02	3.56	3.08	0.29
4	5.56	128.32	27.22	3.26	3.57	2.26	3.62	2.98	0.35
5	8.58	125.32	27.22	3.62	4.55	2.75	3.69	3.70	0.44
6	7.93	90.82	52.78	3.81	4.99	2.98	3.21	4.28	0.44
7	9.64	104.65	59.31	3.85	5.06	2.51	3.54	4.19	0.46
8	9.76	91.6	88.71	4.49	5.76	3.11	3.14	4.90	0.52
9	6.91	97.5	110.0	5.29	5.98	4.5	3.12	4.90	0.57
10	4.47	81	162.5	4.02	7.75	1.88	3.00	10.25	0.55
General Mean	7.42	116.32	47.59	3.60	4.47	2.65	3.50	3.80	0.41
SD	1.92	30.77	9.51	0.24	0.42	0.58	0.45	0.88	0.04
CV	25.87	26.45	19.98	6.78	9.52	22.08	13.10	23.12	11.65

possessing high yield potential, with high degree of resistance may be selected as parents for formulating a sound breeding programme in order to develop hybrids resistant to bacterial wilt and alternaria disease. The lines possessing long-styled flowers will be utilized to find out the extent of cross-pollination for production of hybrids without emasculation (natural cross pollination).

References

Murthy BR (1979) Selection of parental material, breeding methods and evaluation procedures in developing improved crop varieties. *Indian J. Genet.* **39:** 305-315.

Mahalanobis PC (1936). On generalized distance in Statistics. *Proc Nat. Acad. Sci* (India) **2:** 49-55.

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

Determination of Leaf Area in *Dioscorea alata* L. – A Critical Analysis

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An attempt was made to compare the leaf area factor (F = 0.71) by linear measurement method reported earlier and the regression equation Y = 5.7789 + 0.77x, where 'x' = length × breadth, based on measurements made by Ravi and Chaudhary (1989) on two released varieties and 100 accessions of *D. alata* comprising 19 morphotypes collected from different agro-ecological niches in peninsular India. The results favours the use of the newly identified factor (F_1 = 0.82) and the linear regression equation Y = 100.319 + 22.79x, where x = breadth of the leaf for leaf area estimation in *D. alata* over the previous one. From the critical analysis following different means, it was found that the leaf factor for *D. alata* as 0.82 and the regression equation, Y = 100.319 + 22.79x, where x = breadth of the leaf, showed least percentage of deviation from the actual leaf area.

Key Words: ***Dioscorea alata,*** **Leaf Factor, Morphotype, Percentage Deviation, Regression Equation**

Determination of leaf area is an important aspect that matters greatly in preliminary evaluation of any crop germplasm since leaf area influences the canopy structure and, hence, photosynthetic efficiency and productivity of plants. The net dry matter produced by a plant per unit time is more dependent on the size of its total assimilatory system (Watson, 1952). Of the different means for the estimation of leaf area, linear measurement method based on the linear regression relationship between leaf length (L), leaf breadth (B) and product of length and breadth (P) with leaf area (A) has been reported as a simple and reliable method for estimation of leaf area in *Dioscorea alata* (Ravi and Chaudhary 1989). In this method leaf factor for *D. alata* has been reported as 0.71 and the regression equation as Y = 5.7789 + 0.77x, where x = length × breadth based on measurements made only in two varieties.

The present study was undertaken to critically compare the factors obtained and regression equations formulated for the estimation of leaf area based on measurements in 100 different accessions belonging to 19 different morphotypic entities of *D. alata*, with varying morphologic expressions. These morphotypic entities were grouped on the basis of subjective judgement and comparison of qualitative characters of both above ground and underground plant parts (Velayudhan *et al.*, 1991). These morphotypes are logical groups of collections in which individual collections vary very little from one another in major qualitative characters, but with considerable variation in quantitative traits.

Materials and Methods

Based on the subjective morphotypic classification of *D. alata,* 100 different accessions collected from different agro-ecological regions in peninsular India, were grown at the farm of National Bureau of Plant Genetic Resources, Regional Station, Thrissur, during the cropping season 1999-2000. Package of practices as recommended by Kerala Agricultural University, were followed.

Fully-grown and mature leaf samples at 1m height were collected from 100 accessions belonging to 19 distinct morphotypes at fourth month of crop growth. The length (L) of the leaf was measured from the leaf tip to the lamina-petiole joint and maximum width was measured across the margin for breadth (B). The actual area (A) of the leaf was measured by graphical means (Winter *et al.*, 1956).

For critical analysis following steps were computed

1. Product of length (L) and breadth (B) = P
2. Actual area of individual leaves by graphical method = A
3. Linear regression equation Y = a + bx where x = L; x = B; or x = L × B (Snedecor and Cochran, 1967)
4. Leaf factor F_1 = A/P
5. Leaf area with regression equation Y = 5.7789 + 0.77x, (Ravi and Chaudhary, 1989) where x = P
6. Leaf area as P × 0.71 (Ravi and Chaudhary, 1989; F = 0.71)
7. Leaf area as P × F_1 (present study)

The percent deviation over actual leaf area was analyzed by following means.

a. (A – (P x 0.71)/A) × 100

b. (A-(P x 0.82)/A) x 100

c. [(A-(5.7789 + 0.77 x))/A] x 100

d. [(A-(-100.319 + 22.79 x B))/A] x 100

e. [(A-(10.726 + 0.7679 x P))/A] x 100

f. [(A-(-62.896 + 13.57 x L))/A] x 100

Results and Discussion

The estimation of leaf area in 100 accessions belonging to 19 different morphotypes of *D. alata* was carried out and comparative analysis of the present results with the reported linear regression equation and leaf factor (F) (Ravi and Chaudhary 1989) showed significant variation. The calculation of actual area and leaf factor (F_1) for different morphotypes has been given in Table 1 and the average value was found to be 0.82 as against earlier reported value of 0.71 (Ravi and Chaudhary, 1989). The actual area ranges between 63.81 cm^2 and 290.26 cm^2 and a mean value of 175.829 cm^2 in contrast to leaf area of 216.684 cm^2 obtained by multiplying length and breadth.

The computation of regression equation Y = a + bx, where x = L or B or L x B and their coefficient of determination (Table 2) showed maximum r^2 value when breadth was taken into consideration. The maximum r^2 value for this regression equation using breadth as the variable was a significant deviation over the earlier suggested model (Ravi and Chaudhary 1989) using (L × B) as the variable for the leaf area estimation in this species.

The circumspection of the percentage deviation over actual leaf area using six different theoretical formulae ('a' to 'f') are given in Table 3. The minimum percent deviation from actual leaf area (-0.706%) was obtained in the theoretical formula against item 'd' using breadth as the variable in the linear regression equation. But maximum deviation (11.908%) over actual area was shown by the formula 'a' which was based on the earlier reported leaf factor, 0.71 (Ravi and Chaudhary,1989). At the same time the calculated leaf area using leaf factor F_1 (0.82) showed the least and negligible deviation from actual leaf area. The formula 'b' using F_1 showed – 1.74% deviation which is much lesser as compared to 11.908%. The negative value in percentage indicate the decrease in value over actual leaf area. Even though the deviation from actual area is lesser while using the regression equation with product of length and breadth

Table 1. Comparison of leaf measurements in morphotypes of *D. alata*

Morphotype No.	Morphotype name	No. of accessions	Length (L)	Breadth (B)	L × B	Actual area	F_1
1	Chorakkachil	18	16.75	11.553	193.512	155.172	0.80
2	Parakkachil	6	16.517	11.433	188.838	150.438	0.80
3	Rosakampankachil	4	21.25	12.825	272.531	196.353	0.70
4	Kappakkachil	1	18.80	12.400	233.12	163.400	0.70
5	Mudiyankachil	1	24.20	15.000	363.00	241.980	0.67
6	Thonielayankachil	5	15.90	11.900	189.21	183.740	0.97
7	Kuttikkachil	4	15.125	09.825	148.603	125.882	0.84
8	Muzhayankachil	1	180.40	10.500	193.2	143.300	0.74
9	Neelankachil	1	15.00	09.000	135.00	90.090	0.67
10	Neelankachil	2	17.95	11.400	204.63	154.740	0.76
11	Kaiyyankachil	5	13.62	08.680	118.221	097.608	0.82
12	Kulambukachil	9	16.944	11.156	189.027	158.506	0.82
13	Thalavannankachil	27	18.744	13.030	244.234	206.168	0.85
14	Aanikachil	4	19.575	14.700	287.752	222.410	0.77
15	Pachamullankachil	1	15.60	14.000	218.4	195.440	0.89
16	Vattayilakachil	4	16.425	14.075	231.181	220.852	0.95
17	Chuvannamullankachil	1	15.60	13.100	204.36	168.970	0.83
18	Karimpachamullankachil	4	17.20	14.575	250.69	211.225	0.84
19	Thalikayilakachil	2	18.25	13.800	251.85	213.380	0.85

Table 2. Regression Equations and their coefficient of determination

S.No.	Equations	r^2%
1	Y = -62.896 + 13.57L	48.5*
2	Y = -100.319 + 22.79B	89.2*
3	Y = 10.726 + 0.7639 x (LxB)	83.3*

* Significant at 5% level

Table 3. Percentage deviations over actual leaf area

	Range	Mean
Actual leaf area	63.81 – 290.26	175.829
A	- 15.238 – 33. 212	11.980
B	- 33.091 – 22.864	- 1.74
C	- 29.585 – 24.066	0.865
D	- 28.135 – 20.051	- 0.706
E	- 33.19 – 21.266	- 1.956
F	- 56.126 – 37.71	- 4.306

as the variable (formulas 'c' and 'e'), the percent values obtained, viz., 0.865 and-1.956 are higher than the derived by the formula 'd'. Regression equation using length as the variable was neglected because of minimum r^2 value and the percentage deviation calculated over actual area also showed much higher variation (Formula 'e',– 4.306).

The test of significance for the percent deviations using T-test revealed that the deviation 11.908% while using the leaf factor 0.71 was significant over –1.74% obtained while using 0.82, the newly identified factor for *D. alata.* Moreover, the deviations – 0.076% and – 1.956% were not significant over 0.865 obtained while using the earlier reported regression equation.

Even though several methods have been devised for estimating leaf area like destructive, non-destructive, direct and indirect methods, the most common approach is to develop ratio and regression estimators using easily measurable leaf parameters such as length and breadth (Venkateswarlu and Biradar, 1980; Birader *et al.,* 1978). From a comparative study on linear measurement and leaf dry weight methods, it has been reported that linear measurement method is practically feasible and unbiased one for the calculation of leaf area in *Dioscorea* species (Ravi and Chaudhary, 1989).

But in the present study, it has been found that the leaf factor derived for *D. alata* including variable morphological forms grown in tropical humid climate varied from the earlier reported factor (F) for this species. The discrepancy in these value may be attributed to the fact that in the earlier study, measurements were based only on two varieties, which could not account for the extreme extent of morphologic variations occurring in a collection from a wide geographical area. In the present study, the selection of wide form a broad eco-geographic area and regeneration in identical situations might have reduced this deviation.

The critical analysis of deviation over actual leaf area using different means ('a' to 'f') also offered more chances for selection of a better value for leaf factor (0.82) and the regression equation using breadth as the variable with the minimum deviation. From this critical analysis it is clear that the regression equation $Y = -100.319 + 22.79x$, where x = breadth of leaf and the leaf factor 0.82 is more accurate in determination of leaf area in *D. alata.*

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References

Biradar RS, T Venkateswaralu and N Hrishi (1978) Leaf area estimation in *Colocasia. J. Root Crops.* **4:** 51-53.

Ravi V and S Roy Choudhary (1989) A method for leaf area determination in *Dioscorea. J. Root Crops.* **15:** 45-48.

Snedecor GW and WG Cochran (1967) *Statistical Methods.* Iowa State University Press Amer, USA.

Venkateswaralu T and RS Biradar (1980) Leaf area determination in tannia. *J. Root Crops* **6:** 45-74.

Velayudhan KC, VK Muralidharan, VA Amalraj and TA Thomas (1991). *Genetic Resources of Dioscorea alata* L. Sci. Monograph No. 1. National Bureau of Plant Genetic Resources, New Delhi.

Watson DJ (1952) The physiological variation in field yield. *Advan. Agron.* **4:** 101-145.

Winter EJ, PJ Salter, G Stanhill and JKA Bleadsdale (1956) Some methods of measuring leaf area. In: Miltrope FL (ed), *The Growth of Leaves,* Butterworths, London, 195p.

Ethnic Knowledge System on Wild *Dioscoreas* (yams) by the Kanikkars of Southern Western Ghats, Kerala

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Indigenous people with historical background of traditional resource utilization and management possess a vast assemblage of various knowledge systems on the complex behavioral pattern in relation to the ecological systems existing in their own localities. *Kanikkar*, a group of South Indian tribes found in the extreme southern end of Western Ghats has a traditional knowledge base transmitted from generation to generation. They acquired a sound knowledge on the various aspects including uses of cultivated crops and their wild allies. They use a wide array of wild yams for food. In this paper, an overview of the classification of these wild yams and their traditional uses by these indigenous people are summarized. A good relationship exist between the folklore etymology and taxonomic epithets of all the wild yams of the locality.

Key Words: *Dioscorea*, Ethnobotany, Indigenous Technical Knowledge, *Kanikkar*

Kanikkar popularly known as *Kani* is a South Indian tribe found in extreme South Kerala, around Agastyarkudam and Mahendragiri peaks of the Western Ghats in Kerala and nearby areas of the state of Tamil Nadu (Madhava Menon, 1996). They were nomadic agriculturists, but owing to diminution of edible roots and game, they practice settled agriculture, which enables them to live in one place and accumulate the necessities of life (Sashi, 1994). Rice, cassava, aroids and edible fruits form their staple food.

Generally, these tribals establish their dwellings in the semi-evergreen and moist deciduous forests of the southern Western Ghats at an elevation ranging from 90 m to 700 m and the habitat is mountainous. Climate is hot and humid in the plains with little variation throughout the year. Their dwellings are called 'Kanikkudi' and are mostly situated near water sources. Even though many of the settlements are trying to cope up with the development outside their traditional dwelling, they still, to a great extent, lead the traditional life in which many of the wild relatives of cultivated crops are used for their food requirements.

In the past, livelihood of the *Kanis* was totally forest based. Shifting cultivation, collection of Non-wood forest products (NWFP), hunting and fishing were their economic activities for survival and for obtaining a surplus for exchange and trade. The NWFP collected by these tribes are marketed through the Girijan Service Co-Operative Societies, because of the restrictions imposed in collection.

The areas of investigation included various 'Kani settlements' at the foothills of southern Western Ghats at an altitude of about 120 m to 330 m. Each settlement comprises a minimum of 10 families and it varies up to 45 having different literacy status. They have a better type of dwelling and bamboo forms the main building material. The area comes under the mountainous zone of Trivandrum district. The soil is forest loam of varying depth and of black colour. The area receives both South West and North-East monsoons. The average rainfall is about 1874 mm.

Materials and Methods

As a part of the exploration conducted in the extreme southern end of Western Ghats, five representative 'Kani settlements' in Thiruvananthapuram forest division between 8° 34' 995" and 8° 49' 178" N latitude and 77° 02' 960" and 77° 10' 083" E longitude have been surveyed for the traditional knowledge on tuber crops. The settlements include Chonampara in Kottur reserve, Potomav in Sanghili, Mottamood in Kallar, Chathankode and Chemmankala in Agastyavanam Biological Park. Informants from these settlements include local vaidyas and housewives. A survey was made around the settlement areas to assess the diversity and frequency of occurrence of wild yams. The wild yams have been recognized as NWFP under the section 'Kattukachil' of the group edible products. Information was collected from the tribe on the folk system of identification, classification and traditional uses of yams.

Results and Discussion

The area surveyed is a potential site for variability in wild relatives of crop plants especially, yams, *Piper, Vigna, Curcuma* and medicinal and aromatic plants. This

floristically rich area is relatively less explored for wild relatives.

Of the different wild allies of cultivated crops, much diversity and variability was noticed among wild yams (Prain and Burkill, 1936). Out of the 14 species of wild yams reported from southern region (Velayudhan *et al.*, 1998), seven different species occurred in this area showing much variation in their distribution. Among the seven different species of *Dioscorea* that have been collected (Table 1), *D. oppositifolia* was rare, while, *D. wallichii* and *D. tomentosa* were uniformly distributed. Others were found in occasional situations. Intra-specific variability was maximum in *D. pentaphylla* and *D. tomentosa.*

Identification and Classification of Wild Yams by Kanikkars

Traditional people have their own system for identification and classification of plant groups based on the uses and characteristics of resources. *Kanikkars* identify the genus *Dioscorea,* designated as *Kattukizhangu* or *kattukachil* by the nature of stem and leaves. Based on the external morphology of stem, colour, spininess and nature of leaves, they distinguish 7 different groups in wild yams (*Dioscorea*). The method of grouping and naming of the wild yams have been given in Table 1.

Table 1. Traditional grouping and naming of wild yams

Species	Traditional name	Frequency	Uses
Dioscorea wallichii	Neduvan	Uniform	Edible
Dioscorea pubera	Nadunooli	Occasional	Edible
Dioscorea tomentosa	Nooli	Uniform	Antidote for insect bite
Dioscorea oppositifolia	Kavalakizhangu	Rare	Edible
Dioscorea hispida	Thekizhangu (Naykuttykachil)	Occasional	Poisonous
Dioscorea bulbifera	Thampakizhangu	Occasional	Medicinal
Dioscorea pentaphylla	Nooran, Keerinooran	Occasional	Edible/for swelling

They classify each group by a different name and naming signifies the nature specific to the group. Their system of grouping and characters that forms the baseline of this grouping are summarized below:

Kattukizhangu/Kattukachil – Genus *Dioscorea*

I. Neduvan *(Dioscorea wallichii)*

Distinction of this group is identified by the shining, dark, smooth stem and simple glabrous cordate leaves with purple petiole. Tubers elongated, highly coiled, thin, hairy and fibrous. Because of the long thin tubers, they call this *Neduvan* (Neduvan = elongated) (Coll No.: AM/99-22; AM/ 99-62; Voucher Herb. Accn. No. 2027).

II. Nadunooli/Pulayankadan *(Dioscorea pubera)*

The identification of this group is effected by the green, highly pubescent aerial parts, dark green, cordate, highly pubescent leaves, very deep yellow tubers and with ovate aerial bulbils (Coll. No: AM/99-3; AM/99-27; AM/99-61)

III. Nooli *(Dioscorea tomentosa)*

They identify this group by the tomentose nature of aerial parts combined with simple to penta-foliate leaves. The distinctive feature of this group is the exudation of mucilage while breaking the tuber, which later forms a net, hence, the name 'nooli' (Coll. No.: AM/99-2; AM/99-24; Voucher Herb.Accn. No. 2029).

IV. Kavalakizhangu *(Dioscorea oppositifolia)*

Generally, the identification of this group is by the distinction of opposite leaves and the presence of smooth stem. This is the most precious edible tubers for the Kanis. They distinguish two different forms of this species:

(1) Kavalakizhangu – Having dark green leaves and black stem (Coll. No.: AM/99-37).

(2) Pinnankizhangu (Parakizhangu) – With purple stem and green leaves (Coll. No.: AM/99-58; Voucher Herb. Accn. No. 2035).

V. Thekizhangu (Naykutty kachil): *(Dioscorea hispida)*

Identification of this species is by the large, green trifoliate leaves and thick, spiny stem. The tubers are highly poisonous. The tubers are spherical to amorphous, flesh yellowish and are harvested in bulk. The name *Naykutty* is from the shape of the tuber resembling a mild puppy. (Coll No.: AM/99-10; AM/99-31; AM/99-46).

VI. Thampakizhangu: *(Dioscorea bulbifera)*

The angular wiry stem with very large cordate dark green leaves with numerous large aerial bulbils, form the identifying features. The name finds its origin by the fact of formation of numerous, large, warty, round

aerial bulbils on kampu (Thampu = stem). The tubers are spherical and brown (Coll. No.: AM/99-10A; AM/99-43).

VII. Nooran and Keerinooran *(Dioscorea pentaphylla)*

They distinguish two different types within this species.

a. Nooran: The tubers of these are edible and its leaves varied from simple to trifoliate (mainly 3-foliate). (Coll. No.: AM/99-45).

b. Keerinooran: The tubers are not edible, causes irritation and itching. Leaves are trifoliate. The food is a favourite one for *Keeri* (Mongoose), hence, the name *Keerinooran* (Coll. No.: AM/99-23; Voucher Herb. Accn. No. 2028).

Traditional Uses

1. *D. bulbifera:* Eaten as vegetable at times of scarcity; dried, powdered and applied to ulcers; also used for piles and dysentery. Tubers are used for liver ailments. These tubers are eaten by those who propose to become saints because of the development of hatred towards food.
2. *D. hispida:* Food at times of scarcity. The tubers are poisonous and are consumed after detoxification
3. *D. oppositifolia:* Tubers are ground and applied to swellings. This is the most favoured edible tuber.
4. *D. pentaphylla:* Tubers used for swellings and flowers are consumed as vegetable. Tubers of one form designated by them as 'Nooran' is edible and the other form, viz., Keerinooran is not edible.
5. *D. pubera:* Tubers and aerial bulbils are edible and are used only after detoxification in boiling water.
6. *D. wallichii:* Tubers are edible.
7. *D. tomentosa:* Tubers are not edible but used for medicinal purpose. The extract from the leaves are used as an antidote for insect bite, especially by bees.

It is vital that the value of the knowledge-practice belief complex of indigenous peoples relating to conservation of biodiversity is fully recognized, if ecosystem and biodiversity are to be managed sustainably (Gadgil, 1993). Moreover, conservation of traditional knowledge would be most appropriately accomplished through promoting the community based resource management system of indigenous people.

The societies with considerable dependence on hunting and gathering in their immediate neighborhoods are most likely to have accumulated long series of historical observations of relevance to sustainable resource use and conservation of biodiversity. Moreover, self-regulatory mechanisms tend to evolve in such societies when they are faced with resource limitations.

As *Kanikkars* were nomadic agriculturists and have considerable dependence on hunting and gathering from the ancestral period, they might have faced with resource limitations. Such a scarcity period might have forced them for search of more and more edible products. That may be the reason for the utilization of most of the *Dioscoreas* as edible ones. As a result of shifting cultivation, colonization of new territories occur. This may also have contributed for the use of most of the species of *Dioscorea* as edible ones. As far as the safeguarding and sustainable utilization of wild yams are concerned, some of the types like *Nadunooli* and *Kavalakizhangu,* which they prefer for their food, are being grown by them near their settlements or they preserve the plants in its natural habitat so that they can harvest the tubers in a sustainable manner during the next growing season.

Traditional way of classification based on the above ground morphology by these tribal people was found to tally with the taxonomic delimitation of the species in this genera. Even the distinction of two different forms in *D. pentaphylla* and *D. oppositifolia* by these people is an indication towards varietal classification for these species.

Even though much of the knowledge acquired by the pre-scientific societies are qualitative and based on observations on a rather restricted geographical scale, most of these diachronic observations (traditional knowledge transmitted from generation to generation) form the baseline for the synchronic observations of modern science.

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References

Gadgil M (1993) Indigenous knowledge for biodiversity conservation. *Ambio* **22:** 151-156.

Madhava Menon T (1996) Encyclopaedia of Dravidian Tribes. Vol. I and Vol. II. International School of Dravidian Linguistics.

Prain D and I H Burkill (1936-38) An account of the genus *Dioscorea* in the east. *Ann. Roy. Bot. Gard.* **14:** 1-528.

Sashi SS (1994) *Encyclopaedia of Indian* Tribes. Anmol Publications Pvt. Ltd., New Delhi.

Velayudhan KC, VK Muralidharan, VA Amalraj and KI Asha (1998) Genetic resources of yams of Western Ghats. *Indian J. Plant Genet. Resour.* **11:** 69-80.

Combining Ability over Environments for Yield and Yield Contributing Traits in Six-Rowed Barley (*Hordeum vulgare* L.)

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Ten parents and their 45 F_1s and F_2s were evaluated for grain yield and its component characters over three different environments (sowing dates). Highly significant variation was observed due to genotypes and environments for all 10 characters studied. Both *gca* and *sca* variances showed significant interactions. The genotypes RD-2552 and RD-2035 were found to be good general combiners and 15 crosses have been identified as good specific combiners for grain yield and other related traits. The crosses RD-2552 × RD-387, RD-2052 × RD-2508 and RD-2035 × RD-2552 were the best crosses for grain yield and most of the yield contributing traits.

Key Words: Barley, Combining Ability, *gca* × Environment Interaction, *sca* × Environment Interaction

Combining ability effects are considerably influenced by environments and for a more precise and valid conclusion, studies under different environments reveal the impact of genotype x environment interaction on the estimates. The present investigation was carried out in three different environments to study the combining ability of ten genotypes for different quantitative characters in six-rowed barley (*Hordeum vulgare*).

Materials and Methods

Ten varieties/strains of six-rowed barley, namely, RD-2035, RD-2052, RD-2503, RD-2508, RD-2552, RD-2585, RD-387 (Rajkiran), BL-2, ISBYT-4 and ISBYT-17 of diverse genetic origin were crossed in half diallel fashion. The parents along with 45 F_1s and F_2s were grown in randomized block design with three replications during *rabi* 2000-01 under early, normal and late sown conditions. Each plot consisted of two rows of 2 m length of non-segregating materials i.e. parents and F_1s and four rows of segregating materials *i.e.* F_2s with a spacing of 30 cm between the rows and 10 cm between plants. Ten competitive plants in parents and F_1s and 30 plants in F_2s progenies were selected randomly for recording observation under each environment separately. The statistical analysis for combining ability based on mean values was done as per method–II model–I of Griffing (1956). The pooled analysis over environments was carried out by the method of Singh (1973).

Results and Discussion

Pooled analysis of variance revealed significant variation among parents for all the traits, indicating adequate genetic variability among the parental lines used in the present study (Table 1). The genotype interacted significantly with the environments for all the traits. Combining ability analysis reveled that *gca* and *sca* variances were highly significant for all the traits. Both *gca* and *sca* showed significant interaction with environments for all the traits. The significant *gca* x environment and *sca* x environment interaction indicated that the estimates of both additive and non-additive gene

Table 1. Pooled analysis of variance for combining ability for various traits over three environments

Source of Variance	df	Days to heading	Plant height (cm)	Tillers/ plant	Flag leaf area(cm²)	Spike length(cm)	Spikelets/ spike	Grains/ spike	1000-grain weight(g)	Harvest index	Grain yield/ plant (g)
GCA	9	17.50*	47.01**	0.44**	0.46**	0.30**	19.17**	17.82**	6.11**	1.71**	8.16**
SCA	45	13.09*	27.57**	0.29*	0.16*	0.19*	14.52**	15.82**	5.23**	1.26**	3.83**
Env.	2	28.78*	80.25**	1.33*	0.12	0.98**	11.81*	12.13*	0.97	4.39*	5.40*
GCA x Env.	18	14.42*	32.04*	0.83*	0.67*	0.36*	14.13**	13.11*	11.09**	1.86*	15.81**
SCA x Env.	90	15.01**	51.93**	0.51**	0.52**	0.27*	15.53**	14.71**	6.69**	2.06**	9.26**
Error	594	5.46	10.73	0.12	0.14	0.13	3.38	2.75	1.48	0.56	1.11

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

effects are prone to change with the environment. Similar results were also reported by Vazquez and Sanchez (1987), Bhatnagar and Sharma (1995) and Singh *et al.* (1999).

The estimates of *gca* effects (Table 2) on the basis of pooled analysis revealed that the genotypes RD-2585, RD-2035 and RD-2552 for days to heading, BL-2 for plant height, RD-2508 and RD-2552 for tillers/plant, RD-2508, RD-2552 and RD-2052 for flag leaf area, RD-2503, RD-2035 and RD-2052 for spike length, RD-2552 for spikelets/spike, RD-2552 and RD-2035 for grains/spike, RD-2508, RD-2552, RD-2503 and RD-2585 for 1000-grain weight, RD-2503, RD-2508, RD-2052 and RD-2035 for harvest index and RD-2552, RD-2503, RD-2035 and RD-2052 for grain yield/plant.

Present finding revealed that the parent *viz.*, RD-2552 and RD-2035 offered the best possibilities of exploitation for development of improved high yielding genotypes of six-rowed barley.

Fifteen crosses which showed highest significant positive *sca* effects for grain yield are presented in Table 3. The crosses RD-2052 × RD-2508, RD-2503 × ISBYT-4 and RD-2503 × RD-387 exhibited desirable negative non significant *sca* effects for days to heading, whereas RD-2052 × RD-2508 and RD-2552 × RD-2585 showed desirable negative significant *sca* effects for dwarf ness. The cross RD-2552 × RD-387 exhibited positive and significant *sca* effects for tillers/plant, flag leaf area, spike length, spikelets/spike, grains/spike, harvest index and grain yield/plant. The crosses ISBYT-4 × ISBYT-17, RD-2035 × RD-2508, RD-2052 × ISBYT-17 and RD-2552 × BL-2 showed significant positive *sca* effects for 1000-grain weight. For the trait grain yield/plant the crosses, *viz.*, RD-2552

Table 2. Pooled estimates of general combining ability effects for various traits over different environments

Genotypes	Day to heading	Plant height (cm)	Tillers/ plant	Flag leaf area (cm^2)	Spike length (cm)	Spikelets/ spike	Grains/ spike	1000-grain weight (g)	Harvest index	Grain yield/ plant (g)
RD-2035	-0.64*	-0.80	-0.07**	0.03	0.08**	0.35	0.56*	0.13	0.08*	0.17*
RD-2052	1.24**	0.30	0.02	0.06*	0.06**	0.42	0.33	-0.48**	0.18**	0.16*
RD-2503	0.21	-0.76	0.00	0.00	0.10**	0.36	0.14	0.30*	0.23**	0.27**
RD-2508	-0.38	0.11	0.16**	0.10**	-0.01	-0.71*	-0.64*	0.52**	0.23**	0.08
RD-2552	-0.63*	1.09*	0.12**	0.06*	0.07**	1.24**	1.35**	0.48**	0.05	0.63**
RD-2585	-.092**	1.51**	0.00	-0.05*	-0.05**	-0.88**	-0.93**	0.25**	-0.19**	-0.27**
RD-387	-0.30	0.41	-0.12**	-0.09**	-0.05**	-0.29	-0.27	-0.09	-0.12**	-0.31**
BL-2	0.15	-1.21*	-0.07**	-0.05*	-0.11**	-0.22	-0.03	-0.36**	-0.02	-0.19*
ISBYT-4	0.83*	-0.57	0.03	0.02	-0.07**	-0.46	-0.56*	-0.70**	-0.27**	-0.46**
ISBYT-17	0.45	-0.08	-0.08**	-0.09**	-0.02	0.18	0.05	-0.05	-0.19**	-0.09
SE(gi)±	0.26	0.42	0.02	0.02	0.01	0.23	0.20	0.09	0.03	0.07

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

Table 3. Estimates of specific combining ability effects of the best 15 specific crosses over different environments

Crosses	Day to Heading	Plant height (cm)	Tillers/ plant	Flag leaf area (cm^2)	Spike length (cm)	Spikelets/ spike	Grains/ spike	1000-grain weight(g)	Harvest index	Grain yield/ plant(g)	*gca* status
RD-2035 x RD-2052	0.44	-0.54	0.32	0.32*	0.46**	3.06**	3.32**	0.67	0.79*	2.39**	H × H
RD-2035 x RD-2508	-0.27	-0.39	-0.06	0.01	0.09	2.22	1.18	1.73**	0.62	0.92	H × M
RD-2052 x RD-2508	-1.37	-5.55*	0.24	0.16	0.10	4.79**	4.37**	1.29*	0.69	3.06**	H × M
RD-2052 x ISBYT-17	3.79**	3.40	0.67**	0.70**	0.14	0.54	-0.12	1.64*	1.31**	2.07**	H × L
RD-2503 x RD-2585	2.64*	1.06	0.65**	0.62**	0.21	2.41*	1.57	-2.13**	0.67	1.53**	H × L
RD-2503 x RD-387	-1.10	3.94	0.14	0.02	0.42**	1.34	1.54	-0.38	0.62	1.10	H × L
RD-2503 x ISBYT-4	-1.11	-0.68	0.40	0.34*	0.35**	1.96	1.52	-0.94	0.40	1.41*	H × L
RD-2508 x ISBYT-4	2.03	0.15	0.34	0.35*	0.19	-1.10	-2.27	-0.30	0.70	1.06	M × L
RD-2508 x ISBYT-17	2.19	5.41*	0.71**	0.61**	0.19	1.59	1.39	0.12	0.68	1.32*	M × L
RD-2552 x RD-2585	2.70*	-5.05*	0.41*	0.53**	-0.08	-0.93	-1.00	0.49	1.50**	0.81	H × L
RD-2552 x RD-387	2.08	-0.58	0.76**	0.49**	0.53**	5.84**	5.40**	0.37	1.10**	3.34**	H × L
RD-2552 x BL-2	0.63	4.77	0.22	0.14	0.12	5.75**	5.55**	1.41*	0.94*	2.48**	H × L
RD-2552 x ISBYT-4	0.28	-1.64	0.25	0.22	0.53**	3.04**	3.63**	0.45	0.77*	2.04**	H × L
BL-2 x ISBYT-17	-0.79	-2.68	-0.08	-0.17	0.28*	3.20**	3.02**	0.50	0.46	1.46*	L × L
ISBYT-4 x ISBYT-17	-0.13	-0.03	0.04	-0.10	0.16	2.75**	2.60*	2.05**	0.74*	1.81**	L × L
Se (gi) ±	1.24	2.42	0.20	0.15	0.13	1.11	1.03	0.64	0.37	0.56	

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

× RD-387, RD-2052 × RD-2508, RD-2552 BL-2, RD-2035 × RD-2052 and RD-2052 × ISBYT-17 exhibited positive significant *sca* effects.

The crosses with significant positive *sca* effects for grain yield/plant involved parent with low × low or low × high *gca* effects indicating the presence of non-allelic interactions and also manifested heterosis of higher magnitude. Both parents with high *gca* effects when crossed had probably low magnitude of non-additive gene effects resulting in the small degree of *sca* effects and heterosis. The present findings are in agreement with the earlier results of Singh (1983) and Bhatnagar and Sharma (1995). Therefore, recurrent selection for *sca* could be followed in the segregating generation of the crosses RD-2035 × RD-2508, RD-2052 × RD-2508, RD-2052 × ISBYT-17, RD-2503 × RD-2585, RD-2503 × RD-387, RD-2503 × ISBYT-4, RD-2552 × RD-2585, RD-2552 × RD-387, RD-2552 × BL-2 and RD-2552 × ISBYT-4, as this type of relation was proposed on the assumption that an important part of heterosis results from the non-linear interaction of genes at different loci, from interaction between alleles at the same locus or from both causes in combination. It is possible to obtain substantial improvement with regard grain yield in addition to other desirable traits like tillers/plant, spike length, grains/spike, 1000-grain weight and harvest index. Heterosis breeding could be suggested for hybrid development but are not utilized so far in barley for commercial exploitation of heterosis.

References

Bhatnagar VK and SN Sharma (1995) Diallel analysis for combining ability for grain yield and its components in barley. *Indian J. Genet.* **55:** 228-232.

Griffing B (1956) Concept of general and specific combining ability in relation to diallel crossing systems. *Aus. J. Biol. Sci.* **9:** 463-493.

Singh D (1973) Diallel analysis for combining ability over several environments. *Indian J. Genet.* **33:** 469-481.

Singh I, SL Dashora, SN Sharma, EVD Sastry and I Singh (1999) Inheritance of some quantitative characters in six rowed barley. *Indian J. Genet.* **59:** 99-101.

Singh RP (1983) Combining ability in barley breeding. *Madras Agril. J.* **70:** 441-445.

Vazquez JF and EM Sanchez (1987) Correlations, Epistasis and Heterosis of plant height and internode length in barley. *Genome* **29:** 532-536.

Characterization of Some Macromutations Induced by Single and Combination Treatments of Gamma Rays, EMS and SA in Urdbean (*Vigna mungo* L. Hepper)

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Two improved cultivars of urdbean (*Vigna mungo* L. Hepper), namely, PDU1 and T9 were treated with single and combination doses/concentration of gamma rays, ethyl methane sulphonate (EMS) and sodium azide (SA). A number of various types of morphological macromutations were induced in M_2 generation. Out of these, 14 mutants from PDU1 and 13 from T9 were identified as true breeding for plant morphology, pod and seed characters and early maturity in M_3 generation. Many macromutants showed significant improvement in yield and other yield components as compared to their parents.

Key Words: Ethyl Methane Sulphonate (EMS), Gamma Rays, Macromutations, Sodium Azide, Urdbean (*Vigna mungo*)

Urdbean (*Vigna mungo* L. Hepper) is an important pulse crop of India grown on an area of about 3.15 million hectares with a production of 1.49 million tonnes. But the productivity is only 473 kg/ha in the country. The productivity of this crop is very low, particularly when compared with pigeonpea and chickpea. Since urdbean is a highly self-pollinated crop, the natural variability available is far less to make selections for its improvement. Induced mutagenesis has immense potential in creating genetic variability among naturally exhausted population which is utilized in selection programme for obtaining desirable improvement. The present study was conducted to induce and isolate useful macromutants which could be utilized for genetic improvement of this crop.

Material and Methods

Two improved cultivars of urdbean (*Vigna mungo* L. Hepper), namely, PDU1 and T9 were used as experimental materials. Three hundred pure, healthy and dry seeds of each cultivar were use for each treatment. The seeds were irradiated with gamma rays at 15, 30, 45 and 60 kR doses from Gamma Cell-200 having a 2000 Curie ^{60}Co source available at the Division of Genetics, Indian Agricultural Research Institute (IARI), New Delhi, in 1996. For chemical mutagenic treatments, the seeds were pre-soaked in distilled water for 6 h and then treated with ethyl methane sulphonate (0.02, 0.04, 0.06 and 0.08 M concentrations) in freshly prepared phosphate buffer (pH 7.0) or sodium azide (2, 4, 6, and 8 mM concentrations) in phosphate buffer (pH 3.0). For combination treatment, the gamma irradiated seeds at 15-60 kR doses were pre-soaked in distilled water for 6 h and then treated with 0.02 M EMS or 4 mM SA in the manner described earlier. The mutagen treated seeds were thoroughly washed in running water for 1 h to avoid traces of the chemicals, if any.

The mutagen treated seeds along with the untreated control seeds were sown in five rows each measuring 5 m with 30 × 10 cm spacing to raise M_1 generation. The surviving plants were harvested separately and individual plant progenies were raised in M_2 generation. A number of macromutations were induced in various treatments in M_2 generation. The macromutants having sufficient seeds were grown in M_3 generation in Randomized Block Design (RBD) with three replications and they were characterized and also confirmed for their breeding behaviour. The observations were recorded on 10 competitive plants from each replication for various yield and yield components in M_3 generation.

Results and Discussion

Several types of macromutations were induced by different mutagenic treatments in M_2 generation with respect to growth habit, leaf structure, days of mature and days to flower, pod and seed characteristics in both the cultivars, namely, PDU1 and T9. A dose dependent increase in the frequency and spectrum of macromutations was recorded in M_2 generation. A total of 31 and 34 types of macromutants were induced in cvs. PDU1 and T9, respectively. A wide spectrum of viable mutations can be expected in a mutation experiment. The probable causes of these macromutations may be chromosomal changes and most probably point or gene mutations. Most of these macromutations are reported to be

polygenic in nature (Yadav and Singh, 1988; Saini and Mahana, 1989; Thakur and Sethi, 1993).

Fourteen and 13 true breeding macromutants were derived from cultivars PDU1 and T9, respectively, for plant morphology, pod and seed characters and early maturity, were isolated in M_3 generation. These macromutants showed distinct morphological features as compared to their parents (Table 1 and 2). Eleven macromutants derived each from both the cultivars showed significantly higher seed yield than their parents. In case of the remaining macromutants, the performance was either equal or even less than the parents. The characteristic features of these macromutants are described below:

Growth Habit Mutants

The *dwarf, tall, bushy, spreading, tendriller* and *long peduncled* mutants were isolated in M_3 generation, The

Table 1. Mean values of yield and yield attributing traits of macromutants in cv. PDU1 in M_3 generation

S. No.	Macromutant	Mutagen treatment	Plant height (cm)	Days to maturity	Number of branches/ plant	Number of pods/ plant	Pod length (cm)	Number of seeds/ pod	Seed yield/ plant (g)	100-seed weight (g)
1.	Tall	30 kR + 4mM SA	52.50**	79.20	5.36**	36.40**	4.25	5.85	7.50**	4.50
2.	Bushy	45 kR	42.82	81.50	6.90**	34.86**	4.36	5.60	7.30**	4.25
3.	Spreading	30 kR + 4mM SA	40.24	85.50**	7.58**	27.60**	4.35	5.85	7.10**	4.40
4.	Dwarf	30 kR + 4 mM SA	31.10**	75.60**	3.15*	20.15**	4.10	5.58	6.15	4.25
5.	Broad-leaved	0.08 M EMS	38.63*	85.25**	4.50	20.58**	3.90**	5.15**	5.90	4.05
6.	Anthocyanin pigmented	30 kR	44.52	81.36	4.16	22.60	4.05**	5.35**	5.75*	4.20
7.	Hairy	45 kR + 0.02 M EMS	38.36**	82.37	4.52	18.22**	4.40	5.86	5.35**	3.90**
8.	Bold-podded	0.02 M EMS	39.52	82.50	3.92	32.86**	5.05**	6.80**	7.32**	4.82**
9.	Short-podded	0.08 M EMS	44.50	81.85	4.35	35.68**	3.25**	4.90**	6.10	3.85**
10.	Bold-seeded	8 mM SA	45.50**	80.68	4.55	32.87**	4.75**	6.25**	7.25**	5.45**
11.	Small-seeded	45 kR	42.56	82.86	4.55	30.50**	3.90**	4.80**	4.85**	3.05**
12.	Round-seeded	15 kR + 0.02 M EMS	41.96	84.85**	3.90	30.80**	3.95**	4.95**	5.05**	3.50**
13.	Brown-seeded	4 mM SA	46.80**	82.90	4.35	32.80**	4.35	5.70	6.90**	4.50
14.	Early maturing	15 kR + 0.02 M EMS	35.50**	65.00**	4.05	20.15**	4.15	5.56	5.15**	4.15
		Control	42.00	80.50	4.25	25.50	4.30	5.75	6.25	4.30
		SE ±	1.29	1.30	0.296	1.64	0.105	0.136	0.237	0.147

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

Table 2. Mean values of yield and yield attributing traits of macromutants in cv. T9 in M_3 generation

S. No.	Macromutant	Mutagen treatment	Plant height (cm)	Days to maturity	Number of branches/ plant	Number of pods/ plant	Pod length (cm)	Number of seeds/ pod	Seed yield/ plant (g)	100-seed weight (g)
1.	Tall and erect	15 kR + 4 mM SA	44.28**	80.55**	5.15**	28.62**	4.29	5.75	6.75**	4.35
2.	Tendriller	60 kR	30.65**	82.86	2.05**	15.70**	4.05	4.95**	4.58**	4.50**
3.	Bushy	0.08 M EMS	37.85*	83.07	5.90**	32.86**	4.25	5.80	6.50**	4.15
4.	Narrow leaved	4 mM SA	37.26**	82.80	4.25	18.75**	4.26	5.26	4.75**	4.08
5.	Dwarf	45 kR + 4 mM SA	25.60**	78.65**	2.75**	19.80	4.10	5.16**	5.16	4.36
6.	Early maturing	60 kR	32.82*	70.56**	3.65	20.85	4.25	5.75	4.80**	4.46**
7.	Anthocyanin pigmented	15 kR + 0.02 M EMS	38.75**	81.27*	4.05	16.87**	4.60**	5.95**	4.75**	4.35
8.	Hairy	30 kR	32.46**	85.26	3.70	18.26**	4.25	5.65	4.62**	4.26
9.	Bold and long podded	15 kR + 0.02 M EMS	40.81**	84.67	4.50*	30.65**	5.25**	6.95**	6.90**	4.55**
10.	Long-peduncled	30 kR + 4 mM SA	38.52**	86.80**	4.95**	20.26	4.58**	6.05**	5.10	4.10
11.	Bold-seeded	0.08 mM SA	36.75	80.37**	4.25	27.55**	4.75**	6.50**	6.60**	5.35**
12.	Chocolate-seeded	60 kR + 4mM SA	30.56**	86.82**	4.50*	25.86*	4.25	5.62	6.05*	4.35
13.	Short-podded	0.08 M EMS	38.20*	82.80	4.15	30.86**	3.05**	4.30**	4.25**	3.90
		Control	35.25	83.50	3.90	22.50	4.15	5.50	5.50	4.20
		SE ±	1.31	1.09	0.255	1.53	0.127	0.127	0.246	0.090

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

dwarf mutants were characterized by condensed nodes, shorter internodes and lower yield as compared to the control. The plants exceeding the height of the respective controls by at least 10 cm were placed in tall category. The *bushy* mutants were also induced in both the cultivars which were characterized by shorter internodes, compact stature and with higher number of pods. The *spreading* mutant exhibited branching paralled to the ground and covered more area than the normal plants. In the *tendriller* mutant, the leaflets were modified into tendrils. The *long peduncled* mutant had the characteristic of increased peduncle length joining the pods. Similar mutants have been reported by Pande and Raghuvanshi (1988) and Singh and Yadav (1991) in greengram and Thakur and Sethi (1993) and Gautam and Mittal (1998) in blackgram.

Leaf Mutants

The two true breeding leaf mutants, namely, *narrow-leaved* from T9 and *broad-leaved* from PDU1 were isolated in M_3 generation. The *broad-leaved* mutant exhibited increased leaf area and with significantly reduced plant height and number of pods/plants. The *narrow-leaved* mutant showed reduced leaf area with decreased seed yield as compared to the parents. Many types of leaf mutants have been reported in urdbean following mutagenesis (Singh and Raghuvanshi, 1985; Thakur and Sethi, 1993; Gautam and Mittal, 1998).

Early Maturing Mutants

The *early* maturing mutants were isolated from both the cultivars in M_3 generation. These mutants matured 10 to 15 days earlier than the normal period of the control and yielded lower than the respective controls. The *early* maturing mutants have been reported in urd (Sinha, 1988; Gautam and Mittal, 1998) and mung (Singh and Yadav, 1991).

Hairy and Anthocyanin Pigmented Mutants

These included the *hairy* and *anthocyanin* pigmented mutants. The *hairy* mutants had the characteristic of hairy growth all over the above ground parts, particularly on stem and pods. These mutants showed significantly reduced number of pods/plant and low seed yield than the control. This kind of mutant has been reported by Gautam and Mittal (1998) in urdbean. The presence of anthocyanin pigment, particularly on stem and branches of the plant was the characteristic feature of *anthocyanin*-pigmented mutant. This mutant also yielded significantly lower seed yield than its parent. Such mutants have been reported by Tickoo (1987) and Singh and Yadav (1991) in mungbean.

Pod Mutants

The *short-*, *bold-* and *long*-podded mutants were induced by different mutagenic treatments in both the cultivars in M_3 generation. The *short-podded* mutants had relatively less number of seeds per pod with lower yield than the control. Such mutants have been reported by Thakur and Sethi (1993) and Gautam and Mittal (1998) in urdbean. The *bold-* and *long-podded* mutants had significantly increased pod length, greater number of seeds/pod and more seed yield over their parents. Gautam and Mittal (1998) observed such mutants in urdbean.

Seed Mutants

The *brown* and *chocolate* testa colour mutants were isolated in M_3 generation as compared to the black testa colour of the parent varieties. Both the mutants exhibited a significant increase in the seed yield over the respective parents. The *bold*-seeded mutants were induced in both the cultivars which showed significantly increased pod length, number of seeds/pod, 100-seed weight and seed yield as compared to the controls. The *small-* and *round*-seeded mutants were also induced which showed significantly lower yield than the parents. The seed mutants for varied testa colours, shapes and sizes have been reported by Ali Khan and Veerswamy (1974) in redgram and Singh *et al.*, (1982) in greengram. These coloured testa mutants are likely to involve single genes.

Increasing mutation frequency is a very important aspect for improvement of mutation breeding programme. Gamma rays, EMS and SA have been demonstrated in induce mutations by different mechanisms. The combination of these mutagens in appropriate sequences has been shown to cause a synergistic increase in mutation frequency as observed during the present study as well as in the past (Cheng, 1987; Cheng and Gao, 1988). The combined treatments induced a higher mutation frequency, resulting in a higher mutation efficiency and an expansion of the spectrum of morphological mutations, thus, offering more opportunities for selection in mutation breeding practice.

Many mutants such as *tall, bushy, early* maturing, *long-* and *bold-podded, bold-seeded, hairy,* etc. induced during the present study show the desirable characteristics from the breeders' point of view and hold promise for isolation of improved types from their progenies in the later generations.

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References

Ali Khan WM and R Veeraswamy (1974) Mutations induced in redgram (*Cajanus cajan* L. Millsp) by gamma radiation and EMS. *Rad. Bot.* **14:** 237-242.

Cheng XY (1987) Physiological and mutagenic effects of sodium azide alone or in combination with gamma rays on rice (*Oryza sativa* L.) *Application of Atomic Energy in Agriculture* **No. 1,** pp 7-14.

Cheng XY and MW Gao (1988) Biological and genetic effects of combined treatments of sodium azide, gamma rays and EMS in barley. *Environ. Exp. Bot.* **28:** 281-288.

Gautam AS and RK Mittal (1998) Induced mutations in blackgram (*Vigna mungo* L. Hepper). *Crop Res.* **16:** 344-348.

Pande K and SS Raghuvanshi (1988) Gamma ray induced high yielding dwarf mutants in *Vigna radiata* L. Wilczek. *Mutation Breed Newsl.* **32:** 6-7.

Saini RG and SK Mahana (1989) Induction of mutations in mungbean. *J. Phytol. Res.* **2:** 61-68.

Singh RK and SS Raghuvanshi (1985) Pentaphyllus mutant in *Vigna mungo* (Urd). *Curr. Sci.* **54:** 1286-1287.

Singh VP, RDS Yadav, RM Singh, BD Singh and RB Singh (1982) Note on a golden yellow seed coat colour mutant of mungbean (*Vigna radiata* L. Wilczek) induced by gamma irradiation. *Legume Res.* **5:** 111-114.

Singh VP and RDS Yadav (1991) Induced mutations for qualitative and quantitative traits in greengram (*Vigna mungo* L. Wilczek) cv. T44. *J. Genet. Breed.* **45:** 1-5.

Sinha RP (1988) Early maturing dwarf mutants of urdbean (*Vigna mungo* L. Hepper). *J. Nucl. Agric. Biol.* **17:** 61-62.

Thakur HL and GS Sethi (1993) Characterization and segregation pattern of some macromutations induced in black gram (*Vigna mungo* L. Hepper). *Indian J. Genet.* **53:** 168-173.

Tickoo JL (1987) Spectrum and frequency of induced macromutants in mungbean. In: KS Gill, AS Khera, MM Verma and KS Bains (eds.) *First Symposium on Crop Improvement,* 23-27 Feb. Ludhiana Crop Improvement Society, India, pp 116-117.

Yadav RDS and PD Singh (1988) Induced synchronized mutant in mungbean. *Natl. Acad. Sci. Lett.* **11:** 271.

Genetic Divergence and Potentiality of Castor (*Ricinus communis* L.) Germplasm Collected from North-East India

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Eighty-nine accessions collected from North-east India were studied for genetic divergence and potentiality for yield and other economic traits. A number of accessions were identified as sources of traits of breeders' interest. Sources of resistance to fusarium wilt, jassids and serpentine leaf miner were identified. Eighty-nine accessions were grouped into six clusters. The diverse clusters derived could be used in hybridization programme to generate a wide range of transgressive segregates in populations for development of high yielding, disease and insect resistant castor varieties.

Key Words: Castor, Diversity, Germplasm, Resistance

Castor is grown across the country in semi wild to wild forms and semi-cultivated to cultivated forms in India. In order to collect indigenous castor germplasm, several explorations were taken up in India. As a part of it, an exploration was conducted in North-east India (Ajnani *et al.* 1994). The paper presents the diversity and potentiality of wild castor types collected from North-east India.

Materials and Methods

Eighty-nine accessions collected from Assam (32), Meghalaya (31), Mizoram (5), Nagaland (5) and Manipur (16) were evaluated under rainfed situation at Directorate of Oilseeds (DOR), Hyderabad, Rajasthan Agricultural University, Mandore, and All India Coordinated Research Project (Castor) Centre, Jalna, in an augmented block design, with five checks after every 10 accessions. Each accession was planted in a single row of 5 m length with 45 x 90 cm spacing. Recommended dose of NPK and plant protection measures were adopted. Data were recorded on plant height (cm), number of nodes to primary spike, days to 50% flowering, day to 50% maturity, total length of primary spike (cm), length of primary spike covered by capsules (cm), total number of productive spikes/plant, 100-seed weight (g), oil content (%), seed yield/plot (g) at 120, 150, 180 and 210 days after planting (DAP). Data from each centre were subjected to analysis separately.

Dispersion matrix of data of Hyderabad centre was used for studying genetic diversity using Mahalanobis's D^2 analysis, clustering was done according to Tocher's method. Adjusted mean values were used for the analysis. Screening against *Fusarium* wilt was carried out in high wilt sick plot at DOR, Hyderabad in 1999, 2000 and 2001. Leaf miner screening was done under natural heavy infestation from 1994-1997 at Hyderabad. Screening against jassids was done under natural heavy infestation by taking up late sowing in 1997 and 1998.

Results and Discussion

Potentiality of North-east Collection

In the present paper, only those accessions that consistently performed high at all the three locations are presented and their adjusted values were averaged to identify promising stable sources of agronomic and economic traits. Accessions suitable for each location were also selected based on their performance at the particular location. In castor, short plant height is desirable for easy harvesting, crossing and selfing. Three accessions, namely, RG 2034, RG 2042 and RG 1940 were identified for short plant height (46-49 cm). The number of nodes to primary spike on main stem was assumed as a good indicator of earliness (Singh and Yadav, 1981) of any specific castor genotype. The less the node number the earlier the accession. Three accessions (RG 1961, RG 1965 and RG 2047) possessed low node number (12). Primary spike contributes about 40-50% of yield in castor. Therefore, any improvement in length of primary spike would increase the yield. Eight North-eastern collections, namely, RG 1922, RG 1952, RG 1960, RG 1974, RG 1979, RG 1981, RG 1984 and RG 2029 had long primary spikes (41-51 cm). The inflorescence of castor is a raceme with unisexual, monoecious flowers. Male flowers are arranged at the lower part of the spike and female flowers at the upper part. Therefore, more the length of spike covered by capsules the more productive it would be. The accessions RG 1922, RG 1952, RG 1974, RG 1979 and RG 1981 possessed long length of primary spikes covered by capsules (34-38 cm). Seed weight is one of the important yield contributing component. In North-eastern collection, there accessions, namely, RG 1959, RG 1969 and RG 2029 possessed heavy seeds (37-41

g/100 seed). Total number of spikes/plant is another important yield contributing factor in castor. In our collection, seven accessions (RG 1978, RG 1987, RG 1993, RG 2014, RG 2017, RG 2018 and RG 2049) produced high number of productive spikes/plant (14-18). As castor is indeterminate in nature, harvesting was done at 120, 150, 180 and 210 DAP. Fifty per cent higher yield/plot was realized from RG 1952 (440 g) over the highest yielding check GCH 4 (290 g) at 120 DAP. At 210 DAP, very high yields were realized from RG 1961 (358 g) and RG 1968 (350 g) over GCH 4 (80 g).

Sources of Resistance Diseases and Insect pests

Fusarium wilt is the major disease of castor, which can cause up to 90% yield losses in traditional castor growing regions. Ten accessions (RG 1922, RG 1923, RG 1929, RG 1938, RG 1941, RG 1963, RG 2019, RG 2046, RG 2048 and RG 1925) were identified as wilt resistance sources. Wilt incidence in these accessions was 0%; and 40% and 80% in resistant check GCH 4 and susceptible check Aruna, respectively. These accessions are being used by breeders as sources of wilt resistance in crossing programmes. Four accessions, namely, RG 1982, RG 2000, RG 2001 and RG 2031 were identified as sources of resistance to jassid. There was no incidence of hopper burn and number of jassids/ leaf was three in the resistant accessions, while these were 80% and 200-300 in susceptible check Aruna. The accessions RG 1930 and RG 2008 were identified as the sources of resistance to serpentine leaf miner (*Liriomyza trifolii*) in the entire castor germplasm in India. Leaf infestation was 0% and number of larval mines/plant was 0 in these accessions, whereas in susceptible checks the infestation was 71-78% and larval mines/plant were 41-69. The resistance was attributed to the presence of high total phenols in these accessions (Prasad and Anjani, 2001). Since, the leaf miner is reportedly resistant to most insecticides, the integration of resistant genes is the only solution for its management. Hence, these are being utilized extensively in ongoing breeding programmes in the country to incorporate leaf miner resistance.

Diversity in North-East Collection

To measure the diversity in North-East collection, the adjusted mean values of eight important traits recorded at Hyderabad centre were used. The analysis of dispersion for the test of significance of differences in the mean values based on Wilk's criterion revealed highly significant differences between the genotypes for the aggregation of eight characters. The cluster composition and intra- and inter-cluster divergences are given in Table 1 and 2, respectively. Eighty-nine accessions were grouped into six diverse clusters. The main criterion for selection of diverse parents for hybridization using D^2 analysis is the inter-cluster distance. Genotypes included in clusters with maximum inter-cluster distance are obviously more divergent. In the present study, the highest inter-cluster (D) value was between cluster II and VI and the lowest was between V and VI. Selection of parents for hybridization has to be made from cluster II and VI to derive wide variability among segregates. The genotypes in cluster II had maximum intra-cluster distance showing the within cluster divergence. Crossing among the accessions in cluster II would yield diverse recombinants.

Table 1. Clustering of 89 accessions of castor

Cluster	Accessions
I	RG1922, RG1952, RG1926, RG 1976, RG1993, RG1947, RG1979, RG1981, RG1939, RG2009, RG1938, RG1960, RG1977, RG1936
II	RG1974, RG1980, RG2029, RG1929, RG1941, RG1967, RG1982, RG2013, RG1969, RG1942, RG2046, RG2030, RG1957, RG1973, RG1930, RG1948
III	RG1963, RG2003, RG1964, RG2011, RG1970, RG1997, RG1996, RG1962, RG1968, RG1971, RG1978, RG1987, RG1923, RG1958, RG1940
IV	RG1965, RG1949, RG1966, RG1953, RG1955, RG1959, RG1984, RG1927, RG1975, RG2001, RG2041, RG1928, RG1934, RG1931
V	RG1946, RG2032, RG1935, RG2019, RG2031, RG2043, RG1924, RG2012, RG1956, RG2042, RG2014
VI	RG1932, RG1972, RG1954, RG2047, RG1961, RG1992, RG2018, RG2034, RG2015, RG1993, RG2036, RG2017, RG2049, RG2035, RG2037, RG2040, RG2010, RG1925, RG2008

Table 2. Intra- and inter-cluster distance in 89 accession of castor

	I	II	III	IV	V	VI
I	**2.9**	4.3	4.1	3.5	4.8	4.5
II		**4.8**	4.3	4.4	4.7	5.2
III			**3.6**	3.9	3.9	4.4
IV				**2.6**	2.9	3.0
VI					**2.1**	2.7
V						**2.3**

The cluster mean values for different traits showed wide variability (Table 3). Cluster VI has the highest value for total number of spikes/plant and Cluster I had the highest value for total primary spike length and length of primary spike covered by capsules. Accessions possessing highest seed weight were grouped in cluster II. Therefore, crossing among these three groups

Table 3. Intra-cluster mean values for different characters in castor

	Plant height (cm)	Number of nodes	Total length of primary spike (cm)	Length of primary spike covered by capsules (cm)	Days to 50% flowering	Days to 50% maturity	100-seed weight	Total spikes/ plant
I	144	21	39	28	96	135	23	4
II	173	23	31	19	107	147	25	3
III	130	22	27	17	111	154	22	5
IV	113	18	31	19	77	116	24	4
V	100	16	23	14	83	117	17	5
VI	86	16	29	16	73	111	18	8

would produce recombinants having desirable high yield traits. The wilt resistant accessions were grouped in five clusters (I, II, III, IV and VI). Leaf miner resistant accessions were grouped in two different clusters (II and VI) and jassid resistant accessions were found in II, IV and V clusters. The diverse clustering of resistant sources indicates that the resistant sources are quite diverse in their performance. Cluster II is the most potential one; as it was comprised of wilt, jassid and leaf miner resistant sources. Crossing with cluster II would produce diverse recombinants with resistance to diseases/insect pests.

The isolation of genetically diverse genotypes and grouping of less diverse ones, and identification of disease and insect resistant sources in the present study would greatly help castor breeders, to select the promising base material to generate desirable recombinants for high yield and disease and insect resistance.

References

Anjani K, SK Chakravarty and MVR Prasad (1994) Collecting castor (*Ricinus communis* L.) germplasm in North-eastern Hill Province of India. *IBPGR Newsletter for Asia, the Pacific and Oceania* **17:** 13.

Prasad YG and K Anjani (2001) Resistance to serpentine leaf miner (*Liriomyza trifolii*) in castor (*Ricinus communis*). *Indian J. Agric. Sci.* **71**: 351-352.

Singh H and TP Yadav (1981) Genetic analysis of days to flower, maturity and yield in castor. *Haryana Agric.Univ. J. Res.* **11:** 54-59.

Quarantine Risk Associated with Exchange of Plant Genera Carrying Hidden Infestation

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A large number of plant germplasm samples are being exchanged throughout the world for crop improvement programmes. In addition, the liberalized trade in the present global scenario (WTO regime) has increased the flow of agricultural commodities across different countries. These exchanges always carry the risk of inadvertent introduction and spread of exotic pests. Such pests, if established may prove more devastating in the new geographical areas in the absence of natural enemies and competitors. The risk of introduction of exotic pests could be minimized by undertaking quarantine of the planting material under exchange. The effective implementation of quarantine measures at National Bureau of Plant Genetic Resources (NBPGR) has resulted in the interception of a number of exotic pests. These include *Acanthoscelides obtectus* in *Cajanus cajan, Phaseolus vulgaris* and *Vicia faba* from Brazil, Bulgaria and Malawi; *Anthonomus grandis* in *Gossypium* sp. and *Hibiscus* spp. from USA; *Bruchophagus gibbus* in *Medicago* spp. and *Trifolium* spp. from France, Germany, Italy, USA and USSR; *Leptinotarsa decemlineata* in potato from Europe and USA; *Popillia japonica* in root stocks of nursery crops from Japan, USA and USSR.

There are groups of insects infesting seeds, *viz.*, seed wasps (Hymenoptera: Chalcidoidea), pulse beetles (Coleoptera: Bruchidae), and a few weevils/borers (Coleoptera:Curculionidae/Scolytidae) which infest the developing seeds without showing external symptoms of their presence within. Such an infestation is called hidden or latent infestation.

The quarantine risk becomes much higher with the exchange of seeds with hidden infestation because these are not detectable through routine visual inspection. There are several examples of movement of such insects across the geographical boundaries. The douglas fir seed chalcid (*Megastigmus spermotrophus* Wachtl.) has spread from its original home in western United States to Scotland (Mac Dougall, 1926), France (Vayssiere, 1931), Germany (Escherich, 1938) and New Zealand (courlay, 1930) alongwith the shipment of douglas fir (*Pseudotsuga taxifolia*) seeds. The rose seed chalcid [*Megastigmus aculeatus* (Swedrus)] was introduced into New Jersey (USA) through the seeds of *Rosa multiflora* from Japan (Weiss, 1917). The crop losses reported to have been caused by various introduced chalcid pests include seed damage over 80% by *Bruchophagus roddi* in the seeds of alfalfa (Strong, 1962) and about 40% by *Systole albipennis* in various umbelliferous seeds (Gupta, 1962). Seed damage to the extent of about 40% has been reported in *Trifolium alexandrium* by bruchids, viz., *Bruchidius alfieri* and *Bruchidius trifolii* (Abou-Raya, 1954).

Detection of Hidden Infestation

During quarantine processing, the seeds of *Glycyrrhiza glabra* imported from Iraq were suspected to carry hidden infestation. Hence, these were detained to observe the emergence of any insect. The insects emerged during detention were identified as eurytomids (Chalcidoidea), *Bruchophagus glycyrrhizae* (Wadhi, 1963, 1967) and bruchid, *Bruchidius* sp. (Wadhi *et al.*, 1966). This highlighted the possibility of escape of such pests during routine quarantine inspection due to hidden nature of infestation and the need for development of specialized detection procedures. Therefore, X-ray radiography technique was standardized for the detection of hidden infestation in seeds at National Bureau of Plant Genetic Resources (Wadhi *et al.*, 1967). The seeds are spread on a sheet of paper that is placed on an envelope containing the Agfa Rapid X-ray film and are exposed to soft X-rays generated at 22 Kv, 3 mA, at a distance of 30 cm from the source for 15 seconds. The envelope containing the exposed film is removed gently without disturbing the seed geometry and the film is developed/ fixer prepared for the purpose. Infested seeds are marked on the X-ray plate and corresponding (infested) seeds are then hand picked from the seed sample with original geometry retained on the paper. The dose, however, is varied with the size, shape or thickness of the seeds

for better resolution of image on the X-ray plate. The dose is also standardized for different seeds as and when required, as was done in case of mango stones (exceptionally large seeds) for detection of mango stone weevil, *Sternochaetus mangiferae* (Kapur *et al.*, 1997).

The seed transparency technique (Kaura, 1959) is used for detection of hidden infestation in small seeds as it is difficult to screen them through X-ray radiography. The seeds are boiled in lactophenol solution containing distilled water, phenol crystalsl, lactic acid and glycerine till these are sufficiently transparent to reveal the internal infestation. However, the fumes of phenol (skin irritant) are hazardous to the workers and also the valuable imported material under test gets destroyed during the process. These two techniques have been extensively used to screen the seeds of plant genera carrying hidden infestation since 1967 (Wadhi *et al.*, 1968).

Techniques such as X-ray micrography or projection micrography need to be developed so that the radiograph of small seeds could be enlarged and accurately analysed. This would overcome the limitations of two techniques.

Need to Identify the Plant Genera Carrying Hidden Infestation

X-ray radiography is a cumbersome and time consuming process. It also requires enormous funds and, thus, it is practically impossible to screen all the exotic seed material. Therefore, need was felt to identify the plant genera which can carry the latent infestation so as to reduce the workload of X-ray radiography and to minimize the quarantine risk of introduction of pests causing latent infestation. Consequently, two lists namely one for plant genera reported to be infested by one or the other species of *Phytophagous chacidoids* (Wadhi, 1967) and other for bruchids of the genus *Bruchidius* (Wadhi and Verma, 1971) were drawn from the published reports. These two lists comprised 148 plant genera that were designated as the *listed plant genera* and their seeds were compulsorily subjected to X-ray radiography (Wadhi, 1980).

Later, during the quarantine processing, seeds of genera other than the listed plant genera were also suspected to carry infestation and the same was confirmed through X-ray screening. The bruchid, *Pachymeus lacerrdae* (Coleoptera: Bruchidae) was intercepted in the nuts of *Orbignya phalerata* from Brazil (Kapur *et al.*, 1988); seed chalcid, *Eurytoma* sp. in the seeds of *Urginea maritima* from Cyprus (Kapur *et al.*, 1992); seed chalcids, *Quadrastichodella eucalypti* in seeds of *Eucalyptus* and *Bootanomyia* sp. In seeds of *Casurina* sp. from Australia (Mathur and Lal, 1996). Analysis of pest risk in respect of various crops through perusal of literature (Kapur *et al.*, 1989) and over experience of exposing the doubtful seeds to X-ray radiography resulted in addition of many more genera to the listed plant genera, requiring X-ray screening. The list was further updated by extensive scrutiny of the catalogues on family bruchidae (Udayagiri and Wadhi, 1989) and phytophagous chalcidoidea (Muesebeck *et al.*, 1975; Krombein, 1958; Peck, 1963), review of Agricultural Entomology, Series A (Anonymous, 2000) and available literature. The list now comprises 340 plant genera belonging to 75 plant families. The families of plant genera (Jackson, 1977a,b; Usher, 1984; Terrell *et al.*, 1986) have been included for future reference because it is well known that the host plant relationship exists between specific taxonomic groups of plants and insects. This would help as a precaution against other plant genera also belonging to these families which may harbour similar infestation. The updated list (Table 1) shows plant genera known to carry hidden infestation of bruchids (194), chalcids (72), both bruchids and chalcids (71) and others as curculionids/scolytids (3).

Table 1. Plant genera in their seeds which carry hidden infestation of bruchids, chalcids and others

S.No.	Genus	Family	S.No.	Genus	Family
1.	*Abelmoschus*[b]	Malvaceae	33.	*Astrocaryum*[b]	Palmae
2.	*Abies*[c]	Pinaceae	34.	*Attalea*[b]	Araecaceae
3.	*Abrus*[b]	Fabaceae	35.	*Atylosia*[b]	Fabaceae
4.	*Abutilon*[b]	Malvaceae	36.	*Baccharis*[b]	Compositae
4.	*Acacia*[b]	Fabaceae	37.	*Bactris*[b]	Arecaceae
6.	*Acer*[c]	Aceraceae	38.	*Bambusa*[c]	Poaceae
7.	*Achillea*[c]	Asteraceae	39.	*Banisteriopsis*[b]	Malpighiaceae
8.	*Acrocomia*[b]	Arecaceae	40.	*Baptisia*[b]	Fabaceae
9.	*Acuan*[b]	Fabaceae	41.	*Barcena*[b]	Fabaceae
10.	*Adenocarpus*[b]	Fabaceae	42.	*Bauhinia*[b]	Fabaceae
11.	*Aeschynomene*[b]	Fabaceae	43.	*Bellis*[c]	Compositae
12.	*Albizzia*[b]	Fabaceae	44.	*Bixa*[b]	Bixaceae
13.	*Alhagi*[b]	Fabaceae	45.	*Bonjeanea*[bc]	Fabaceae
14.	*Allocasuarina*[c]	Casuarinaceae	46.	*Borago*[b]	Boraginaceae
15.	*Aloe*[c]	Aloeaceae	47.	*Bothriochloa*[c]	Poaceae
16.	*Amelanchier*[c]	Rosaceae	48.	*Bradburia*[b]	Compositae
17.	*Ammi*[bc]	Apiaceae	49.	*Brassica*[b]	Brassicaceae
18.	*Ammodendron*[b]	Fabaceae	50.	*Bromus*[bc]	Poaceae
19.	*Amomum*[b]	Zingiberaceae	51.	*Buchenania*[b]	Anacardiaceae
20.	*Amorpha*[b]	Fabaceae	52.	*Bupleurum*[bc]	Apiaceae
21	*Anethum*[c]	Apiaceae	53.	*Butea*[b]	Fabaceae
22.	*Annona*[c]	Annonaceae	54.	*Cachrys*[bc]	Apiaceae
23.	*Anthyllis*[bc]	Fabaceae	55.	*Caesalpinia*[b]	Fabaceae
24.	*Apeiba*[b]	Tiliaceae	56.	*Cajanus*[b]	Fabaceae
25.	*Apium*[c]	Apiaceae	57.	*Calapogonium*[b]	Fabaceae
26.	*Apoplanesia*[b]	Fabaceae	58.	*Calliandra*[b]	Fabaceae
27.	*Arachis*[b]	Fabaceae	59.	*Calycotome*[bc]	Fabaceae
28.	*Arenaria*[b]	Caryophyllaceae	60.	*Calystegia*[b]	Convolvulaceae
29.	*Argyreia*[b]	Convolvulaceae	61.	*Camellia*[c]	Theaceae
30.	*Artemisia*[b]	Asteraceae	62.	*Canavalia*[b]	Fabaceae
31.	*Ascelpias*[c]	Asclepiadaceae	63.	*Capparis*[b]	Capparaceae
32.	*Astragalus*[bc]	Fabaceae	64.	*Caragana*[bc]	Fabaceae

S.No.	Genus	Family
65.	*Cassia*[b]	Fabaceae
66.	*Casuarina*[b]	Casuarianceae
67.	*Caucalis*[bc]	Apiaceae
68.	*Cedrus*[c]	Pinaceae
69.	*Cenchrus*[c]	Poaceae
70.	*Centaurea*[bc]	Asteraceae
71.	*Centranthus*[b]	Velarianeae
72.	*Centrosema*[b]	Fabaceae
73.	*Ceratonia*[b]	Fabaceae
74.	*Cercidium*[b]	Fabaceae
75.	*Cercis*[b]	Fabaceae
76.	*Chamaecrista*[b]	Fabaceae
77.	*Chamaecruistata*[c]	Pinaceae
78.	*Chaemaecyparis*[b]	Cupressaceae
79.	*Chesneya*[b]	Fabaceae
80.	*Chrysanthemum*[bc]	Asteraceae
81.	*Cicer*[b]	Fabaceae
82.	*Cichorium*[c]	Asteraceae
83.	*Cissus*[bc]	Vitaceae
84.	*Cnidoscolus*[c]	Euphorbiaceae
85.	*Coccothrinax*[c]	Arecaceae
86.	*Cocos*[b]	Arecaceae
87.	*Colutea*[b]	Fabaceae
88.	*Combretum*[bc]	Combretaceae
89.	*Condalia*[b]	Rhamnaceae
90.	*Convolvulus*[b]	Arecaceae
91.	*Copernicia*[b]	Arecaceae
92.	*Cordia*[b]	Boraginaceae
93.	*Coriandrum*[c]	Apiaceae
94.	*Coronilla*[bc]	Fabaceae
95.	*Coursetia*[b]	Fabaceae
96.	*Cracca*[b]	Fabaceae
97.	*Crataegus*[c]	Rosaceae
98.	*Crotalaria*[b]	Fabaceae
99.	*Cryptomeria*[c]	Coniferaceae
100.	*Cumin*[c]	Apiaceae
101.	*Cupressus*[bc]	Cupressaceae
102.	*Cyamopsis*[bc]	Fabaceae
103.	*Cybistax*[b]	Bignoniaceae
104.	*Cymbosema*[b]	Fabaceae
105.	*Cynoglossum*[c]	Boraginaceae
106.	*Cytisus*[b]	Fabaceae
107.	*Dactylis*[c]	Poaceae
108.	*Dahlia*[c]	Compositae
109.	*Dalbergia*[b]	Fabaceae
110.	*Dalea*[b]	Fabaceae
111.	*Daubentonia*[b]	Fabaceae
112.	*Daucus*[bc]	Apiaceae
113.	*Dendrocalamus*[c]	Poaceae
114.	*Desmanthus*[b]	Fabaceae
115.	*Desmodium*[bc]	Fabaceae
116.	*Desmonchus*[b]	Plamae
117.	*Dialium*[b]	Fabaceae
118.	*Dichostachys*[bc]	Fabaceae
119.	*Dioclea*[b]	Fabaceae
120.	*Diospyros*[bc]	Ebenaceae
121.	*Dodonaea*[b]	Sapindaceae
122.	*Dolichos*[bc]	Fabaceae
123.	*Dombeya*[b]	Sterculiaceae
124.	*Dorycnium*[b]	Fabaceae
125.	*Draba*[c]	Cruciferae
126.	*Drypetes*[b]	Euphorbiaceae
127.	*Earleocassia*[b]	Fabaceae
128.	*Echium*[c]	Boraginaceae
129.	*Elaeis*[b]	Arecaceae
130.	*Enterolobium*[b]	Fabaceae
131.	*Epilobium*[b]	Onagraceae
132.	*Eriosema*[b]	Fabaceae
133.	*Errazurizia*[b]	Fabaceae
134.	*Eryngium*[bc]	Apiaceae
135.	*Erythraea*[b]	Gentianaceae
136.	*Erythrina*[b]	Fabaceae
137.	*Eucalyptus*[c]	Myrtaceae
138.	*Eugenia*[bc]	Myrtaceae
139.	*Eupatorium*[b]	Asteraceae
140.	*Euphorbia*[bc]	Euphorbiaceae
141.	*Euterpe*[b]	Arecaceae
142.	*Fagopyrum*[b]	Polygonaceae
143.	*Festuca*[c]	Poaceae
144.	*Ficus*[c]	Moraceae
145.	*Foeniculum*[c]	Apiaceae
146.	*Galactia*[b]	Fabaceae
147.	*Galega*[bc]	Fabaceae
148.	*Genista*[bc]	Fabaceae
149.	*Gleditschia*[bc]	Fabaceae
150.	*Glycine*[bc]	Fabaceae
151.	*Glycyrrhiza*[bc]	Fabaceae
152.	*Gossypium*[bc]	Malvaceae
153.	*Guarea*[b]	Meliaceae
154.	*Guazuma*[b]	Sterculiaceae
155.	*Gymnosperma*[b]	Compositae
156.	*Haematoxylon*[c]	Fabaceae
157.	*Halimodendron*[bc]	Fabaceae
158.	*Hardwickia*[b]	Fabaceae
159.	*Hedysarum*[bc]	Fabaceae
160.	*Helianthemum*[b]	Cistaceae
161.	*Helianthus*[b]	Asteraceae
162.	*Heracleum*[c]	Umbelliferae
163.	*Heteropterys*[b]	Malpighiaceae
164.	*Hibiscus*[b]	Malvaceae
165.	*Hippocrepis*[bc]	Fabaceae
166.	*Hippomane*[b]	Euphorbiaceae
167.	*Hoffmanseggia*[b]	Fabaceae
168.	*Holcus*[c]	Poaceae
169.	*Hosackia*[b]	Fabaceae
170.	*Hymenaena*[b]	Fabaceae
171.	*Hymenoclea*[b]	Compositae
172.	*Icma*[b]	Compositae
173.	*Ichthymethia*[b]	Fabaceae
174.	*Ilex*[c]	Aquifoliaceae
175.	*Indigofera*[bc]	Fabaceae
176.	*Inodes*[b]	Palmae
177.	*Inula*[c]	Asteraceae
178.	*Impmoea*[b]	Convolvulaceae
179.	*Isatis*[c]	Brassicaceae
180.	*Juniperus*[c]	Cupressaceae
181.	*Lab lab*[b]	Fabaceae
182.	*Laburnum*[bc]	Fabaceae
183.	*Lagonychium*[b]	Fabaceae
184.	*Larix*[c]	Pinaceae
185.	*Laserpitium*[c]	Umbelliferae
186.	*Lathyrus*[bc]	Fabaceae
187.	*Lechea*[b]	Cistaceae
188.	*Lens*[bc]	Fabaceae
189.	*Lepidium*[c]	Brassicaceae
190.	*Leptoglottis*[b]	Fabaceae
191.	*Lespedeza*[bc]	Fabaceae
192.	*Leuceana*[b]	Fabaceae
193.	*Leuzea*[b]	Compositae
194.	*Lisaea*[b]	Umbelliferae
195.	*Lithraea*[b]	Anacardiaceae
196.	*Lonchocarpus*[b]	Fabaceae
197.	*Lotus*[bc]	Fabaceae
198.	*Luchia*[b]	Tiliaceae
199.	*Ludwigia*[b]	Onagraceae
200.	*Lupinus*[bc]	Fabaceae
201.	*Lysiloma*[b]	Fabaceae
202.	*Lythrum*[b]	Lythraceae
203.	*Macroptilium*[b]	Fabaceae
204.	*Malus*[c]	Rosaceae
205.	*Mangifera*[b]	Anacardiaceae
206.	*Mecadamia*[b]	Proteaceae
207.	*Medicago*[bc]	Fabaceae
208.	*Meibomia*[b]	Fabaceae
209.	*Melanoxylon*[b]	Fabaceae
210.	*Melilotus*[bc]	Fabaceae
211.	*Mentha*[bc]	Lamiaceae
212.	*Merremia*[b]	Convolvulaceae
213.	*Mimosa*[b]	Fabaceae
214.	*Mucuna*[b]	Fabaceae
215.	*Myobroma*[b]	Fabaceae
216.	*Myrcia*[b]	Myrtaceae
217.	*Nelumbo*[b]	Nelumbonaceae
218.	*Neptunia*[b]	Fabaceae
219.	*Nissolia*[b]	Fabaceae
220.	*Nitraria*[b]	Zygophyllaceae
221.	*Ochroma*[b]	Bombacaceae
222.	*Olea*[c]	Oleaceae
223.	*Olneya*[b]	Fabaceae
224.	*Onobrychis*[bc]	Fabaceae
225.	*Ononis*[bc]	Fabaceae
226.	*Orbignya*[b]	Arecaceae
227.	*Ornithopus*[bc]	Fabaceae
228.	*Oryza*[b]	Poaceae
229.	*Oxytropis*[bc]	Fabaceae
230.	*Pachyrrhizus*[b]	Fabaceae
231.	*Panax*[c]	Araliaceae
232.	*Pandanus*[b]	Pandanaceae
233.	*Panicum*[b]	Poaceae
234.	*Parkia*[b]	Fabaceae
235.	*Parkinsonia*[bc]	Fabaceae
236.	*Parryella*[b]	Fabaceae
237.	*Parthenium*[b]	Asteraceae
238.	*Parthenocissus*[c]	Vitaceae
239.	*Pavonia*[c]	Malvaceae
240.	*Pennisetum*[b]	Poaceae
241.	*Petalostemon*[b]	Fabaceae
242.	*Petit*[bc]	Verbenaceae
243.	*Pettaria*[bc]	Fabaceae
244.	*Phaseolus*[b]	Fabaceae
245.	*Phleum*[c]	Poaceae
246.	*Phoenix*[0]	Arecaceae
247.	*Physocarpus*[c]	Rosaceae
248.	*Physostigma*[b]	Fabaceae
249.	*Phytelephas*[b]	Arecaceae
250.	*Picea*[c]	Pinaceae
251.	*Piliostigma*[b]	Fabaceae
252.	*Pimpinella*[b]	Apiaceae
253.	*Pinus*[c]	Pinaceae
254.	*Piptadenia*[b]	Fabaceae
255.	*Piscidia*[b]	Fabaceae
256.	*Pistacia*[c]	Anacardiaceae
257.	*Pisum*[b]	Fabaceae
258.	*Pithecellobium*[b]	Fabaceae
259.	*Plantago*[0]	Plantaginaceae
260.	*Poinciana*[b]	Fabaceae
261.	*Podocytisus*[bc]	Fabaceae
262.	*Prangos*[bc]	Umbelliferae
263.	*Primula*[c]	Primulaceae
264.	*Prosopis*[bc]	Fabaceae
265.	*Prunus*[c]	Rosaceae
266.	*Pseudabutilon*[b]	Malvaceae
267.	*Pseudosamanea*[b]	Fabaceae
268.	*Pseudotsuga*[c]	Pinaceae
269.	*Psidium*[c]	Myrtaceae
270.	*Psophocarpus*[b]	Fabaceae
271.	*Pterocarpus*[b]	Fabaceae
272.	*Pueraria*[b]	Fabaceae
273.	*Pyrus*[c]	Rosaceae
274.	*Quercus*[c]	Fagaceae
275.	*Reseda*[c]	Resedaceae
276.	*Rhamnus*[b]	Rhamnaceae
277.	*Rhus*[c]	Anacardiaceae
278.	*Rhynchosia*[b]	Fabaceae
279.	*Ricinus*[b]	Euphorbiaceae
280.	*Rbinia*[bc]	Fabaceae
281.	*Rosa*[bc]	Rosaceae
282.	*Rosmarinus*[c]	Lamiaceae
283.	*Ruellia*[b]	Acanthaceae
284.	*Sabal*[b]	Arecaceae
285.	*Salvia*[bc]	Lamiaceae
286.	*Samanea*[bc]	Fabaceae
287.	*Sarothamnus*[b]	Fabaceae
288.	*Sauvagesia*[b]	Ochnaceae
289.	*Scheelea*[b]	Plamae
290.	*Schinus*[b]	Anacardiaceae
291.	*Schrankia*[b]	Fabaceae
292.	*Scorpiurus*[bc]	Fabaceae
293.	*Senna*[b]	Febacea
294.	*Sesamum*[c]	Pedaliaceae
295.	*Sesbania*[bc]	Fabaceae
296.	*Sesbastiana*[b]	Euphorbiaceae
297.	*Sideroxylon*[b]	Sapotaceae
298.	*Silybum*[c]	Asteraceae
299.	*Smilax*[c]	Smilacaceae
300.	*Smirnowia*[c]	Fabaceae
301.	*Soja*[b]	Fabaceae
302.	*Sophora*[bc]	Fabaceae
303.	*Sorbus*[c]	Rosaceae
304.	*Spartium*[bc]	Fabaceae
305.	*Sphaerophysa*[b]	Fabaceae
306.	*Spiraea*[c]	Rosaceae
307.	*Spondias*[bc]	Anacardiaceae
308.	*Strombocarpus*[b]	Fabaceae
309.	*Strophostyles*[b]	Fabaceae
310.	*Stylosanthes*[b]	Fabaceae
311.	*Tachigalia*[b]	Fabaceae
312.	*Tamarindus*[b]	Fabaceae
313.	*Tamarix*[c]	Tamaricaceae
314.	*Taverniera*[b]	Fabaceae
315.	*Tectona*[b]	Verbenaceae
316.	*Tephrosia*[bc]	Fabaceae
317.	*Termindalia*[b]	Combretaceae
318.	*Tetragonolobus*[b]	Fabaceae
319.	*Theobroma*[b]	Sterculiaceae
320.	*Thermopsis*[bc]	Fabaceae
321.	*Thusyopsis*[b]	Coniferaceae
322.	*Tillandsia*[b]	Bromeliaceae
323.	*Trifolium*[bc]	Fabaceae
324.	*Trigonella*[bc]	Fabaceae
325.	*Triumfetta*[b]	Tiliaceae
326.	*Tsuga*[c]	Pinacceae
327.	*Ulex*[bc]	Fabaceae
328.	*Ulmus*[c]	Ulmaceae
329.	*Urena*[b]	Malvaceae
330.	*Urgined*[b]	Liliaceae
331.	*Vachellia*[b]	Mimosaseae
332.	*Verbascum*[c]	Scrophylariaceae
333.	*Veronica*[bc]	Scrophylariaceae
334.	*Viburnum*[c]	Caprifoliaceae
335.	*Vicia*[b]	Fabaceae
336.	*Vigna*[b]	Fabaceae
337.	*Vitis*[bc]	Vitaceae
338.	*Voandzeia*[b]	Fabaceae
339.	*Zea*[b]	Poaceae
340.	*Zizyphus*[b]	Rhamnaceae

b = Plant genera known to carry hidden infestation of Bruchids

c = Plant genera known to carry hidden infestation of Chalcids

bc = Plant genera known to carry hidden infestation of Bruchids and Chalcids

0 = Plant genera known to carry hidden infestation of other (Curculionids/ Scolytids etc.)

Several interceptions of exotic bruchids, chalcids etc. of quarantine significance have been made in the Plant Quarantine Division as a result of X-ray screening of the listed plant genera (Verma, 1980; Chandel and Singh, 1987; Mathur and Lal, 1996). This information is of paramount importance for the exchange of seeds including transgenics among different countries. Therefore, it is suggested to expose the listed plant genera to X-ray radiography at all the ports of entry.

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References

Anonymous (2000) *Review of Agricultural Entomolgy Series A,* CAB, UK.

Abou-Raya AK (1954) *Bruchidius alfieri* Pic a biologic race of *Bruchidius trifolii* Motsch. (Coleoptera: Bruchidae). *Bull. Soc. Fouad I. Ent.* **38**: 193-203.

Chandel KPS and BM Singh (1987) *Research Achievements-A Decade. NBPGR Sci. Monogr.* **No. 11,** 170p.

Escherich K (1938) The phytophagous species of *Megastigmus* as destroyer of the seeds of conifers. *Rev. Appl. Ent.* (A) **27**: 230.

Gourlay ES (1930) Some parasitic hymenoptera of economic importance in New Zealand. *N.Z.J. Sci. Tech.* **11**: 319.

Gupta SC (1962) Occurrence of exembryonate seeds in the umbelliferae. *Curr. Sci.* **31**: 203-205.

Jackson BD (1977a) *Index Kewensis-An Enumeration of the Genera and Species of Flowering Plants.* Otto Koeltz Science Publishers, West Germany. **1**: 1268p.

Jackson BD (1977b) *Index Kewensis-An Enumeration of the Genera and Species of Flowering Plants.* Otto Koeltz Science Publishers, West Germany. **2**: 1300p.

Kapur Manju Lata, BR Verma and B Lal (1988) Interception of *Pachymerus lacerdae* (Coleoptera: Bruchidae) from imported nuts of *Orbignya phalerata* (Palmae)–a new host record. *J. Young Ent. Quart.* **6**: 31-32.

Kapur Manju Lata, B Lal and BR Verma (1989) Studies on pest risk involved in import of medicinal plants. *Indian J. Pl. Genet. Resour.* **2**: 55-59.

Kapur Manju Lata, B Lata and BR Verma (1992) *Eurytoma* intercepted from imported seeds of *Urginea maritima*–A first record. *Indian J. Ent.* **55**: 451-52.

Kapur Manju Lata, BR Verma and Shashi Bhalla (1997) Quarantine detection of mango stone weevil, *Sternochaetus mangifera* (F.) in mango through X-ray radiography. In: *Souvenir and Abstracts: Symposium on Integrated Pest Management for Sustainable Crop Production,* IARI, New Delhi, pp. 59.

Kaura (1959) A new transparency method for detecting internal infestation in grains. *Grain Storage Newslet.* **1**: 12.

Krombein Karl V (1958) *Hymenoptera of America North of Mexico. USDA Agriculture Monogr.* **2:** 305p.

Mac Dougall RS (1926) The *Megastigmus* of the douglas fir seed. *Trans. R. Scot. Arbor. Soc.* **19**: 52-65.

Mathur VK and A Lal (1996) *Plant Quarantine Activities at NBPGR (1976-1996). NBPGR Sci. Monogr.* **No. 6:** 96p.

Muesebeck CFW, Karl V Krombein and Henry K Townes (1951) *Hymenoptera of America North of Mexico.* USDA, 1420p.

Peck O (1963) *A Catalogue of the Nearctic Chalcidoidea (Insecta: Hymenoptera).* Canadian Entomologist Supplement No. 30, 1092p.

Strong FE (1962) Laboratory studies on the biology of the alfalfa seed chalcid, *Bruchophagus roddi* Guss. (Hymenoptera: Eurytomidae). *Hilgardia* **32**: 229-249.

Terrell EE, SR Hill, JH Wierseman and WE Rice (1986) *A Checklist of the Name of 3,000 Vascular Plants of Economic Importance.* USDA, ARS, Agriculture Handbook, 505p.

Udayagiri S and SR Wadhi (1989) *Catalogue of Bruchidae. Mem. Amer. Ent. Inst.* **No. 45,** 300p.

Usher G (1984) *A Dictionary of Plants Used by Man.* CBS Publishers & Distributors 620p.

Vayssiere P (1931) Appartition en France du *Megastigmus spermotrophus* Wachtl. parasite des semences du *Pseudotsuga douglasii* Harr. *Rev. Appl. Ent.* (A) **19**: 586.

Verma BR (1980) Pests intercepted from planting material imported during the period from January, 1956 to December, 1979. In: SR Wadhi (ed) *Plant Quarantine Activity at the National Bureau of Plant Genetic Resources. NBPGR Sci. Monograph* **No. 2,** pp 55-71.

Wadhi SR (1963) Interception of *Bruchophagus glycyrrhizae* Nikolskaya from liquorice seeds. *Indian J. Ent.* **25**: 382-384.

Wadhi SR (1967) Seed infesting chalciodoids and plant quarantine. *Indian J. Ent.* **29**: 252-260.

Wadhi SR (1980) *Plant Quarantine Activity at the National Bureau of Plant Genetic Resources. NBPGR Sci. Monogr.* **2:** p. 99.

Wadhi SR and BR Verma (1971) Quarantine problem posed by *Bruchidius* species. *Indian J. Ent.* **33**: 34-41.

Wadhi SR, BR Verma, Thomas Soares, Nirmolini Singh and Rattan Lal (1967) Detection of phytophagous chalcidoids in seeds for quarantine purpose. *Indian J. Ent.* **29**: 197-199.

Wadhi SR, BR Verma, Thomas Soares, Nirmolini Singh and Rattan Lal (1968) Insects intercepted from the seed samples imported and exported for plant introduction work during January, 1965 to December, 1996. *Indian J. Ent.* **30**: 303-308.

Wadhi SR, Thomas Soares and Rattan Lal (1966) Insect interceptions from the seed samples imported and exported for plant introduction work during the period from August, 1960 to December, 1964. *Indian J. Ent.* **28**: 494-500.

Weiss HB (1917) *Megastigmus aculeatus* Swedrus-introduced into New Jersey from Japan. *J. Econ. Ent.* **6**: 402-403.

Geographical Distribution of Mulberry *(Morus)* Species in India

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In India, genus *Morus* is represented by four species viz., *M. indica, M. alba, M. serrata* and *M. laevigata* (Hooker, 1885; Brandis, 1906). The natural distribution of the genus has considerably changed because of its extensive cultivation for silkworm rearing. Vavilov (1926) while reviewing the centre of origin of crop plants placed the genus *Morus* in China-Japan region which includes East China, Korea and Japan. There are about 68 species recognized in the genus of which 24 species are represented in China, 19 in Japan, 6 in Korea, 4 each in Taiwan and India, 3 each in Myanmar and Indonesia, 2 each in Thailand, Vietnam and Afganistan and 1 each in Arabia, Oman and Muscat. Further, 14 species are found in North America and 7 in Central and South America (Sanjappa, 1989). Parkinson (1923) reported the availability of *M. laevigata* in Andaman and Nicobar islands. Sreekumar *et al.* (1995) have extensively explored Kerala and collected mulberry resources from farm backyard/ cultivated gardens, tea and coffee estates. The wide spread urbanization, for agricultural used and denudation of forest areas, threatens the natural habitats of mulberry particularly the primitive and obsolete varieties available in different parts of the country (Chauhan and Thakur, 1995; Sanjappa, 1989). The genus *Morus* is distributed naturally in the Sub-Himalayan region up to an altitude of 2200 m extending between Indus and Brahmaputra rivers with varying climate from temperate to tropical. *M. serrata,* the Himalayan mulberry is available in natural habitat in North-western Himalaya. The natural and sacred mulberry tree, belongs to *M. serrata* at Joshimath, is the oldest and about 1200 years old (Rau, 1967; Tikader *et al.,* 1999). Therefore, regular explorations are essential to identify the different locations of mulberry resources available in natural and cultivated habitats and to document the diversity of mulberry for further utilization in mulberry crop improvement programme.

Materials and Methods

Regular surveys and explorations were conducted in various geographical regions of the country in two different seasons (February-April and September-November) in every year during 1993-2000. The exploration sites are indicated in Fig. 1. To expedite the process of exploration in different areas, the geographical regions of the country were grouped into 4 zones, viz., North-east, North-west, Central and South India.

Accordingly, the zones were covered to identify the mulberry germplasm. Random sampling in case of wild forms and biased sampling procedure were used when the population was above 25 plants i.e. at least 10% of the population were sampled. Healthy, mature, disease-free shoots with dormant buds were collected for further multiplication in the nursery and subsequent establishment in the field genebank.

Results and Discussion

A total of 367 mulberry germplasm accessions were collected from different zones and states are presented in Table 1. The distribution pattern revealed that in India two species *M. laevigata* and *M. serrata* exist as wild trees (Fig. 2). *M. serrata* exists in North-western India up to an altitude to 2200m (Dandin *et al.,* 1993, 1995; Tikader *et al.,* 1999, 2000) growing with oak plantation in natural habitat. *M. laevigata* grows in varied climates both in wild and cultivated forms. The natural distribution of *M. laevigata* was observed in Eastern Himalaya, North West India and Andaman and Nicobar Islands. Cultivated forms of *M. laevigata* was observed in Central India, North-West India, South India which are grown as shade trees in tea and coffee estates. In Andaman and Nicobar Islands, wild trees of *M. laevigata* differ in characteristics from main landforms. *M. serrata* is the only representative of North-west India and confined to higher altitude in Sub-Himalayan belt (750-2200 m).

The variation observed in different species are presented in Table 2. *M. laevigata* collected from different parts of the country indicates lot of variation. The important characters of the species is ½ phyllotaxy, long inflorescence and big size leaf.

M. indica, the wild and cultivated mulberry for sericulture, possess varied leaf shape. Leaf serration varied from serrate to crenate. The special characteristic features of the species is long leaf, acuminate, style long hairy, female flower spike short, ovoid. Fruit spikes slightly enlarged, dark purple, black when ripened and tastes sour to sweet.

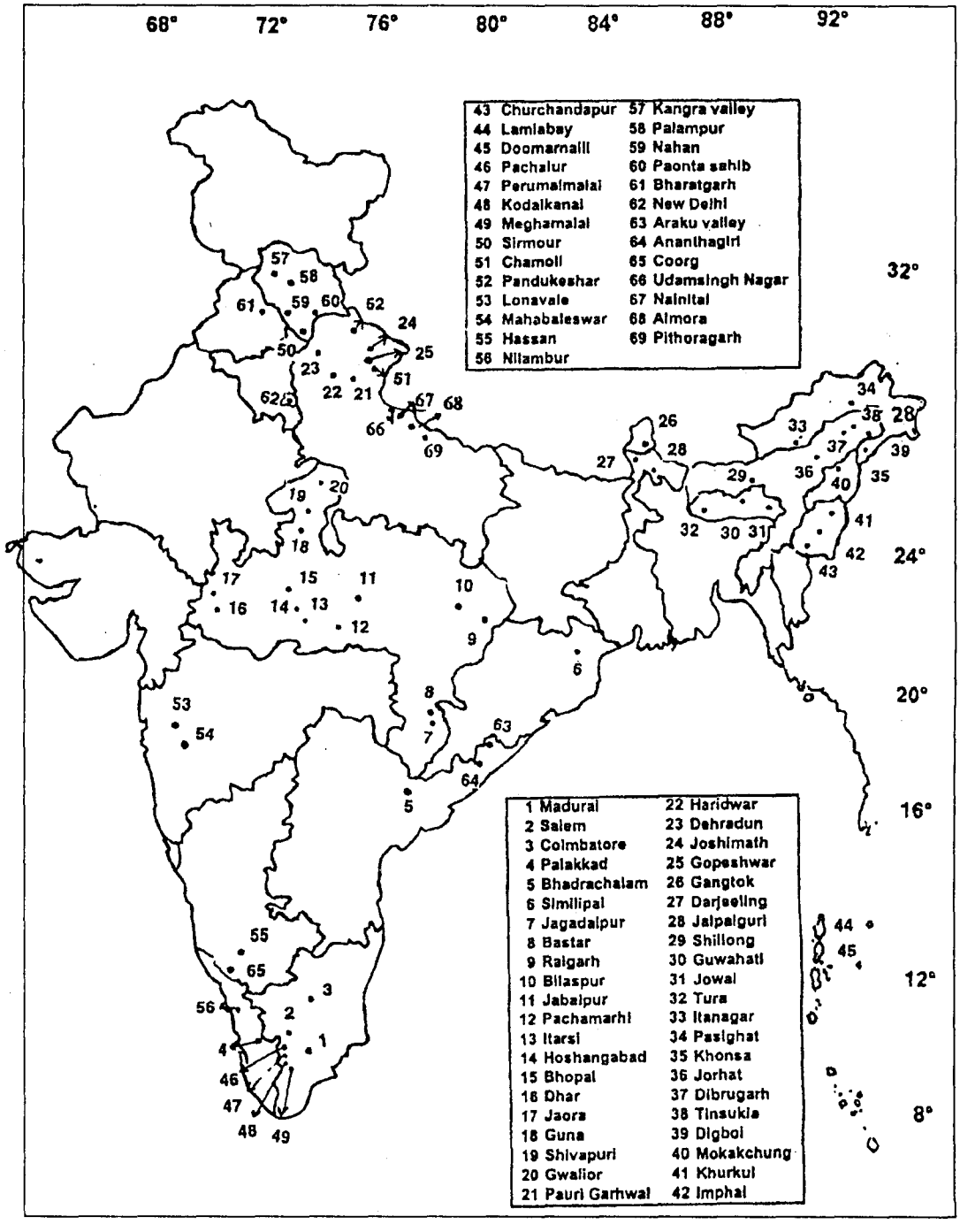

Fig. 1. Exploration sites of Morus Indica, M. alba, M. laevigata and *M. serrata in India*

Table 1. Number of mulberry germplasm accessions collected under each species and zones

Zone	Species					
	M. alba	*M. indica*	*M. laevigata*	*M. serrata*	*Unidentified*	*Total*
North-East India	—	32	33	—	4	69
North-West India	16	60	14	34	—	124
Central India	2	8	8	—	—	18
South India *(A&N islands)*	2	49	59	—	46	156
Total	20	149	112	34	50	367

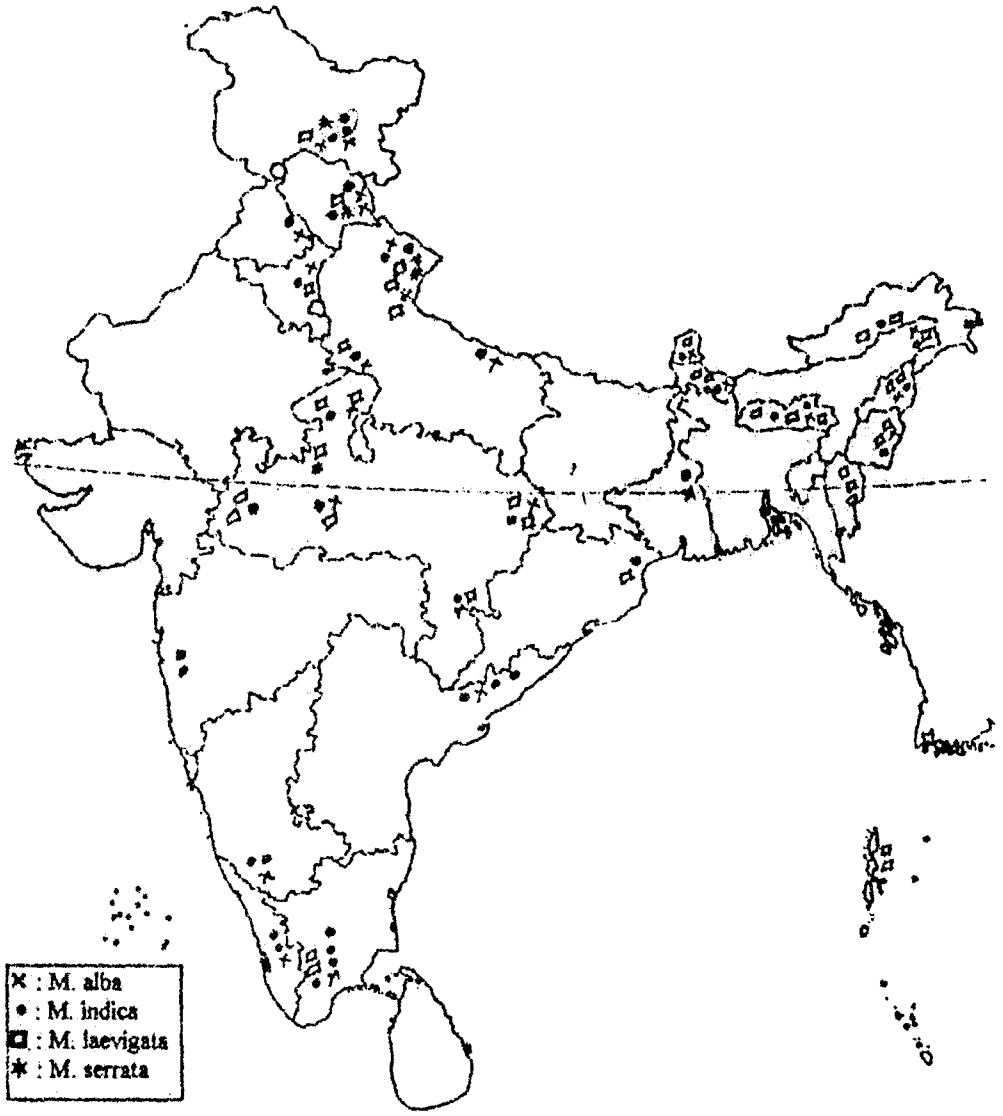

Fig. 2. Distribution of Morus species in India

Morus alba is known as white mulberry for its white fruit colour. The species is cultivated mainly for silkworm rearing. The species has small to medium leaves. The leaf apex is acuminate and leaf texture smooth. The style is short, minute hairy and united partly at the base. Fruiting spikes are dark purple or white when ripened and very sweet to taste.

Morus serrata is called the Himalayan mulberry as it is confined to North-western Himalayan belt. The bark colour varied from red brown to dark brown and blackish brown. Phyllotaxy is mixed type i.e. *½. 1/3* and *2/5*. Internodal distance varied from 3.5 to 7.5 cm. Fruit colour ranged from black to pink, very sweet to taste and mucilage (Tikader *et al.*, 1999, Tikader *et al.*, 2000).

All over India a good number of mulbery varieties have been introduced replacing the traditional ones. In eastern India the improved variety S1, S1635, Tr10, BC 259 have replaced the traditional varieties. In South India, the improved variety K2, S13, S36, V1 have replaced the traditional varieties. In North-West India, S146, Chinese white have replaced the local varieties. Till date about 60% area are covered by improved varieties. In the present circumstances, more germplasm is required for evolving new varieties. The collected germplasm (367) includes different species which were not collected earlier. The collections are being maintained in field genebank for characterization, evaluation and further utilization in crop improvement.

Table 2. Characteristic features of different mulberry germplasm collected from different zones of India

No.	Characters	*M. laevigata*	*M. indica*	*M. alba*	*M. serrata*
1	Bark colour	Brown, grey, grey white, greenish grey, grey blackish	Brown, dark brown, blackish brown	Brown, dark brown	Brown, dark brown, blackish brown
2	Leaf lobation	Lobed, unlobed, mixed	Lobed, unlobed, mixed	Unlobed	Lobed, unlobed, mixed
3	Leaf texture	Chartaceous, coriaceous	Chartaceous, coriaceous	Chartaceous, coriaceous	Chartaceous, coriaceous, leathery
4	Leaf shape	Ovate, long ovate, wide ovate	Ovate, narrow ovate	Ovate, narrow ovate	Ovate, narrow ovate, wide ovate
5	Leaf margin	Serrate, minute serrate,	Serrate, crenate, dentate	Serrate	Serrate, dentate
6	Leaf surface	Smooth, slightly rough, rough	Smooth, slightly rough, rough	Smooth	Smooth, slightly rough, rough
7	Leaf size Range (LxB)cm	15 x 11-32x16	10 x 8-20x12	14 x 12-15x12	15 x 10-20x20
8	Sex	Male, female	Male, female	Male, female	Male, female
9	Catkin length (cm)	4.0-10.0	1.5-3.5	1.5-2.5	2.5-3.5
	Male,				
	Female	5.0-12.0	1.5-3.5	1.2-2.5	3.0-4.0
10	Fruit length (cm)	6.0-12.0	1.2-4.0	1.8-2.6	3.5-4.5
11	Fruit colour	Green, pink, white, black	Black	Pink, white	Black, pink
12	Phyllotaxy	1/2	1/2,1/3,2/5	1/2,1/3	1/2,1/3,2/5
13	Internodal distance (cm)	4.0-10.0	3.8-5.5	3.5-4.5	4.0-7.0
14	Altitude (m)	150-1350	350-1340	400-1350	750-2200

References

Brandis D (1906) Indian trees London. pp 612-613.

Chauhan NS and S Thakur (1995) Conservation of plant genetic resources of Himachal Pradesh. *Indian J. Forest* **18:** 226-238.

Dandin SB, R Basavaiah Kumar and HV Venkateshaiah (1993) Phytogeographical studies in genus *Morus* L. I. Geographical distribution and natural variation of *Morus serrata* Roxb. *Indian J. Plant Genet. Resour.* **7:** 223-226.

Dandin SB, R Basavaiah Kumar and RS Mallikarjunappa (1995) Phytogeographical studies in genus *Morus* L. II. Geographical distribution and natural variation of *Morus laevigata* Wall ex Brandis. *Indian J. Plant Genet. Resour.* **8:** 129-131.

Hooker JA (1885) Flora of British India.V: 491-493. Bishen Singh Mahendra Pal Singh, Dehradun.

Parkinson CE (1923) *A Forest Flora of Andaman Islands.* Bishen Singh and Mahendra Pal Singh Dehradun, p155.

Rau MA (1967) The Sacred Mulberry Tree of Joshimath U.P. *Indian Forester* **93:** 333-335.

Sanjappa M (1989) Geographical distribution and exploration of the genus *Morus* L. (Moraceae). In: K Sengupta and SB Dandin (eds) *Genetic Resources of Mulberry and its Utilization* Central Silk Research and Training Institute, Mysore, pp 4-7.

Sreekumar H, S Kumaresan, J C Jose, S K Jayalakshmi, R Satheesh and PKK Nair (1995). Exploration and collection of mulberry genetic resources in Kerala. *J. Environ. Resour.* **3:** 14-17.

Tikader A, AA Rao and P Mukherjee (1999). *Ex situ* conservation of the oldest mulberry tree. *Indian Silk* **38:** 17-18.

Tikader A, S Ravindran, V Girish Naik, A Ananda Rao, SB Dandin, P Mukherjee and SR Ramesh (2000). Geographical distribution and variation in Indian mulberry genetic resources. Paper presented at "National Conference on Strategy for Sericulture Research and Development" at Central Silk Research and Training Institute, Mysore, 13p.

Vavilov NI (1926). Studies on the origin of cultivated plants. *Trudy Byuro Prikl. Bot.* **16:** 139-248.

Genetic Divergence and Selection of Promising Types of Aonla (*Emblica officinalis* L.) from Seedling Population in Solan Area of Himachal Pradesh

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To assess the nature and magnitude of genetic divergence in *Emblica officinalis*, a survey was conducted during 2000 in Arki area of Himachal Pradesh and non-hierarchical Euclidean cluster analysis was performed for 66 seedling trees taking 15 fruit characters of each tree. Coefficient of variability ranged from 3.57% for pulp percentage (volume basis) to 39.26% for pulp volume. All the genotypes got clustered into 14 clusters which revealed that their distribution is in more than one cluster showing, non-parallelism between geographic and genetic diversity. Number of trees were minimum (1) in cluster 7 and 14 and maximum (12) in cluster 13. Mean value of most of the fruits was higher in cluster 14. Intra-cluster distance varied from 0 (cluster 7 and 14) to 1.81 (cluster 3). Maximum inter-cluster distance of 13.00 was observed between cluster 1 and 14. Based on various important fruit characters, four promising seedling trees will be propagated vegetatively for further testing and release in the growing area.

Key Words: Aonla, *Emblica officinalis*, Genetic Divergence, Selection, Variability

Aonla (*Emblica officinalis* L.) is an important fruit of family Euphorbiaceae. It is said to be indigenous to tropical South-East Asia, particularly in central and southern India (Firminger, 1947). Aonla is an important minor fruit crop of commercial significance. It is quite hardy, a prolific bearer and highly remunerative even without much care. The fruit is highly nutritive and is the richest source of vitamin C among fruits except Barbados cherry. The fruits are made into preserve, sauce, candy, dried chips, tablets, jellies, pickles, toffees and powder. In India, there is limited systematic plantation of aonla and mostly plants of seedling origin are grown. The seed-propagated trees exhibit a tremendous genetic divergence with respect to fruit and other characters, which in turn offers a great scope for selection of promising types. Earlier improvement work of aonla has taken place through selection only. Keeping in view the above importance the present survey was conducted in Arki area of district Solan in Himachal Pradesh.

Materials and Methods

The present survey was conducted during 2000 in Arki area of district Solan in Himachal Pradesh which is situated at an elevation of 1000 to 1200 m above mean sea level. The microclimate of the survey area is subtropical to subtemperate. Hence, there is slight variation in the microclimate of the area from which the trees were sampled. In this area aonla was found growing in wild form in neglected areas and grasslands. Based on preliminary information from farmers, fruits were collected from 66 trees, out of a total population of 400 trees in the area. Twenty-five fruits from each tree were randomly harvested in mid December and were used for recording data on various fruit characters. Data were statistically analysed by using non-hierarchical Euclidean cluster analysis (Spark, 1973). The multivariate analysis was performed by using statistical package Spar-1. Based on various fruit characters like fruit weight, length, diameter, volume, pulp weight, pulp percentage and seed:pulp ratio, the promising types were selected and the fruits from selected types were subjected to chemical analysis following the methods suggested in AOAC (1975).

Results and Discussion

Highest coefficient of variability was observed as 39.26 % for pulp volume followed by pulp weight (38.81%), fruit volume (36.44%), fruit weight (36.39%), seed:pulp ratio weight basis (35.60%), seed:pulp ratio volume basis (34.46%), seed weight (23.21), seed volume (21.43%), fruit diameter (12.53%), fruit length (11.52%), TSS (10.15%), seed length, (9.91%), seed diameter (8.93%), pulp percentage (3.61%) on the basis of weight and pulp percentage (3.57%) on the basis of volume (Table 1).

All 66 aonla genotypes got clustered into 14 clusters and distribution of genotypes from different areas into these clusters was apparently random. Number of genotypes in each cluster varied from 1 in cluster 7 and 14 to 12 in cluster 13. The number of trees in different clusters (1-14) were 4, 2, 9, 3, 8, 4, 1, 3, 2, 7, 7, 3, 12 and 1, respectively.

Table 1. Range, mean, standard deviation and coefficient of variability for different fruit characters in seedling trees of aonla

Characters	Range	Mean	Standard deviation (SD)	Coefficient of variability (CV)
Fruit weight (g)	2.30-12.50	6.10	2.22	36.39
Fruit length (mm)	14.69-14.62	19.45	2.24	11.52
Fruit diameter (mm)	15.73-29.05	22.18	2.78	12.53
Fruit volume (cc)	3.00-11.00	5.68	2.07	36.44
Seed weight (g)	0.230-0.855	0.56	0.13	23.21
Seed length (mm)	8.40-12.86	10.09	1.00	9.91
Seed diameter (mm)	8.16-12.61	10.08	0.90	8.93
Pulp weight (g)	1.756-11.640	5.54	2.15	38.81
Pulp percentage (weight basis)	76.35-95.57	89.98	3.25	3.61
Seed:pulp ratio (weight basis)	3.23-21.60	10.00	3.56	35.60
TSS (°B)	9.00-15.00	12.41	1.26	10.15
Pulp volume (cc)	1.625-10.250	5.123	2.041	39.26
Seed volume (cc)	0.250-0.750	0.56	0.12	21.43
Pulp percentage (volume basis)	83.33-95.02	89.27	3.19	3.57
Seed:pulp ratio (volume basis)	4.33-19.08	9.17	3.16	34.46

The mean fruit weight (12.50 g), fruit length (24.62 mm), fruit diameter (29.05 mm), fruit volume (11 cc), seed weight (0.86 g), seed length (11.43 mm), seed diameter (12.61), pulp weight (11.65 g), pulp volume (10.25 cc) and seed volume (0.75 cc) were highest in cluster 14 while cluster 7 had maximum pulp percentage (95.57%) and seed : pulp ratio (1:21. 60) on their weight basis. Similarly, cluster 7 had highest mean value (14.50° B) of TSS while cluster 14 had maximum pulp percentage (94.55%) and seed : pulp ratio (1:17.59) on volume basis (Table 2).

Minimum intra-cluster distance (0) was observed in cluster 7 and 14 while it was maximum (1.810) in cluster 3. Similarly inter-cluster distance varied from 0.046 between cluster 2 and 3 to 13.000 between cluster 1 and 14. Cluster 9 and 14 are separated from each other by a distance of 12.846 while 11.260 distance was recorded between cluster 7 and 14.

Different characters have different magnitude of percentage towards diversity. It ranged from 0.00% in pulp percentage seed : pulp ratio (volume basis) to 58.10% in fruit weight. Fruit weight (58.10 g), length (21.73 cm), diameter (5.94 cm), volume (4.85 cc), seed weight (4.12 g) and seed length (1.37 cm), thus explaining 96.10% variation.

Based on various characters like fruit weight, fruit length, fruit diameter, pulp weight, pulp percentage, seed: pulp ratio (weight and volume basis) and TSS, Tree No. 31, 59, 64 and 66 were found to be promising and were selected. Fruits from all these trees were green in colour. The various fruit characters of selected types are presented in Table 3. Acidity in selected types varied from 2.01 (Tree no. 59) to 2.48% (Tree No. 31), while ascorbic acid ranged from 305 to (Tree No. 59) to 515 mg/100 g of fruit (Tree No. 31). Similarly, total and reducing sugars varied from 8.62% (Tree No. 64) to 10.01% (Tree No. 59) and 5.23% (Tree No. 66) to 6.13% (Tree No. 59), respectively.

In the present investigation a great extent of genetic divergence was recorded from various fruit characters. Coefficients of variability in pulp volume, pulp weight and fruit weight as 39.26, 36.44 and 36.39%, respectively. Similar type of variation was also observed by Singh *et al.* (1987) and Chandra *et al.* (1998) in aonla varieties and seedling trees, respectively. All the 66 genotypes got clustered unsystematically into 14 clusters thus, cutting across geographic boundaries demonstrating that geographic isolation is not the only factor causing genetic diversity. Intra-cluster distance varied from 0 to 1.810. These relatively low values depicted the presence of narrow range of genetic diversity within a cluster. The 0 value of intra-cluster distance is due to the fact that only a single plant entered in this cluster. The inter-cluster distance varied from 0.04 between cluster 2 and 3 to 13.00 between cluster 1 and 14. The parents for hybridization could be selected on the basis of their large inter-cluster distance for isolating useful recombinants in the segregating generation. So to improve various fruit characters the members of cluster 1 and 14 can be used for hybridization programme as well as for introgressing their useful traits in commercial aonla cultivars. Aonla is a less exploited crop and mostly the improvement work was undertaken through selection. These four selected types

Table 2. Cluster mean, standard deviation and coefficient of variability of 14 clusters for different fruit characters in seedling trees of aonla

Characters	Para-meters	Clusters													
		1	2	3	4	5	6	7	8	9	10	11	12	13	14
Fruit weight	Mean	3.10	8.10	4.37	8.47	5.66	9.93	7.30	6.87	2.80	6.86	5.74	10.62	4.84	12.50
	SD	0.48	0.14	0.41	0.49	0.46	0.66	0.00	0.59	0.71	0.47	0.68	0.48	0.91	0.00
	CV	15.48	1.73	9.38	5.79	8.13	6.65	0.00	8.59	25.36	6.85	11.85	4.52	18.80	0.00
Fruit length	Mean	15.90	21.72	18.13	21.52	19.31	22.66	17.24	22.56	15.67	20.02	19.05	23.25	18.28	24.62
	SD	0.43	0.37	0.92	0.99	0.75	0.30	0.00	0.48	1.39	0.61	1.64	1.14	0.93	0.00
	CV	2.70	1.70	5.07	4.60	3.88	1.32	0.00	2.13	8.87	3.05	8.61	4.90	5.09	0.00
Fruit diameter	Mean	18.12	24.44	20.42	24.33	21.95	26.69	18.57	23.10	16.77	23.91	20.87	27.11	21.49	29.05
	SD	0.79	0.18	1.08	1.82	0.80	0.75	0.00	0.75	1.48	0.96	1.79	0.87	1.27	0.00
	CV	4.36	0.74	5.29	7.48	3.64	2.81	0.00	3.25	8.83	4.02	8.58	3.21	5.91	0.00
Fruit volume	Mean	2.70	8.45	3.92	7.83	5.04	9.38	3.50	6.13	3.40	6.39	5.27	10.03	4.93	11.00
	SD	0.48	0.78	0.58	0.06	0.52	0.63	0.00	0.35	3.28	0.46	0.73	0.40	0.59	0.00
	CV	17.78	9.23	14.80	0.77	10.32	6.72	0.00	5.71	8.24	7.20	13.85	3.99	11.97	0.00
Seed weight	Mean	0.40	0.70	0.43	0.50	0.65	0.71	0.32	0.55	0.54	0.70	0.45	0.59	0.57	0.86
	SD	0.06	0.01	0.06	0.04	0.08	0.07	0.00	0.06	0.00	0.07	0.05	0.10	0.05	0.00
	CV	15.00	1.43	13.95	8.00	12.31	9.86	0.00	10.91	0.00	10.00	11.11	16.95	8.77	0.00
Seed length	Mean	8.73	10.70	9.43	10.57	10.56	11.12	8.60	11.19	10.00	10.33	9.39	9.28	10.46	11.43
	SD	0.29	0.26	0.56	1.08	1.08	0.72	0.00	0.70	0.15	0.78	0.95	0.71	0.75	0.00
	CV	3.32	2.43	5.94	10.22	10.23	6.47	0.00	6.26	1.50	7.55	10.12	7.65	7.21	0.00
Seed diameter	Mean	9.06	10.85	9.24	9.66	10.76	10.51	8.20	9.89	10.20	10.89	9.36	10.14	10.33	12.61
	SD	0.67	1.07	0.55	0.28	0.42	0.30	0.00	0.35	0.08	0.56	0.55	0.87	0.64	0.00
	CV	7.40	9.86	5.95	2.90	3.90	2.85	0.00	3.54	0.78	5.14	5.88	8.58	6.20	0.00
Pulp weight	Mean	2.70	7.40	3.94	7.96	5.01	9.22	6.98	6.32	2.26	6.16	5.29	10.03	4.27	11.65
	SD	0.44	0.13	0.38	0.47	0.47	0.59	0.00	0.59	0.71	0.45	0.67	0.39	0.91	0.00
	CV	16.30	1.76	9.64	5.90	9.38	6.46	0.00	9.34	31.42	7.31	12.67	3.89	21.31	0.00
Pulp per cent age (weight basis)	Mean	86.92	91.31	90.20	94.07	88.46	92.87	95.57	91.97	79.99	89.82	92.06	94.46	87.82	93.16
	SD	1.64	0.04	1.13	0.38	1.73	0.28	0.00	1.10	5.15	1.06	1.13	0.74	2.36	0.00
	CV	1.89	0.04	1.25	0.40	1.96	0.30	0.00	1.20	6.44	1.18	1.23	0.78	2.69	0.00
Seed:pulp ratio (weight basis)	Mean	6.75	10.52	9.33	15.91	7.84	13.05	21.60	11.62	4.17	8.91	11.83	17.27	7.49	13.62
	SD	1.09	0.03	1.17	1.09	1.38	0.56	0.00	1.87	1.33	0.94	1.90	2.62	1.61	0.00
	CV	16.15	0.29	12.54	6.85	17.60	4.29	0.00	16.09	31.89	10.55	16.06	15.17	21.50	0.00
TSS (°B)	Mean	11.50	12.50	11.33	12.17	12.27	13.25	14.00	14.50	10.25	12.29	12.50	13.17	12.79	14.00
	SD	1.35	0.00	1.32	0.29	1.24	0.65	0.00	0.50	1.77	0.70	1.29	0.29	0.81	0.00
	CV	11.74	0.00	11.65	2.38	10.11	4.91	0.00	3.45	17.27	5.70	10.32	2.20	6.33	0.00
Pulp volume	Mean	2.23	7.74	3.49	7.29	4.82	8.67	3.06	5.55	2.88	5.72	4.83	9.49	4.41	10.25
	SD	0.42	0.80	0.54	0.01	0.51	0.61	0.00	0.35	0.28	0.44	0.70	0.43	0.57	0.00
	CV	18.83	10.34	15.47	0.14	10.58	7.04	0.00	6.31	9.72	7.69	14.49	4.53	12.93	0.00
Seed volume	Mean	0.47	0.71	0.43	0.55	0.72	0.70	0.44	0.58	0.52	0.67	0.44	0.555	0.52	0.75
	SD	0.06	0.03	0.08	0.07	0.02	0.06	0.00	0.07	0.00	0.06	0.05	0.07	0.03	0.00
	CV	12.77	4.23	18.60	12.73	2.78	8.57	0.00	12.07	0.00	8.96	11.36	12.73	5.77	0.00
Pulp per cent age (volume basis)	Mean	82.51	91.59	88.92	93.03	85.62	92.48	87.49	90.47	84.51	89.51	91.60	94.55	89.30	93.18
	SD	1.01	1.08	2.00	0.82	1.71	0.67	0.00	1.29	1.29	0.99	0.87	0.80	0.99	0.00
	CV	1.22	1.18	2.25	0.88	2.00	0.72	0.00	1.43	1.53	1.11	0.95	0.85	1.11	0.00
Seed:pulp ratio (volume basis)	Mean	4.73	10.99	8.31	13.48	6.03	12.39	6.99	9.63	5.48	8.61	11.01	17.59	8.42	13.67
	SD	0.33	1.54	1.78	1.61	0.74	1.27	0.00	1.47	0.54	0.90	1.22	2.52	0.86	0.00
	CV	6.98	14.01	21.42	11.94	12.27	10.25	0.00	15.26	9.85	10.45	11.08	14.33	10.21	0.00

Table 3. Fruit characters of some selected promising seedling trees

Characters	Tree Number			
	31	59	64	66
Fruit weight (g)	10.10	11.05	10.90	12.50
Fruit length (mm)	23.15	24.44	22.56	24.62
Fruit diameter (mm)	26.22	27.95	27.81	29.05
Fruit volume (cc)	9.80	10.50	10.00	11.00
Seed weight (g)	0.475	0.643	0.801	0.855
Seed length (mm)	8.46	9.69	11.94	11.43
Seed diameter (mm)	9.27	11.01	10.65	12.61
Pulp weight (g)	9.625	10.407	10.099	11.645
Pulp percentage (weight basis)	95.23	94.18	92.65	93.16
Seed:pulp ratio (weight basis)	1:20.26	1:16.19	1:12.61	1:13.62
TSS (°B)	13.5	13.0	14.0	14.0
Pulp volume (cc)	9.312	9.975	9.250	10.25
Seed volume (cc)	0.488	0.525	0.750	0.750
Pulp percentage (volume basis)	95.02	95.00	92.50	93.18
Seed:pulp ratio (volume basis)	1:19.08	1:19.00	1:12.33	1:13.67
Acidity (%)	2.48	2.01	2.40	2.36
Ascorbic acid (mg/100g of fruit)	515	305	350	460
Reducing sugar (%)	6.04	6.13	5.34	5.23
Total sugar (%)	9.91	10.01	8.62	8.87

of aonla seem to be promising and to avoid adaptability problem of exotic types, these will be now multiplied vegetatively for further testing and release. Similar type of selection study was also conducted in Meghalaya (Chandra *et al.*, 1998) and three promising trees were selected.

References

AOAC (1975) *Official Methods of Analysis Analytical Chemist.* Washington DC, USA.

Chandra R, R Srivastava, S Govind, DK Hore and AS Singh (1998) Collection of genetic diversity of aonla (*Emblica officinalis* L.) from Garo hills of Meghalaya. *Indian J. Hill. Farmg.* **11:** 116-123.

Firminger TA (1947) *Firminger's Manual of Gardening for India* (8th edition). Thacker Spink Co. Ltd., Calcutta.

Singh BP, IP Singh, SP Singh and KA Kumar (1987) Physico-chemical composition of different cultivars of aonla. *Indian Fd. Pack.* **41:** 7-10.

Spark DN (1973) Euclidean cluster analysis. Algorithm As 58. *Appl. Stats.* **22:** 126-130.

Evaluation of Genetic Diversity in Indian Durum Wheat with RAPD Markers

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Genetic variability among 26 released varieties/local cultivars of *Triticum durum* was estimated by RAPD marker analysis and the results discussed in view of their centre of breeding and the pedigree. A total of 4 series of primers were used to screen the polymorphic primers and the profiles generated by 15 of such types were used for analysis. The primers OPA3 and OPP6 were the most polymorphic primers and can be used in conjugation with the morphological markers for the identification of the varieties. The varieties developed by the selection among the local race Bansi were grouped together. The highest degree of polymorphism was between the local landrace Malvaraj with Motia and Jay. The clustering on the basis of RAPD markers in the present study was clearly on the pattern of their parentage. The varieties developed through the selection in the CIMMYT material were widely dispersed and therefore can be used along with the local landraces in the breeding programme to diversify the genetic base. The grouping of the germplasm particularly the landraces by RAPD markers can be used in developing the Indian durum wheat cultivars with wider genetic base.

Key words: Diversity, Genetic Similarity, RAPD Markers, *Triticum turgidum* (durum)

Durum wheat, [*Triticum turgidum* var. *durum* Dest.] is a tetraploid species with extremely hard grains and generally used for macaroni, spaghetti and other pasta products. Knowledge about the extent of genetic variation in cultivated durum and its comparison with that of landraces is important for conservation of genetic resources and breeding. Durum wheat has longer evolutionary history than *T. aestivum* and also have been exploited to lesser extent and therefore, likely to possess sufficient polymorphism. The germplasm collection have been selected and crossed in search of new gene or gene combinations and in the process yield increase have been accompanied by increase in total biomass production, harvest index and changes in yield components such as number of spikes/unit area and spike fertility (CIMMYT, 1988). In India, durum breeding did not receive as much emphasis as aestivum wheat as it is less widely grown because of its non-suitability for *chapati* and bread making. Breeders have largely used the landraces either directly for selection or for improving the adaptability of the high yielding exotic lines. Therefore, the extent of genetic diversity present in the Indian released varieties have always been a debatable issue. The morphological characters have been used both for plant variety identification and for the diversity analysis (Yang *et al.*, 1991). Greater variation was found among the characters but not among the countries by Porceddu (1976). The use of morphological descriptors have been criticised because of environmental and epistatic interactions and the unknown genetic control of the traits (Smith and Smith, 1989). The use of biochemical markers involving seed storage protein and isozymes have been questioned due to poor genomic sampling. The pedigree analysis of the varieties released have been used by many workers to account for genetic variation and in many cases have found the narrow genetic base (CIMMYT, 1987, Martin *et al.*, 1991). Random amplified polymorphic DNA (RAPD) is one of the several multiple arbitrary amplicon profiling technique used to characterize plant varieties at the molecular level. It uses a single primer of arbitrary nucleotide sequence to generate relatively complex DNA profile (William *et al.*, 1990, Welsh and McClelland,1990). The degree of polymorphism generated by PCR based techniqu es ensures the higher level of differentiation of plant varieties in comparison to morphological and biochemical markers. The germplasm used in durum breeding in India largely comprises landraces, released Indian cultivars and improved material received from CIMMYT and ICARDA. The breeders, generally, involve these germplasm in their breeding on the performance *per se* or the pedigree which many times does not lead to highly segregating population of desired types. The characterization and grouping of the germplasm in the distinct clusters is very important for improving the breeding efficiency. The objective of the present research was to study the level of diversity present in local and released cultivars of Indian durum wheat and the results are then discussed in view of the pedigree record of the variety.

Material and Methods

Plant Material

A total of 26 local and released cultivars of *T. turgidum* var. *durum* were used for the present study. Seeds were obtained from the collections maintained at Directorate of Wheat Research Karnal, Haryana. The plant material include the varieties bred by different centres of durum breeding and the local cultivars. A complete list of the varieties along with their origin and status is presented in Table 1.

DNA Isolation

DNA was isolated from 7-day-old seedlings germinated on towel paper incubated in a seed germinator at 20°C. Plant tissues (5-10 g) were ground in liquid nitrogen and mixed immediately with 20 ml of CTAB extraction buffer 2X(1.4M NaCl, 100 mM Tris, 20 mM EDTA, 2% mercaptoethanol, 1.5% CTAB; pH 8.0). The samples were incubated at 60°C for 1 h. Chloroform: isoamyl alcohol (24:1) was then added and mixed gently by inverting the tubes for 5 min. The aqueous phase was recovered after centrifugation at 17,000 rpm for 10 min. This was followed by DNA precipitation in 2/3rd volume of isopropanol. The precipitated DNA was then spooled out and stored in 70% alocohol at 4°C. DNA was washed twice in 70% alcohol and dried under vacuum. The DNA pellet was dissolved in 10:1 TE (10 mM Tris, 1mM EDTA; pH 8.0) solution. This solution then was treated with RNAase, which was followed by two extractions. DNA was reprecipitated by adding 1/10 volume of 3M NaOAc and 2.5 volume of distilled ethanol. DNA was collected and washed, followed by drying under vacuum and dissolving in TE. The samples were then stored at -20^0 C.

PCR Reaction

For amplification of random genomic sequences in reproducible way, the reaction condition was rigorously optimized (10 mM tris -Cl pH8.3, 500 mM KCl, 200 µmols each of d NTPs, 3.25 mM $MgCl_2$, 0.5 µM primer, 0.75 U Taq DNA polymerase and 20 ng template DNA; total volume 25 µl). The PCR reaction were carried out in Perkin Elmer thermal cycler programmed for initial denaturation at 92°C for 3 min, followed by 40 cycles of 1min at 94°C, 1 min at 35°C and 1 min at 72°C.

Table 1. Durum wheat varieties/lines used in the study with their pedigree and origin

S.No.	Name	Pedigree	Origin and remarks
1	PBW 34	AASIB/FGOSIB	PAU, Ludhiana, released variety selected from the CIMMYT material
2	Jairaj	YAGULATE(Pol)/4/PI/3/ZENATI/BTL//WLS	Jabalpur (MP), released variety selected from the CIMMYT material
3	Motia	Selection from local Bansi	Niphad (Maharastra), released cultivar
4	PDW 215	Raj911//AASIB/D#2E/3/DWL5002	PAU, Ludhiana, released variety
5	Vizapur 8	Local strain	Vizapur, local strain
6	Bijaga Yellow	Bijaga Red Sib	Bijapur (Gujarat), released variety
7	A-9-30-1	A 206/ GAZA	Arnej (Gujarat), released variety
8	A-624	Selection from local	Arnej (Gujarat), released cultivar
9	HI 8381	JO 69 SIB/AASIB//FGOSIB	IARI, Indore, released variety through selection in the CIMMYT material
10	HD 4502	PISIB/2* BY//TC60/3/Zena/TI/BTL//WLS	IARI, released variety through selection in the CIMMYT material
11	Amrut	ANLC/GAZA	Annigeri (Karnataka), released variety
12	N-59	-	Niphad (Maharastra), released variety
13	Malvaraj	Selection from local	Indore (MP), local improved
14	MACS 1967	GULAB/5/ BYE*2/TCTE//4*TC60/3/BYE *2/TC60/STW63/4?AASIB/CITSIB	Pune (Maharastra), released variety
15	Vizapur 10	Vizapur (Gujarat)	Vizapur (Gujarat), local
16	GW2	GS SIB//A206/NP200	Junagarh (Gujarat), released variety
17	Raj 1555	CIT/RAJ911	RAU, Durgapura (Raj), released variety
18	NP 404	GAZA/EKD6	IARI, Indore, released variety
19	MPO 215	Narmada 215	Powerkhera (MP), released variety
20	Gulab	Selection in local Bansi	Niphad (Maharastra)
21	HD4530	TPT/MOGHK/4/PI/TML//2 *TC60/3/3ZENTI/BTL//WLS	IARI, Delhi, released variety through selection in the CIMMYT material
22	NW 51	Unclassified germplasm	Not known
23	PDW 233	-	PAU, Ludhiana, released variety
24	DWL 5023	CR/LDS//PLC/Gaza	PAU, Ludhiana released variety through selection in the CIMMYT material
25	Jay	Motia/KPH	Niphad (Maharastra), released variety
26	GW 1	A206/VSM//A206	Junagarh (Gujarat), released variety

After the last cycle, the sample were kept at 72°C for additional 3 min and then cooled to 4°C. The amplified products with the loading buffer were electophoresed in 1.8% agarose gel at a constant voltage. The gel was stained with ethidium bromide and photographed. Four series of oligonucleotide primers of operon were screened and the primers giving the good polymorphic and reproducible banding pattern were selected and these are presented in Table 2.

RAPD profiles were visually scored for the presence or absence of bands across the lanes. The combined data from all the 15 primers were used to calculate the similarity coefficient for all possible pair-wise combinations. These similarity coefficients were used for cluster analysis to depict the relationship among the genotypes using unweighed pair group method for arithmetic average (UPGMA). All the computational and statistical analyses were performed using NTSYS programme.

Results and Discussion

Four series of the Operon primers, namely, OPA, OPP, OPD and OPM were screened. Most of the primers were found to give average or poor resolution of durum wheat cultivars. Limited polymorphism in wheat in general have also been reported by Devos and Gale, (1996). Moreover, in the present study, the material chosen was from India only and, thus, has a narrow genetic base. Natural selection causes RAPD to have ecogeographical (Fahima *et al.*,1999) adaptation and therefore similar kind of environment in the central and South-West India from where most of landraces originated resulting in poor polymorphism and differentiation in the present study. None of the primers alone or in combination were able to identify all of the varieties.

Table 2. List of arbitrary primers used and the resolution achieved in durum wheat

Primer	Resolution
OPA2	Average
OPA3	Good
OPA10	Average
OPA11	Average
OPA12	Poor
OPP3	Average
OPP6	Good
OPP7	Poor
OPP9	Poor
OPP15	Poor
OPD5	Poor
OPD12	Average
OPD13	Average
OPD15	Average

However, some of the primers like OPA3 and OPP6 gave good resolution and, therefore, could be used in conjugation with the morphological markers for identification of the variety. The phenogram resulting from cluster analysis using UPGMA is shown in Fig.1. The largest divergence was observed between the local race Malvaraj (No.13) selected from the Malva tract of central India with the two other local cultivars of India i.e, Motia (No.3) and Jay (No.25). Except the two entries i.e., PBW34 (No.1) and Jayraj (No.2), the released varieties developed through selection in the CIMMYT advance material were genetically diverse and spread under different nodes and sub-nodes. International organizations like CIMMYT have global collection of germplasm, and therefore, generally the material generated by them are more likely to have the wide genetic base in comparison to the national programme. Three varieties, namely, Motia (No. 3), Gulab (No. 20) and Jay (No. 25) appeared under one node. These varieties have markedly low polymorphism among themselves. This might be due to their common origin and common ancestry as all of these were developed through selection from Local Bansi accession. Similarly, two other varieties like A-9-3-1 and GW1 showed very high similarity. It might also be due to their common ancestry as both of them involve A 206 in their pedigree. However, the close proximity of PDW 215(No. 4) and B.Yellow (No. 6) was quite surprising as both of these neither have the ancestry or their centre of origin common. The limited number of primers used in the study may be one of the reasons and therefore, needs to be confirmed through further screening with large number of primers. The two local cultivars from Vizapur also appear close. Others like Amrut (No. 11) and N 59 (No.12) formed a separate subgroup and both of these cultivars were having the strain GAZA in their pedigree. The clustering on the basis of RAPD markers was clearly on the basis of parentage of the entries involved in the study. Pujar *et al.* (1999) in their study on Indian tetraploid wheat found the highest divergence in wild and less commonly cultivated species along with the sub grouping of Indian released durum cultivars on the basis of their common parentage. The unclassified accessions could not be assigned to any of the groups and therefore the entry is either exotic or some other centre of durum breeding in India with entirely different parentage. The genetic base of improved cultivars of durum wheat in India is largely represented by the local cultivars and landraces and is very narrow, therefore, more vulnerable to biotic and abiotic stresses. Widening of genetic base of any

Table 3. Jaccard's Similarity Coefficients among 26 wheat cultivars

	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
01	1.00																									
02	0.83	1.00																								
03	0.60	0.57	1.00																							
04	0.70	0.71	0.54	1.00																						
05	0.53	0.52	0.60	0.54	1.00																					
06	0.66	0.67	0.59	0.64	0.60	1.00																				
07	0.64	0.72	0.65	0.63	0.54	0.76	1.00																			
08	0.61	0.70	0.61	0.64	0.58	0.57	0.71	1.00																		
09	0.63	0.63	0.62	0.64	0.58	0.58	0.58	0.73	1.00																	
10	0.53	0.57	0.64	0.60	0.59	0.60	0.65	0.57	0.63	1.00																
11	0.59	0.68	0.61	0.63	0.57	0.59	0.68	0.64	0.58	0.68	1.00															
12	0.57	0.62	0.61	0.61	0.62	0.57	0.62	0.63	0.59	0.62	0.77	1.00														
13	0.62	0.62	0.43	0.59	0.45	0.50	0.52	0.51	0.52	0.49	0.54	0.56	1.00													
14	0.57	0.61	0.61	0.59	0.62	0.63	0.66	0.63	0.60	0.59	0.62	0.65	0.55	1.00												
15	0.53	0.51	0.59	0.52	0.71	0.48	0.56	0.60	0.59	0.61	0.53	0.65	0.47	0.65	1.00											
16	0.57	0.61	0.62	0.59	0.51	0.64	0.72	0.61	0.56	0.6	0.60	0.52	0.45	0.65	0.51	1.00										
17	0.57	0.57	0.59	0.63	0.51	0.52	0.62	0.62	0.55	0.56	0.59	0.49	0.54	0.59	0.54	0.70	1.00									
18	0.54	0.55	0.63	0.61	0.61	0.57	0.59	0.62	0.68	0.62	0.54	0.58	0.51	0.70	0.66	0.55	0.60	1.00								
19	0.52	0.57	0.63	0.54	0.54	0.47	0.57	0.66	0.63	0.59	0.57	0.55	0.52	0.60	0.55	0.61	0.65	0.62	1.00							
20	0.54	0.53	0.89	0.49	0.60	0.56	0.61	0.57	0.57	0.60	0.56	0.55	0.38	0.54	0.60	0.56	0.54	0.59	0.60	1.00						
21	0.56	0.58	0.59	0.50	0.48	0.46	0.53	0.57	0.53	0.49	0.55	0.53	0.46	0.57	0.57	0.54	0.66	0.56	0.60	0.61	1.00					
22	0.62	0.57	0.50	0.53	0.46	0.67	0.60	0.45	0.46	0.51	0.46	0.54	0.61	0.51	0.49	0.51	0.47	0.49	0.44	0.46	0.52	1.00				
23	0.52	0.61	0.57	0.56	0.44	0.47	0.55	0.57	0.48	0.62	0.75	0.53	0.54	0.61	0.49	0.66	0.73	0.55	0.61	0.55	0.55	0.46	1.00			
24	0.52	0.60	0.55	0.51	0.53	0.47	0.55	0.55	0.51	0.54	0.54	0.56	0.55	0.60	0.57	0.58	0.66	0.57	0.58	0.49	0.55	0.47	0.68	1.00		
25	0.57	0.55	0.86	0.50	0.58	0.54	0.63	0.57	0.57	0.64	0.60	0.59	0.43	0.55	0.61	0.57	0.57	0.60	0.59	0.85	0.56	0.46	0.62	0.58	1.00	
26	0.56	0.64	0.70	0.60	0.51	0.64	0.79	0.62	0.52	0.61	0.64	0.60	0.55	0.62	0.53	0.65	0.64	0.57	0.56	0.62	0.55	0.54	0.64	0.67	0.74	1.00

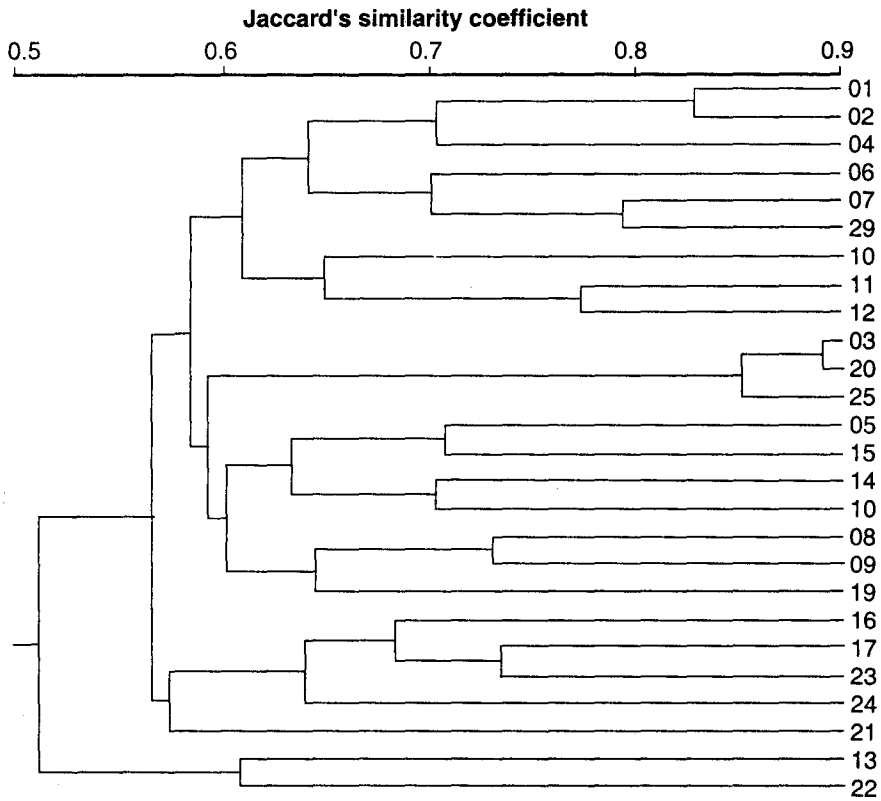

Fig. 1. Jaccard's Similarity Coefficients among 26 wheat cultivars

of the cultivated crop species is very important and the breeding lines/varieties involved in the breeding programme first needs to be characterized for the genetic diversity and due to the narrow range of the descriptors, diversity analysis on the basis of RAPD markers offer a viable alternative. Evaluation of the local cultivars or landraces for morphological and physiological characters is critical to exploit the genetic traits needed for adaptation. Identification of the diverse parents on the basis of agronomic traits, confirming it with the RAPD analysis and using them in crossing programme can maximise the level of variation in the segregating populations. The results confirm the utility of RAPD markers in the estimation of genetic diversity even in the closely related races/varieties. It is clear from the present study that the genetic base of the Indian durum cultivars can be very easily widened by making the crosses between the Indian local landraces and the improved germplasm from CIMMYT.

References

CIMMYT (1987) 1986 Annual Report. International Maize and Wheat Improvement Center, Mexico, D.F.

CIMMYT (1988) CIMMYT report on wheat improvement 1985-1986. International Maize and Wheat Improvement Center, Mexico, DF.

Devos KM and MD Gale (1992) The use of random amplified polymorphic DNA markers in wheat. *Theor. Appl. Genet.* **84:** 567-572.

Fahima T, GL Sun, A Beharav, T Krugman, A Beiles and E Nevo (1999) RAPD polymorphism of wild emmer wheat populations *Triticum dicocoides*, in Israel **98:** 434-437.

Martin JM, TK Black and EA Hockett (1991) Diversity among North American spring barley cultivars based on coefficient of parentage. *Crop Sci.* **31:** 1131-1137.

Porceddu E (1976) Variation for agronomical traits in a world collection of durum wheat. *Z Pflanzenzuchtg* **77:** 314-327.

Pujar S, SA Tamhankar, VS Rao, VS Gupta, S Naik and PK Ranjekar (1999) Arbitrarily primed- PCR based diversity assessment reflects hierarchical groupings of Indian tetraploid wheat genotypes. *Theor. Appl. Genet.* **99:** 868-876.

Smith JSC and OS Smith (1989) The description and assessment of distances between inbred lines of maize. II. The utility of morphological, biochemical and genetic descriptors and a scheme for testing distinctiveness between inbred lines. *Maydica* **34:** 151-161.

Welsh J and M McClelland (1990) Fingerprinting genomes using PCR with arbitrary primers *Nucleic Acid Res.* **18:** 7213-7218.

Williams JGK, ARK Kubelik, JL Livak, JA Rafalsiki and SV Tingey (1990) DNA polymorphisms amplified by random primers are useful as genetic markers. *Nucleic Acids Res.* **18:** 6531-6535.

Yang RC, S Jana and JM Clarke (1991) Phenotypic diversity and associationship of potentially drought responsive characters in durum wheat. *Crop Sci.* **31:** 1484-1491.

Evaluation of some Walnut (*Juglans regia*) Seedling Germplasm in Himachal Pradesh

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In the present study 30 seedlings with desirable traits were selected from total 104 populations. Maximum nut weight, nut length, suture and cheek diameter were recorded in KW 020. KW 012 had the minimum shell thickness (1.44 mm). It also had excellent shelling quality with light yellow kernel colour and excellent taste. Highest shelling percentage (58.5%) was also recorded in KW 012. Therefore, out of 30 seedlings, KW 012 was found to be the most promising selection having all the characters matching with international standards.

Key Words: *Juglans regia*, Seedlings, Shell Nut, Walnut

Walnut is a priced nut crop and grown in India in North-western Himalayas. At present 41,840 ha area is under walnut cultivation in India and the production is 22,000 metric tonnes (FAO, 1998). Still most of the walnuts are grown as scattered seedling trees and not in the form of a well laid-out orchard. The major hurdle in the expansion of area under walnut is non-availability of vegetatively progagated plants of superior strains/ cultivars. Though, some efforts have already been made to select superior walnut seedlings (Nauriyal *et al.*, 1970; Lal and Singh, 1978; Chauhan and Sharma, 1979; Sharma and Chauhan, 1980; Pandey and Sinha, 1984) and to introduce improved cultivars from abroad, seedling selections/cultivars of international standard are available only to a limited extent. The present studies were undertaken to evaluate best seedlings available in the Kotkhai and Theog area of Shimla district of Himachal Pradesh in India. This study is an effort to find out any seedling selection which can meet all the standards needed for the export of walnuts.

Materials and Methods

A survey on walnut was conducted during 1999 in the Kotkhai and Theog area of Shimla district located at an altitude ranging between 1800 to 2000 msl. Out of 104 seedlings, the detailed studies were conducted on 30 seedlings having desirable characters. The others were rejected on the basis of preliminary observations. Data was compiled on 30 nuts selected randomly from the whole harvest of the tree after the nuts were dried to edible stage. The results were expressed on the basis of averages of triplicate sampling and analysed statistically in a completely randomised design. Nut size represents the nut length, suture diameter and the cheek diameter in mm, which were measured with the help of Vernier Callipers. Weight (g) of the in-shell nuts, kernel weight (g) were also recorded from the same nuts. Shelling quality and taste grades were rated on numerical scale such as 5 – excellent, 4-very good, 2 – fair, 1– poor. Shelling percentage was also calculated.

Results and Discussion

The data on nut and kernal characters are presented in Table 1.

Nut Weight

The average nut weight varied from 9.5 g to 21.4 g (Table 1). The highest nut weight was found in KW 020 followed by KW 02. Gouzhen and Yang (1990) reported a variation in nut size in China between 5.8 g to 27 g. For international market an ideal nut should weigh between 12 to 18 g (McGranahan and Leslie, 1990).

Nut Length

The maximum nut length (47.1 mm) was recorded in KW 020 which was significantly higher than all other seedlings.

Suture Diameter

Suture diameter was found to be maximum (38.9 mm) in KW 020 which was statistically at par with KW 013. The minimum suture diameter (29.2 mm) was recorded in KW 05. For commercial grading suture diameter should not be less than 3.13 mm (Serr and Ford, 1956). A suture diameter above 3.7 mm is not considered good, as there are chances of poor filling of larger nuts.

Cheek Diameter

Nuts with maximum cheek diameter (39.1 mm) were

Table 1. Variation in nut characters of different walnut seedlings

Seedling No.	Nut characteristics								Kernel characteristics		
	Weight (g)	Length (mm)	Suture diameter (mm)	Cheek diameter (mm)	Shape	Surface	Shell thickness (mm)	Shelling quality (grade)	Colour	Taste (grade)	Shelling percentage
KW 01	10.7	35.2	31.4	29.2	Conical	R	2.52	3	V	2	37.5
KW 02	20.2	44.1	37.2	39.7	Ovoid	R	1.91	4	Y	4	42.3
KW 03	14.6	38.4	33.2	31.9	Oblong	S	2.15	3	LY	5	38.3
KW 04	12.9	33.2	28.4	29.0	Ovoid	S	1.97	5	Y	4	35.3
KW 05	9.5	30.4	29.2	30.5	Ovoid	R	2.34	4	DY	4	39.3
KW 06	15.7	40.3	32.8	34.2	Oblong	R	2.12	4	Y	3	41.8
KW 07	11.5	36.5	33.4	32.2	Oblong	S	1.84	4	V	2	32.4
KW 08	13.4	42.2	29.5	31.0	Concial	R	2.01	4	Y	3	46.5
KW 09	14.6	39.5	34.3	31.8	Ovoid	R	2.52	3	Y	3	38.4
KW 010	12.4	38.2	31.9	28.8	Conical	S	1.95	2	V	4	35.2
KW 011	10.8	35.1	32.6	33.4	Oblong	R	2.46	3	DY	3	32.4
KW 012	15.4	35.2	36.3	38.4	Ovoid	S	1.44	5	LY	5	58.5
KW 013	19.4	42.5	38.8	38.7	Ovoid	R	2.31	3	LY	5	34.5
KW 014	12.2	38.2	30.4	31.2	Oblong	R	2.18	4	Y	4	37.3
KW 015	9.8	29.2	31.2	30.4	Conical	R	1.91	3	Y	4	33.4
KW 016	14.3	35.0	36.4	32.2	Ovoid	R	2.13	4	LY	5	42.2
KW 017	19.2	41.4	38.4	33.4	Oblong	S	1.88	5	V	3	48.4
KW 018	11.3	33.4	32.2	30.7	Ovoid	S	2.08	5	Y	2	40.4
KW 019	10.2	38.2	32.4	31.4	Oblong	R	1.95	4	Y	4	35.2
KW 020	21.4	47.1	38.9	39.1	Oblong	R	2.28	4	V	3	47.3
KW 021	15.7	39.2	30.2	31.4	Conical	S	2.02	5	Y	4	31.7
KW 022	14.8	37.2	34.4	33.2	Oblong	S	2.62	2	LY	5	28.3
KW 023	13.3	36.5	33.0	32.1	Oblong	R	2.55	3	DY	3	29.4
KW 024	11.7	38.2	30.2	29.4	Conical	R	1.83	4	Y	4	43.7
KW 025	15.3	35.4	33.8	34.2	Ovoid	R	2.57	3	V	2	33.4
KW 026	12.8	37.4	30.2	28.7	Conical	S	1.62	5	DY	3	44.2
KW 027	13.7	35.0	33.2	32.4	Ovoid	R	2.44	4	LY	5	35.2
KW 028	18.4	40.4	35.3	34.7	Oblong	S	2.36	4	DY	4	39.4
KW 029	12.7	37.2	30.4	29.2	Conical	R	2.25	4	Y	3	41.4
KW 030	11.2	33.4	32.2	31.4	Ovoid	S	1.81	4	LY	5	42.3
$CD_{0.05}$	3.62	2.46	3.84	4.27	-	-	0.33	-	-	-	7.84

Nut surface: R-Rough; S-Smooth
Kernel colour: V-Violaceous; DY-Dark yellow; Y-yellow; LY-Light yellow
Shelling quality: 5-Excellent; 4-Very good; 3-Good; 2- Fair; 1-Poor

obtained from KW 020. The minimum cheek diameter (29.0 mm) was found in KW 04.

Nut Shape

Three prominent shapes were recorded in the nuts of different seedlings such as conical, oblong and ovoid. Great variation in the shape of nuts is found in the seeding germplasm. Sharma and Sharma (1998) also found various nut shapes in a survey conducted on 125 walnut seedlings.

Nut Surface

Out of 30 seedlings the nut surface of 18 seedlings was rough and that of 12 was smooth. Shell surface varied from slightly grooved to deeply grooved. Nuts having minimum grooved surface were more desirable. Sharma and Sharma (1998) in a study on 125 seedlings reported that shell surface of nuts of 72 trees were slightly grooved, 46 moderately grooved and 7 deeply grooved.

Shell Thickness

Highest shell thickness (2.62 mm) was recorded in KW 022 whereas it was lowest (1.44 mm) in KW 012. Medium shell nuts can be marketed as in shell and thin shelled nuts as kernels. Bhat *et al.* (1992) found that out of 20 seedlings, 4 were designated as hard shelled, 14 as medium shelled and 2 as thin shelled.

Shelling Quality

Shelling quality is a very important parameter as it determines whether the whole kernel is removed neatly or as broken pieces. Excellent shelling quality was observed in KW 04, KW 012, KW 017, KW 018 and KW 026. Fair shelling quality was found in KW 010 and KW 022.

Kernel Colour

For good quality walnuts, light yellow kernel is a desirable character. KW 03, KW 012, KW 013, KW 016, KW 022, KW 027 and KW 030 all hadlight yellow coloured kernels. Bhat *et al.,* (1992) reported that light amber coloured kernel is not a serious handicap but dark and black kernels are very objectionable.

Kernel Taste

Five local seedlings KW 03, KW 012, KW 013, KW 022 and KW 027 were found to have an excellent taste with numerical value of 5. Taste of KW 01, KW 07, KW 018 and KW 025 was observed to be fair in taste.

Sheelling Percentage

Highest shelling percentage (58.5%) was recorded in KW 012 which was significantly higher than other seedlings. The lowest percentage (29.4%) was, however, recorded in KW 023. According to Serr and Ford (1956) an ideal nut should have above 50% kernel, however, 50 to 60% is desirable. Bhat *et al.* (1992) reported three seedlings namely Wossan-4, P-1 and V-1 having a shelling percentage of 63.60, 63.0 and 62.0, respectively.

The variability in all the characters is mainly due to the heterozygous nature of plants obtained from seeds. Hansche *et al.* (1972) have reported that shell thickness, nut weight and kernel weight have high heritabilities. Therefore, these traits should be considered for the selection programme of seedlings. For international market an ideal nut should weigh between 12-18 g with a clean, strong and thin shell with tight seal and easily removeable light clear and plump kernel weighing at least 50% of the in-shell nut (Mc Granahan and Leslie, 1990). In the present study the nut size of KW 012 was found to be medium (15.4 g) with the highest shelling percentage (58.5%). It is thin shelled (1.44 mm) and also possesses excellent shelling quality and taste. Its hull splits so well that it leaves no stain on the nut. Therefore, KW 012 was found to be the most promising selection for international standard.

References

Bhat AR, HU Ahanger, AA Sofi and NA Mir (1992) Evaluation of some walnut selections of quality parameters in Jammu and Kashmir. In: *Emerging Trends in Temperate Fruit Production in India.* NHB Technical Communications No. **1:** 56-61.

Chauhan JB and SD Sharma (1979) Phenotypic variability in walnut of Kinnaur district of Himachal Pradesh. *Indian J. Agric. Sci.* **49:** 420-423.

FAO (1998) *FAO Production Yearbook,* Rome, Italy.

Gouzhen R and W Yang (1990) Walnut Germplasm in China. *Acta Horticulturae* **284:** 345-51.

Hansche, PE, V Beres and HI Ford (1972) Estimates to quantitative genetic properties of walnut and their implication for cultivar improvement. *J. Am. Soc. Hortic. Sci.* **97:** 279-85.

Lal H and RD Singh (1978) Some promising walnut strains in Chakrata hills of U.P. *Prog. Hortic.* **10:** 61-66.

McGranahan G and C Leslie (1990) Walnuts (*Juglans*). *Acta Horticulturae* **290:** 907-951.

Nauriyal JP, KL Chadha and H Kumar (1970) Some promising walnut trees in the Kullu valley. *J. Res.* PAU **6:** 852-857.

Pandey D and MM Sinha (1984) Some promising selections of walnut from Jaunsar Bhabhar area of Garhwal hill. Morphological studies. *Prog. Hortic.* **16:** 183-187.

Serr EE and HI Ford (1956) Walnut breeding *Proc. Am. Soc. Hortic. Sci.* **68:** 184-94.

Sharma SD and JS Chauhan (1980) A note on variability in nut characters of walnut seedlings. *Punjab Hortic. J.* **20:** 78-79.

Sharma SD and OC Sharma (1998) Studies on the variability in nuts of seedling walnut (*Juglans regia* L.) in relation to the tree age. *Fruit Varieties J.* **58:** 20-23.

Genetic Divergence for Seed Yield, its Components and Oil Content in Sesame*

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Multivariate analysis of divergence among 50 genotypes of sesame for nine quantitative characters revealed considerable genetic diversity in the materials and led to their grouping into five clusters. The cluster I was the largest having 20 genotypes followed by cluster III (13), V (9), II (5) and IV (3). The maximum divergence was revealed between cluster II and IV. The cluster IV was also distantly placed from other three clusters. Oil content contributed maximum, accounting for 45.39% of total genetic divergence followed by number of capsules/plant (18.94%) and seed yield/plant (16.49%). Based on genetic distance, mean performance and clustering pattern, hybridization involving genotypes EC-357023, B-6 and CST-782 are likely to give desirable segregants for developing superior varieties of sesame.

Key Words: D^2 Statistics, Genetic Divergence, Sesame (*Sesamum indicum*)

Sesame (*Sesamum indicum* L.) is one of the most ancient oilseed crop of arid and semi-arid ecosystem. India is considered to be the major centre of genetic diversity for sesame. Sesame yields oil and protein of high quality and holds tremendous potential for export. However, its productivity is very low (332 kg/ha) and fluctuate frequently from location to location and season to season due to the photosensitive nature of the crop. Selection in segregating generations has not led to significant improvement of yield levels. Hence, the situation warrants the exploitations of heterosis either by using effective CMS system or through manual emasculation and pollination for further yield enhancement. The choice of diverse parents with good combining ability is a pre-requisite for an efficient hybridization programme. The heterosis component is largely dependent on parental diversity as suggested by several workers in both self- and cross-pollinated crops.

The concept of genetic divergence provides an idea about the genetic diversity among the parents. In the present investigation, genetic divergence among 50 genotypes of sesame selected from different geographic regions has been worked out using D^2 statistics in order to understand the nature and magnitude of genetic divergence and the relative contribution of different characters to the total divergence.

Materials and Methods

Fifty genotypes of sesame collected from different places of Uttar Pradesh and other states of the country were grown at Oilseeds Research Farm, C S Azad University of Agriculture and Techology, Kanpur, during *kharif* 1998 in a randomized block design with three replications. Each genotypes was planted in single row of 5 m length at row and plant spacing of 30 x 15 cm. Recommended package of practices was followed to raise a good plant stand. Observations were recorded on five randomly selected plants in each strain replication-wise for nine quantitative traits (Table 3).

The oil content was estimated by NMR. The analysis of variance was carried out for all the characters individually. Multivariate analysis was done as per Mahalanobis D^2 statistics and the genotypes were grouped into different clusters, following Tocher's method described by Rao (1952).

Results and Discussion

The analysis of variance for each individual showed highly significant differences among the genotypes for all the characters studied. The pooled divergence for all the characters within the lines, tested by the wilk's criterion, was significant. Hence, the analysis of genetic divergence among genotypes used in the study was considered relevant. The D^2 values for all possible pairs of genotypes were worked out and on that basis, 50 genotypes have been grouped into five clusters (Table 1).

Cluster 1 having 20 genotypes was found to be the largest one followed by cluster III (13), V (9), II (5) and IV (3). Most of the important and related genotypes from the same source were distributed into

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Table 1. Group constellation of sesame genotypes

Clusters	Identity of the genotypes	Total no. of genotypes
I	EC 357016, TC-473, TC-491, IS-131-2-84, IS-234-2-84, IS-646-2-84, IS-600, IS-632-1-84, IS-100, AT-60, AT-61, RT-167, CST-93, TANU-17, TANU-22, OMT-11-6-5, OMT-11, OMT-34, OMT-3	20
II	iS-446-2-84, IS-554, RT-64, TANU-26, OMT-11-6-3	5
III	TC-25, IS-189-1-84, IS-431-2-84, IS-564-B, IS-520, TKG-1-4-6, BT-18-39-3, BT-875, RT-46, JLT-35, JLT-27, HT-20, HT-37	13
IV	EC-357023, B-6, CST-782	3
V	EC-357015, EC-351907, TKG-21, TKG-22, IS-195-1-84B, IS-195-2-84, IS-137, IS-232-96, DORS-0-6	9

different clusters. The results indicated that the geographical diversity alone is not an index of parental diversity as reported earlier by several workers like Thangavelu and Rajasekaran (1983), Swain and Dikshit (1997), Joel *et al.*, (1998) and Singh (2001). It also implies that it is not the geographic origin but selection pressure, which played an important role in determining genetic closeness and divergence among parents.

The divergence within and between clusters indicated divergence among the genotypes of same cluster and distance between different clusters, respectively. The perusal of Table 2 revealed that cluster I showed maximum intra-cluster distance (18.31). The maximum inter-cluster distance was recorded between cluster II and IV (14.32) while the distance was minimum between I and III (6.25).

Table 2. Intra- and inter-cluster distance among 5 clusters in sesame

Cluster	I	II	III	IV	V
I	**18.31**	6.93	6.25	12.35	6.92
II		**7.55**	7.01	14.32	8.68
III			**11.24**	14.05	7.68
IV				**10.68**	10.64
V					**12.11**

Note: Boldface values indicate intra-cluster distance

The cluster mean (Table 3) also substantiates this statistical distance, as means of cluster II and IV are substantially different. Genotypes belonging to these clusters (II and IV) are genetically more divergent and hybridization between genotypes of divergent clusters are likely to produce wide variability with desirable segregants (Dhamu *et al.*, 1983; Solanki and Gupta, 2002). The minimum distance between I and III indicates that the genotypes of these clusters were least genetically diverse and were of almost same genetic architecture.

Cluster II recorded highest mean for harvest index and oil content. Cluster III recorded highest mean value for plant height, capsules/plant and seed yield/plant whereas the cluster IV recorded highest mean for primary branches/plant and flowering duration. Hence, the genotypes of outstanding mean performance from these three clusters may be identified as potential parents and could be utilized in hybridization programme for developing high yielding sesame varieties.

The contribution of characters towards total divergence was carried out in terms of number of times it appeared in first rank (Table 4). Oil content has highest contribution of 45.39% to total divergence followed by number of capsules/plant (18.94%) and seed yield/plant (16.49%). Working on *kharif* sesame, Thangavelu and Rajasekaran (1983), whereas Swain and Dikshit (1997) on *rabi* sesame, reported that oil content contributed maximum towards genetic divergence. Solanki and Gupta (2002) reported maximum contribution of capsules/plant while Singh (2001) observed the maximum contribution of 1000-seed weight to genetic divergence followed by seed yield/plant.

Table 3. Cluster means for nine characters in sesame

Clusters	Plant height (cm)	No. of primary branches/ plant	Day of 50% flowering	No. of capsules/ plant	Days to maturity	Harvest index	1000-seed weight (g)	Oil content (%)	Seed yield/ plant (g)
I	91.95	2.68	40.51*	36.13	84.9	5.9	2.60*	50.73	3.1
II	81.13*	2.62	40.66	27.78*	84.33*	7.57**	2.84	52.88**	2.78
III	95.56**	2.65	40.56	43.28**	85.59	6.43	2.78	51.14	4.30**
IV	93.77	3.81**	48.22**	32.04	86.11	5.16*	3.06	46.87*	2.40*
V	85.51	2.53*	41.62	34.4	87.11**	6.49	3.10**	48.51	3.22

* Lower value ** Upper value

Table 4. Contribution of different characters towards total divergence in sesame

Characters	No. of times appearing first in ranking	Per cent contribution
Plant height	19	1.55
No. of primary branches/plant	26	2.12
Days to 50% flowering	62	5.06
No. of capsules/plant	232	18.94
Days to mature	31	2.53
Harvest index	84	6.86
1000-seed weight (g)	13	1.06
Oil content (%)	556	45.39
Seed yield/plant (g)	202	16.49
Total	**1,225**	**100**

On the contrary the other characters have given very little contribution to total divergence for enabling clear discrimination of the genotypes.

It may be inferred from the present study that the genotypes grouped in cluster II, IV and III are likely to produce potential crosses for exploitation of heterosis on commercial scale and to get desirable segregants for the development of high yielding varieties of sesame with high oil content.

References

Dhamu KP, MK Ayyaswamy and A Shanmugasubramaniam (1983) Genetic diversity in sesamum. *Madras Agric. J.* **70:** 495-498.

Joel AJ, S Alarmelu and S Thangavelu (1998) Genetic diversity in sesame (*Sesamum indicu.* L.). *J. Oilseeds Res.* **15:** 71-75.

Rao CR (1952) Advanced Statistical Methods in Biometric Research. John Wiley and Sons *Inc.* New York, pp 357-363.

Singh PK (2001) Genetic diversity in sesame (*Sesamum indicum* L.). *Indian J. Plant Genet. Resour.* **14:** 168-169.

Solanki ZS and Deepak Gupta (2002) Genetic divergence for seed yield and other characters in sesame (*Sesamum indicum* L.). *J. Oilseeds Res.* **19:** 35-37.

Swain D and UN Dikshit (1997) Genetic divergence in *rabi* sesame (*Sesamum indicum* L.). *Indian J. Genet.* **57:** 296-300.

Thangavelu MS and S Rajasekaran (1983) Genetic divergence in sesamum (*Sesamum indicum* L.). *Madras Agric. J.* **70:** 211-214.

Variability Studies in Kokam (*Garcinia indica*)

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The variability in kokam [*Garcinia indica* (Thouars) Choisy] available in the NBPGR Regional Station, Vellanikkara, Thrissur, Kerala, India was analysed. Major objectives of the study were to explore and document the variability in vegetative, floral and fruiting characters of *G. indica*. This study clearly indicated the existence of variability among the accessions/trees being maintained in the field genebank. Three accessions were found to be promising for separate characters such as IC 136687-3 for individual fruit weight, IC 136687-2 for total yield/tree/year and IC 136685-1 for number of fruits/tree/year.

Key Words: *Diversity, Garcinia indica,* Germplasm, Kokam, Variability

Kokam is one of the potential under-exploited multipurpose crops, currently gaining much commercial and medicinal importance. Botanically Kokam [*Garcinia indica* (Thouars) Choisy] belongs to the family Clusiaceae, formerly known as Guttiferae. It is endemic to the Western Ghats region in Maharashtra, Goa, and Karnataka but rare in Kerala and TamilNadu (Singh, 1993). Its fruits are valued for its nutritional and medicinal properties (Hadankur *et al.*, 1987). The dried rind is used as an excellent substitute for tamarind and lime, in the preparation of non-vegetarian curries especially for fish for imparting a special flavour and taste. It is used in preparing syrup during summer in Goa and Karnataka. Pharmaceutically active ingredient, (-)-hydroxycitric acid (HCA) which accelerates fat burning and inhibits fatty acid synthesis has been reported to occur in fruit rind (Krishnamurthy *et al.*, 1982; Akhtar Husain *et al.*, 1992). The seeds yield valuable fat known as kokam butter, which is edible and suitable as ointment in medicinal preparations for fissures of lips and heel (Singh, 1993).

It is a cross-pollinated and heterozygous crop. South Maharashtra and Goa regions is the centre of origin of this crop. Limited plantations are available in South Maharashtra and Karnataka. However, the bulk of the raw material is derived from wild sources. Due to severe deforestation and habitat destruction, genetic erosion is taking place and so there is a need for its conservation. There are no studies on variability in this crop. Hence, variability of kokam available at NBPGR Regional Station, Thrissur, was studied, where this crop has been introduced from North and South Kanara districts of Karnataka as seedling progenies.

Materials and Methods

Three-year-old 10 seedlings collected from North Kanara and one from South Kanara district of Karnataka were transplanted during the year 1992 at NBPGR Regional Station's farm at Vellanikkara, Thrissur (Table 1). On the day of observation trees were 8-11 years old. Observations on vegetative characters such as tree height (cm), tree spread (cm), leaf length (cm), leaf breadth (cm), leaf area (cm^2), petiole length (cm) and branching nature were recorded. Flower characters such as number of stamens, number of bundles, number of anthers per bundle and percentage of lightly stained pollen grains, deeply stained pollen grains, flowering season and fruiting season were recorded. Fruit characters such as weight (g), fresh rind weight (g), fresh rind thickness (mm), fresh fruit height (mm), fresh fruit diameter (mm), seed number, seed weight (g), seed length (mm), seed width (mm), seed thickness (mm), and pulp weight (g) were recorded. Yield related characters such as year of transplanting, first year of flowering, yield in kg/tree/year and number of fruits/tree/year were recorded. Leaf area was calculated by the method suggested by Lila Mathew *et al.* (1996). A mean of 10 observations on vegetative and fruit characters, five on flower characters, four yearly observations in flowering and bearing characters were subjected to statistical analysis.

Results and Discussion

Among the 10 trees, five were male, four female and one bisexual (Table 2). Data recorded on male, female and bisexual trees (Table 1) revealed, significant variations, the tree height ranged from 480 to 600 cm in male trees, 528 to 612 cm in female trees and the bisexual tree recorded 552 cm. The tree spread varied from 360 to 672 cm in male, 248-720 cm in female and 456 cm in bisexual tree. Significant variations were observed in leaf length and leaf breadth for female, male and bisexual. The trees studied were with both horizontal and drooping branches. Trees with horizontal

Table 1. Variation in vegetative characters of different kokam genotypes

Acc. No.	Tree height (cm)	Tree spread (cm)	Leaf length (cm)	Leaf breadth (cm)	Leaf area (cm^3)	Petiole length (cm)	Branching nature
IC 136682-2	593	492	6.46	2.42	15.32	0.56	Horizontal
IC 136685-1	612	444	7.22	3.30	23.05	0.75	Drooping
IC 136687-1	552	456	7.37	3.19	22.72	0.70	Horizontal
IC 136687-2	556	248	6.69	2.84	18.50	0.89	Drooping
IC 136687-3	528	720	5.96	2.70	15.75	0.73	Horizontal
IC 136684-3	504	456	7.67	3.24	25.53	1.03	Horizontal
IC 136685-2	456	576	6.08	3.19	20.15	0.73	Horizontal
IC 136685-3	480	432	6.54	2.51	17.21	0.60	Horizontal
IC 136682-3	485	360	6.94	2.67	19.30	0.63	Horizontal
IC 136678	600	672	8.37	3.77	32.15	0.99	Horizontal
SE	17.32**	44.28**	0.23	0.13	1.62	0.05	

** Significant at 1% level

branches occupied larger area with fewer yields but trees with drooping branches were promising as the spacing requirements per tree is less. A total of 80% of the trees had horizontal branches, that is all the male trees, two female trees and one bisexual tree recorded horizontal branches and only two female trees recorded the drooping branches.

Regarding female and bisexual trees, flower characters (Table 2) variability was noticed in terms of number of staminodes, there was no variability in terms of number of bundles (4) in both female and bisexual trees studied. Only a limited amount of variability was noticed among the collections in terms of number of staminodes/bundle 8 to 9 and 8.8 for female and bisexual, respectively. The male trees recorded 5 months of flowering period between December to April. The fruiting period in female trees was from January to May.

The physical parameters of fruit (Table 3) varied in respect to fresh fruit weight, fresh rind weight, fresh rind thickness and fruit diameter in female and bisexual trees. The same trend of variation, in female trees and the least value in bisexual trees was recorded in the following seed characters. In contrast, the thickest seed (8.16 mm) was observed in bisexual tree whereas female trees recorded the range from 5.67 to 6.11 mm. The best genotype with respect to fruit weight was IC 136687-3.

In respect of yield characters (Table-4), all the trees came to flowering at the age of eight years except IC 136687-3 which came at the age of nine. Bearing progressed from 1997 to 1999 gradually under minimal cultural practices with farmyard manure (FYM). FYM was applied @ 21 kg/tree/year during 1996-97, 1998-99 and 1999-2000. Because of application of NPK mixture (8:8:16) @ 200 g/tree/year during 1998-99 and NPK mixture (17:17:17) @ 400 g/tree/year during 1999-2000, there was increase in yield in all to the extent of 2 to 21 times during 1999-2000. Among the available data in all the bearing years, the accession IC 136687-2 was found to be the best which recorded 28.77 kg/tree/year. Regarding the number of fruits, the similar trend as to that of yield was followed for fertilizer application. The more number of fruits were recorded in the accession IC 136685-1 which recorded

Table 2. Variation of flower characters of different kokam genotypes

Acc. No.	No. of Staminodes/ Stamens	No. of bundles	No. of staminodes per bundle	Lightly stained pollen grains (%)	Deeply stained pollen grains (%)	Flowering Season	Fruiting season	Sex
IC 136682-2	06-17	4.00	08.80	100	-	Jan-Feb	Jan-May	F
IC 136685-1	05-12	4.00	09.20	99.28	-	Jan-Feb	Jan-May	F
IC 136687-1	06-10	4.00	08.80	99.47	-	Jan-Mar	Mar-May	B
IC 136687-2	06-08	4.00	08.00	98.94	-	Jan-Feb	Jan-May	F
IC 136687-3	06-12	4.00	09.60	100	-	Jan-Feb	Jan-April	F
IC 136685-2	37-44	1.00	40.60	-	92.3	Dec-April	-	M
IC 136678	34-44	1.00	39.40	-	94.48	Jan-Mar	-	M
IC 136684-3	23-38	1.00	30.56	-	91.08	Jan-April	-	M
IC 136685-3	23.36	1.00	29.20	-	83.17	Jan-April	-	M
IC 136682-3	*	*	*	*	*	Jan-April	-	M
SE±	4.75	0.57	04.71		NS	-	-	

* Data not available

Table 3. Variation in physical parameters of fruits from different kokam genotypes

Acc. No.	Fresh Fruit weight (g)	Fresh rind weight t (g)	Fresh rind thickness (mm)	Fruit height (mm)	Fruit diameter (mm)	Pulp weight (g)	Seed number	seed weight (g)	Seed length (mm)	Seed breadth (mm)	Seed thickness (mm)
IC 136682-2	18.53	07.96	2.52	30.04	33.88	07.29	5.10	3.28	17.12	09.31	6.07
IC 136685-1	17.17	08.17	2.63	26.41	33.96	06.26	5.60	2.73	12.84	08.93	5.67
IC 136687-1	06.18	03.11	1.89	22.87	22.07	04.22	1.00	1.96	14.89	08.65	8.16
IC 136687-2	15.54	06.91	2.42	25.91	32.75	05.39	4.40	2.47	15.84	09.77	6.11
IC 136687-3	25.16	10.73	2.41	32.98	37.33	10.72	5.40	3.70	17.35	10.70	6.06
SE±	07.86**	03.18	0.33	04.51**	06.68**	02.24	2.19	0.78	02.12	00.93	1.14

** Significant at 1% level

Table 4. Variation in yield characters of different kokam genotypes

Acc. No.	Year of transplanting	Year of first Flowering	Yield kg/tree year				Number of fruits/tree/year			
			1997	1998	1999	2000	1997	1998	1999	2000
IC 136682-2	1992	1997	0.025	2.041	4.005	19.165	1.00	139	321	2,260
IC 136685-1	1992	1997	0.000	2.705	8.956	19.905	4.00	179	827	3,268
IC 136687-1	1992	1997	0.033	0.000	0.000	00.025	1.00	000	000	0,004
IC 136687-2	1992	1997	0.000	2.791	9.218	28.766	6.00	123	409	2,209
IC 136687-3	1992	1998	0.000	0.009	1.221	26.012	0.00	001	066	1,954
SE±			0.007	0.630	1.910	05.030	1.12	37.03	146.93	533.23

3,268 fruits/tree/year. The accession, which recorded higher number of fruits, gave low yield and *vice versa* this is because of natural adjustment and energy diversion (Muthulakshmi, 1998).

In general, compared to the morphological characters of the fruit, variations observed in flower characters were limited. While demarcating the lines with higher yield and good quality, it was not possible to select kokam accessions with all the characters i.e., high fruit weight, number of fruits, rind thickness, pulp weight, seed number, seed length, breadth and thickness. However, accessions with individual quality characters could be identified which can be utilized for further improvement. The present study indicated the existence of variability among the accessions in terms of vegetative, floral, fruit and yield characters and the existence of distinct male, female and bisexual trees. There is a need for identifying the sex of the plants in the seedling stage itself as is being done in Malabar tamarind (Muthulakshmi, 1998). Since, soft wood grafting in kokam has been found successful (Hadankur *et al.*, 1987), sex determination could be used for large scale multiplication of elite trees. Rapid multiplication needs to be attempted through *in vitro* technology for popularising true-to-type plantations of high yielding lines. Moreover, fruit bearing coincides with summer months which is ideal for drying the rind. Any success in transferring this trait to malabar tamarind (*G. gummigutta*), would be highly useful for the farming community of this locality for rind drying, as it bears fruits during the rainy season.

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References

Akhtar Husain, OP Virmani, SP Popli, LN Mishra, MM Gupta, GN Srivastava, ZAbraham and AK Singh (1992) Dictionary of Indian Medicinal Plants. CIMAP, Lucknow, 218p.

Hadankur PM, MJ Salvi and GD Joshi (1987) Softwood Grafting, Viable Propagation Technique for Kokam Production, *Indian Horticulture,* October-December, 21p.

Krishnamurthy N, YS Lewis and B Ravindranath (1982) Chemical constituents of Kokam fruit rind. *J. Food. Sci.* **19:** 97-100

Lila Mathew, Sarah T George and S Krishnan (1996) Estimation of leaf area in *Garcinia gambojia* (Kodampuli) through linear measurement. *J. Tropic. Agricul.* **34:** 61-62p.

Muthulakshmi P (1998) *Variability Analysis in Garcinia cambogia* Desr. (Malabar Tamarind) M.Sc. (Ag.), Thesis Kerala Agricultural University, Thrissur.

Singh NP (1993) Clusiaceae. In: BD Sharma and M Sanjappa (Eds) *Flora of India*, Vol. 3. Portulaceae – Ixonanthaceae, Botanical Survey of India, Calcutta, pp 87-151.

Genetic Variability, Correlation and Path Analysis in Grain Amaranth

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The present study on grain amaranth revealed presence of genetic variability in seed yield and harvest index. Genetic index and flowering time showed high heritability while genetic advance was high for plant height. Harvest index, plant height, inflorescence length, maturity period, flowering time and test weight had significant positive correlation with seed yield. Path analysis revealed highest positive direct effect of harvest index followed by maturity period, basal girth and plant height. Plant height, inflorescence length and flowering time had substantial indirect contribution through harvest index.

Key Words: Genetic Variation, Grain Amarnath, Heritability, Path Analysis

Grain amaranth is a widely adapted under-utilized crop plant having immense potential for scientific exploitation. This C_4 plant species can be grown in varying agroclimatic conditions ranging from the high altitude temperate Himalayas to the desert plains of Gujarat. In the Himalayan region, it is grown as a *kharif* cash crop in high altitude areas while in the plains it is cultivated in the *rabi* season. For achieving increased production in grain amaranth it is essential to evolve high yielding varieties as very few improved varieties have been evolved in this crop. Planning of any breeding programme requires information on the amount of genetic variability available among the breeding genotypes. The nature of association among easily measurable characters influencing yield determines the success of selection programmes. Current knowledge on genetic variability and character association in grain amaranth genotypes is meagre. The present study was, therefore, undertaken to assess the genetic variation, heritability, correlation and direct and indirect contributions of some quantitative characters on seed yield in a set of diverse grain amaranth genotypes.

Materials and Method

Twenty-two widely adapted grain amaranth genotypes belonging to *Amaranthus hypochondriacus* species received from different regions of the country, were raised at Plant Breeding Research Block, Hill Campus (2100 m asl) of GB Pant University of Agriculture and Technology during 1991-92. The genotypes tested were IC 38269, IC 38280, IC 38658, IC 42255-5, IC 42290-17, IC 42316-1, IC 42374, VHC 7502, VHC 7519, VL 21, VL 33, VL 35, VL 36, VL 38, VL 44, PRA 8701, PRA 8801, PRA 8901, Annapurna, Suvarna, Ranichauri Local and Saonli Local. The experiments were laid out in a randomized block design with three replications. Plot size was 5 rows each of 2.5 m long. Row to row distance was 50 cm while plants within a row were spaced at 15 cm. Recommended agronomic practices were followed with a fertilizer dose of 20:40:0 NPK kg/ha, but no plant protection measures were undertaken since no insect and disease problems were encountered.

Observations were recorded on 10 randomly selected representative plants/plot. Data on flowering time (days taken for 50% head emergence), maturity period (days), plant height (cm), inflorescence length (cm), basal girth of stem at collar region (cm), height: girth ratio, test weight (weight of 10 ml seed in g), seed yield (q/ha) and harvest index (%) were recorded. Analysis of variance were done from the mean data obtained for each character. The phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability in broad sense, genetic advance were calculated following Johnson *et al.*, (1955) and path coefficient analysis following Dewey and Lu (1959).

Results and Discussion

Significant differences were observed among the genotypes for all the characters studied indicating presence of adequate variability. Low estimates of phenotypic and genotypic coefficients of variations revealed in general (Table 1), but grain yield and harvest index showed maximum coefficients of variation. Heritability was high for harvest index and flowering time while genetic advance was high for harvest index and flowering time while genetic advance was high only for plant height (Table 1). The absence of any character combining high heritability as well as high genetic advance in this study suggests that non-additive gene actions are predominantly operating for the characters studied (Liang and Walter, 1968). Lohithaswa *et al.* (1996) in a study in the plains of southern India reported

Table 1. Estimates of genetic variability in grain amaranth

Character	Mean	PCV (%)	GCV (%)	Genetic advance	Heritability (%)
Flowering time	69.3	6.1	5.3	6.7	77.4
Maturity period	131.7	2.8	2.2	4.5	58.7
Plant height	227.5	10.4	7.3	23.9	49.3
Inflorescence length	77.9	14.0	7.1	5.8	25.6
Basal girth	7.9	11.8	6.2	5.3	27.7
Height:girth ratio	3.5	12.1	9.0	0.5	55.2
Test weight	8.6	2.9	1.9	0.2	44.4
Harvest index	16.2	18.0	16.5	5.0	83.6
Seed yield	12.9	27.6	18.2	3.2	43.2

high heritiability but moderate genetic advance for plant height and days taken to 50% flowering only.

The phenotypic and genotypic correlation coefficients are presented in Table 2. Harvest index, plant height, inflorescence length, maturity period, flowering time and test weight had significant positive associations with grain yield. Plant height had significant positive association with all the characters except height:girth ratio. Thus, selection for this characters may result in correlated response in other character including seed yield. The significant positive correlation of test weight, inflorescence length and flowering time with plant height suggests that tall and late flowering plants having longer inflorescence and larger seed size would produce high seed yield. Tall and late maturing genotypes were found to be higher yielders among the Himalayan collections by Joshi and Rana (1991, 1995) also. But, these unfavourable associations may pose difficulty in breeding early maturing genotypes having high seed yield which are of prime importance in the hill farming system where crop growing period is extremely short because of the limitations imposed by cold climatic conditions. The significant positive association of harvest index with seed yield indicates high partitioning ability of the high yielders. Genotypic correlations showed almost similar trend as that of phenotypic correlations but had larger values. Inflorescence length had maximum genotypic correlation with seed yield.

Path coefficient analysis was carried out using phenotypic correlations to estimate the direct and indirect contribution of individual characters on grain yield. Harvest index had the highest positive direct effect on grain yield followed by maturity period, basal diameter, plant height and inflorescence length (Table 3). Height: girth ratio and flowering time had direct negative effects on seed yield. Test weight had negligible direct contribution indicating its minimum influence on seed yield. The indirect effect of harvest index through flowering time was negative but it was positive through other characters. Plant height, inflorescence length and flowering time all had positive indirect contributions through harvest index. Pandey (1981) observed that plant

Table 2. Phenotypic (upper) and genotypic (lower) correlations in grain amaranth

	Maturity period	Plant height	Inflorescence length	Basal diameter	Height: diameter	Test weight	Harvest index	Seed yield
Flowering time	0.535**	0.377**	0.394**	0.228	-0.162	0.246	0.390**	0.284*
	0.734	0.860	0.957	0.694	-0.321	0.460	0.436	0.727
Maturity period	–	0.179	0.150	0.134	-0.052	0.445**	0.207	0.314*
		0.425	0.826	0.368	-0.139	0.646	0.233	0.430
Plant height	–	–	0.613**	0.454**	-0.474**	0.910**	0.399**	0.476**
			1.215	0.134	-0.790	0.263	0.661	0.893
Inflorescence length	–	–	–	0.424**	-0.139	0.181	0.370**	0.385**
				0.696	-0.660	0.657	0.916	1.098
Basal girth	–	–	–	–	0.555**	0.142	0.257	0.240
					0.504	0.324	0.485	0.716
Height:diameter	–	–	–	–	–	0.011	-0.164	-0.233
						-0.030	-0.287	-0.336
Test weight	–	–	–	–	–	–	0.180	0.288*
							0.247	0.302
Harvest index	–	–	–	–	–	–	–	0.536**
								0.965

*, ** Significant at 0.05 and 0.01 probability levels, respectively

Table 3. The direct (bold) and indirect effects of different characters on seed yield in grain amaranth

	Flowering time	Maturity period	Plant height	Panicle length	Basal diameter	Height: diameter	Test weight	Harvest index	Phenotypic correlation with seed yield
Flowering time	**-0.1474**	0.1319	0.0440	0.0412	0.0323	0.0289	0.0002	0.1529	0.284*
Maturity period	-0.0790	**0.2465**	0.0209	0.0157	0.0189	0.0093	0.0004	0.0810	0.314*
Plant height	-0.0556	0.0442	**0.1167**	0.0642	0.0643	0.0848	0.0009	0.1561	0.476**
Inflorescence Length	-0.0580	0.0370	0.0716	**0.1047**	0.0600	0.0249	0.0002	0.1448	0.385**
Basal girth	-0.0337	0.0329	0.0529	0.0443	**0.1417**	-0.0993	0.0001	0.1007	0.240
Height:diameter	0.0239	-0.0128	-0.0554	-0.0145	0.0787	**-0.1789**	0.0001	-0.0640	-0.223
Test weight	-0.0363	0.1098	0.1062	0.0189	0.0201	-0.0020	**0.0010**	0.0706	0.288*
Harvest index	-0.0576	0.0509	0.0465	0.0387	0.0365	0.0293	0.0002	**0.3916**	0.536**

Residual effect = 0.584

height had the greatest direct effect on the number of panicles which is an important yield contributory character.

Thus, in view of the above, it appears that selection of late maturing but early flowering and tall plants having higher partitioning efficiency would result in increased seed yield in grain amaranth. But, this may result into reduced cropping intensity and increased lodging susceptibility. However, the linkage of these unfavourable associations with seed yield could be broken through intensive recombination breeding. The high residual effect suggests that the present set of characters alone were not sufficient in explaining the variability in seed yield and hence more yield contributing characters need to be included in future studies.

References

Johnson HW, HF Robinson and RE Comstock (1955) Estimates of genetic and environmental variability in soybeans. *Agronomy J.* **47:** 314-318.

Joshi BD and RS Rana (1991) Grain Amaranth: The Future Food Crop, National Bureau of Plant Genetic Resources, Regional Station, Shimla, Himachal Pradesh, 152p.

Joshi BD and JC Rana (1995) Genetic analysis for yield and its components in grain amaranth. *J. Hill Res.* **8:** 195-198.

Lohithaswa HC, TE Nagaraj, DL Savithramma and HB Hemareddy (1996) Genetic variability studies in grain amaranth. *Mysore J. Agric. Sci.* **30:** 117-120.

Pandey RM (1981) Path analysis in *Amaranthus hypochondriacus*. *Sci. Cult.* **47:** 64-66.

SHORT COMMUNICATION

Identification of Resistant Sources to *Turcicum* Leaf Blight in Maize

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Key Words: Leaf Blight, Resistant Sources, *Turcicum*

Maize (*Zea mays* L.), is an important staple food crop of mid hills of Himachal Pradesh. Crop losses from *Turcicum* leaf blight may vary from 27.6 to 90.7% in grain yield (Chenulu and Hora, 1962). Reduction in yield depends upon time of first appearance of the disease which is largely determined by the weather conditions (Ulstrup, 1961). The disease can be managed by chemical and cultural management practices but the indiscriminate use of fungicides for the control of disease have several disadvantages particularly the cost of fungicide and their residual effects, which cause health hazards and some time pathogen develops resistance against fungicides. Use of resistant material is the best environment friendly approach, therefore, efforts were made to identify resistant sources to *Turcicum* leaf blight of maize.

Turcicum leaf blight caused by (*Exserohilium turcicum* (Pars.) Leonard and Suggs. (*Setosphaeria turcica* (Luttr.) Leonard and Suggs.) is the most serious and prevalent disease in sub-humid zone of Himachal Pradesh.

Two hundred eighteen and 237 maize genotypes/lines during 1996 and 1997, respectively, were evaluated under artificial epiphytotic conditions at the station (hot spot for the disease). The entries were sown/planted in two row plot of 5 m length. All recommended agronomic practices were followed in raising the crop. All entries were inoculated with dry powdered inoculum (obtained from grinding the heavily infested mature leaves of previous season). The inoculum was inserted in the whorl of each plant. In the dry season water was sprayed to increase the relative humidity. The inoculation was repeated twice at one week interval. The disease data/observation were recorded at dough stage by using 0-5 scale.

The critical evaluation of maize germplasm led to the identification of five highly resistant (<1) genotypes, *viz.*, KH-559-A, KH-5367, Bio-9696, PNZ-117 and Bio-41015 and six resistant (<2) genotypes, viz., X-1283-M, BH-1089, X-1265-D, KH-5364, Pro-320 and Bio-9720. It is concluded that resistance mechanism of these genotypes can be exploited in breeding programme for developing high yielding varieties, resistant to *Turcicum* leaf blight to minimize yield losses. Similar types of results were obtained by Brewbaker *et al.*, (1989) and Rathee *et al.*, (1999).

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References

Brewbaker JL, ML Logrono and SK Kim (1989) Bulletin Research Series 62 Hawaii Institute of Tropical Agriculture and Human Resources, University of Hawaii, Manoa, Hawaii, pp 1-26.

Chenulu VV and TS Hora (1962) Studies on losses due to *Helminthosporium* blight of maize. *Indian Phytopath.* **15:** 235-237.

Rathee VK, BK Sharma and SK Guleria (1999) Screening of maize germplasm against *Turcicum* leaf blight under artificial epiphytotic conditions. *Crop Res.* **1** 268-69.

Ulstrup AJ (1961) *Corn Diseases.* Agriculture Hand book No. **199:** 15.

SHORT COMMUNICATION

Evaluation of Maize Hybrids and Composites against Bacterial Stalk Rot, Brown Stripe Downy Mildew and Maydis Leaf Blight

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Key Words: Bacterial Stalk Rot, Brown Stripe Downy Mildew, Maize, Maydis Leaf Blight, Resistance, *Zea mays*

Maize (*Zea mays* L.) is the third important cereal crop in India after rice and wheat. Predominantly, it is grown during *kharif* season in tropical environments. The productivity in India (1.8 t/ha) is verylow as compared to the temperate areas (7.0 t/ha) and world average (3.8 t/ha). Among various factors for low yield, diseases like bacterial stalk rot (*Erwinia chrysanthemi* pv *zeae*) maydis leaf blight (*Dreschlera maydis)* and brown stripe downy mildew (*Sclerophthora rayssaie* var. *zeae*), cause significant reduction in grain yield (Sharma *et al.,* 1993). These diseases can be managed with biocides. However, resource starved farmers cannot afford to use costly chemicals. Moreover, efficacy of chemicals is usually reduced by continued rains during the cropping season. Hence, losses due to diseases can be mitigated by cultivation of resistant varieties. Keeping this in view, some Indian hybrids and composite stocks were evaluated against these diseases and information on identification of resistant sources is presented.

Two hundred and thirty nine hybrid and composite stocks of Advanced Evaluation Trails received from Directorate of Maize Research, New Delhi, were planted during *kharif* 1999 and 2000 at experimental farm of Regional Research Station, Dhaulakuan following recommended agronomic practices (Anonymous, 1993). Bacterial stalk rot epiphytotics were created by inoculating about 75-100 plants/entry with 48 hold cell suspension of *E. chrysanthemi* pv *zeae* at pre-tasseling stage using hypodermic syringe method (Singh, 1983). The field was innoculum-sick for brown stripe downy mildew, moreover, 30 days old plants were whorl inoculated with downy mildew infected leaf bits (Singh, 1983). The maydis leaf blight observations were based on natural infection. The data on incidence of *Erwinia* stalk rot was recorded as per cent wilted plants 20 days after the inoculations. The data for brown stripe downy mildew and maydis leaf blight were recorded on 1-5 and 0-5 scale, at pre-tasseling and grain formation stage, respectively (Singh, 1983). The left over seed of each entry was evaluated during the subsequent *kharif* season to confirm their reaction to the diseases.

The hybrid and composite stocks showing resistance against *Erwinia* stalk rot, brown stripe downy mildew and maydis leaf blight during the year 1999 and 2000 are given in Table 1. Three hybrids BH 1015, BH 1180 and PRO 311 were free from *Eriwinia* stalk rot and none of the stocks were free from brown stripe downy mildew and maydis leaf blight. Seventeen stocks with less than 10% stalk rot incidence were resistant and thirty-two hybrids/composites with 10-20% disease incidence were moderately resistant to *Erwinia* stalk rot.

Forty-eight entries with disease reaction >2 were resistant and 19 entries were moderately resistant (disease reaction 2-3) to brown stripe downy mildew. It was observed that stocks showing resistance to *Erwinia* stalk rot and brown stripe downy mildew were from full season maturity group. Thirty-six stocks with disease reaction 2.1-2.5 were moderately resistant to maydis leaf blight. Sources of resistance among inbreds, hybrids and composites have already been reported against *Erwinia* stalk rot (Thind and Payak, 1985; Ebron *et al.,* 1987), maydis leaf blight (Khan *et al.,* 1992; Sharma and Payak, 1990) and brown stripe downy mildew (Bains, 1989; Sharma *et al.,* 1993).

It has been observed that hybrids BH 1180, (Comp. 9010 x 9116)#, NECH 106, PHS 4783 and X 519 showed multiple resistance against all the diseases. Stocks JC 3252, PRO 311, X 521, and BH 1015, KH 5991, PRO 340, PMH 9844, Seed Tech 2331 showed

Table 1. List of maize (*Zea mays*) stocks resistant to *Erwinia* stalk rot (*Erwinia chrysanthemi* pv *zeae*) brown stripe downy mildew (*Sclerophthora rayssiae* var *zeae*) and maydis leaf blight (*Dreschlera maydis*)

Erwinia stalk rot

FREE: BH 1015, BH 1180 and PRO 311

RESISTANT (1->10%): (Comp. 9010 x 9116)#, FH 3138, JC 3252, KH 5991, NECH 106, PMH 9844, PHS 4783, PRO 311, PRO 340, Seed Tech 2331, X 519, X 519A, X521

MODERATELY RESISTANT (10-20%): AH 418, AH 422, AH 918, AMZ H 98, BH 1102, BH 1179, BIO 9637, Comp 9110, EH 30425, F 7012, HKH 1159, HKH 1121, Him 129, JK 3251, JKO 682, Kiran, KH 510, NECH 01, NECH 02, NMH 9804, Navjot, PAC 79004, PHS 4757, PHS 4786, PMH 9803, PRO 342, Seed Tech 12, SSFX 411, SSFX 9199, X 1288B, X 1288 D.

Brown stripe downy mildew

RESISTANT: (1-2): AMZ H 98, AH 118, AH 421, AH 422, BH 1015, BH 1025, BH 1178, BH 1179, BH 1180, BH 1181, BH 1183, BIO 9637, EH 30425, F 7001, F 7013, HKH 1100, HKH 1121, HKH 1123, HKH 1140, HKH 1159, JH 2906, JH 3125, JH 3795, JK 0581, KJ 0682, JK 1181, KH 409, KH 5991, Kiran, NECH 02, NECH 105, NECH 106, NMH 9804, Navjot, PAC 79002, PAC 79003, PMH 9803, PMH 9844, PHS 4754, PHS 4783, PMZ 1251, PMZ 127, PRO 340, PRO 342, Seed Tech 2331, SSFX 411, SSFX 9199, Seed Tech 12, X 519, X 1174(w), X 1288B.

MODERATELY RESISTANT (2->2.5): Comp 9110, (Comp 9010 x 9116)#, EH 30422, F 7012, HKH 1138, Him 129, JC 3251, KH 510, MECH 01, PRO 311, PRO 339, PHS 4759, PAC 79001, SSFX 522, Surya, Seed Tech 1250.

Maydis leaf blight

RESISTANT: (1-2): AH 914, AH 918, BH 1180, BH 1183, BIO 9637, Comp 9010 x 9116#, Comp 9110, EH 30425, F 7001, Ganga 11, HKH 1138, JC 3251, JC 3252, JH 2906, JH 3125, JK 1181, JK 06802, KH 510, Kiran, NECH 02, NECH 03, NECH 106, PAC 79001, PAC 79002, PAC 79003, PHS 4783, PHS 4757, PHS 4759, PHS 4786, PMZ 127, PRO 311, SSF X 522, Seed Tech 1250, X 519, X521, X 1138R, X 1288B, X 1288D.

MODERATELY RESISTANT (2.1->3.0): AH 418, BH 1181, EH 30422, F 7012, F 7013, GK 3003, HKH 1100, HKH 1121, HKH 1140, HKH 1159, JH 3795, KJ 0581, KH 409, KH 5991, NECH 105, NMH 9804, Navjot, PAC 79004, PMH 9803, PMH 9844, PMZ 1251, PRO 339, PRO 340, Seed Tech 12, Seed Tech 2350, X 519A.

combined resistance against *Erwinia* stalk rot and maydis leaf blight and *Erwinia* stalk rot and brown stripe downy mildew, respectively. Stocks BIO 9637, EH 30425, F 7001, JK 0682, JH 2906, JK 1181, Kiran, NECH 02, PAC 79003, PMZ 127, PHS 4757, PAC 79002, Seed Tech 12 and X 1288B were resistant to maydis leaf blight and brown stripe downy mildew. As has been recorded in the present studies multiple resistance has been reported against maydis leaf blight and brown stripe downy mildew (Dey *et al.,* 1983), *Turcicum* leaf blight, maydis leaf blight and brown spot (Kaiser and Pradhan, 1990) and *Erwinia* stalk rot, maydis leaf blight and brown stripe downy mildew (Basandrai *et al.,* 2000).

Interestingly, Navjot, PRO 311, HIM 129, BH 9637, Kiran, KH 510, Surya and Ganga 11 are identified varieties, which may be directly recommended in disease-prone areas. Most of the hybrids are from private sector. Availability of parental inbred lines of resistant stocks may help to work out genetics of resistance against these diseases, for their better utilization to develop resistant varieties.

References

Singh J (ed) (1983) *Techniques of scoring for resistance of maize diseases.* All India Coordinated Maize Improvement Project, Indian Agricultural Research Institute, New Delhi, pp 125.

Anonymous (1993) *Package and Practices for Kharif Crops.* Directorate of Extension Education, Himachal Pradesh Krishi Vishvavidyalya, Palampur, 112 p.

Bains SS (1989) Response of *Zea* maize species of *Sclerophthora rayssiae* var *zeae* inoculations. *Indian Bot. Report.* **8:** 161-163.

Basandrai AK, A Singh and V Kalia (2000) Sources of multiple disease resistance in Indian maize hybrids and composites. *Indian J. Plant Genet. Resour.* **13:** 188-190.

Dey SK, BS Dhillon, U Kanta, SS Sekhon, VK Saxena, NS Malhi and AS Khera (1983) Resistance to multibiotic stress in maize (*Zea mays* L.). *J. Ent. Res.* **17:** 73-79.

Ebron LA, MS Tolintino and MM Lantin (1987) Screening for bacterial stalk rot in corn. *Philippine. J. Crop Sci.* **12:** 31-32.

Kaiser SAKM and HS Pradhan (1990) Evaluation of multiple resistance in maize to three foliar diseases. *Enviro. Ecol.* **8:** 25-29.

Khan Ali, Shabeer Ahmed, A Khan and S Ahmad (1992) Genotype assay of maize for resistance to maydis leaf blight under field epiphytotics of Peshawar region. *Sarhad J. Agric.* **8:** 547-549.

Sharma RC, Carlos De Leon and MM Payak (1993) Diseases of maize of south and South-east Asia. Problems and Progress. *Crop Protection* **12:** 414-422.

Sharma RC and MM Payak (1993) Durable resistance to two leaf blights in two maize inbred lines. *Theor. Appl. Genet.* **80:** 443-544.

Thind BS and MM Payak (1985) A review of bacterial stalk rot in maize in India. *Tropical Pest Management* **51:** 311-316.

SHORT COMMUNICATION

Evaluation of Some Strawberry (*Fragaria x Ananassa* Duch) Cultivars under Jammu Plains

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KeyWords: Cultivars, Duch, *Fragaria* x *ananassa*, Strawberry

The cultivated strawberry (*Fragaria* x *Ananassa* Duch) belongs to family Rosaceae is derived from the hybridization of two native American species, namely, *F. chiloensis* Duch and *F. virginiana* Duch, which was first developed in France in the 17th century (Sharma and Yamdagni, 2000). Delicate of flavour and rich in vitamins and minerals, strawberry is now a favoured food in the diet of millions of people around the globe. It can be processed into a variety of products through various processes such as canning in syrup, jamming, drying, freeze drying, candying, freezing etc.

At present, strawberry is grown in all kinds of climates including temperate, mediterranean, sub-tropical and tiaga zones. It offers a quicker return on capital investment than any other fruit since under special methods of cultivation, a crop can be picked as early as the first summer after planting (Hughes *et al.*, 1969). Strawberry yield and quality are greatly influenced by a number of factors (soil, environment, pests, diseases etc.) and as a result, plants of a particular cultivar may grow well in one region but may perform poorly in another where environmental conditions are different (Hancock *et al.*, 1996). The fruiting potential of individual cultivars can be exploited only after growing it in the optimum/suitable soil and climatic conditions which need testing.

In spite of being a highly remunerative crop for Jammu plains, very little attention has been given by the researchers to assess the suitability of individual strawberry cultivation. The present study was made to identify the suitable and locally adaptable cultivars(s) for commercial cutlivation in the sub-tropical conditions of Jammu region.

The present study was conducted at KVK Farm, Udheywalla, RS Pura, during 2000-2001 on eight strawberry cultivars, namely, Addie, Belrubi, Brighton, Chandler, Confitura, Fern, Gorella and Selva, planted on 15.11.2000 at 45 x 30 cm. The plants were planted on raised beds (3.00 x 1.35 m) in three rows. The experiment was laid out in Randomised Block Design and replicated thrice. For recording data, 15 plants (out of 30 plants) of each cultivar in a replication were selected randomly. Total number of flowers of selected plants were recorded throughout the fruiting season and expressed as per plant basis. Fruit set (%) was calculated as per the formula given by Westwood (1978). Total number of malformed/deformed fruits from selected plants were counted and expressed in per cent. Duration of picking was calculated by counting the days between first picking to last picking. For calculating yield/plant the weight of total fruits of selected plants was measured and expressed on per plant basis.

The fruits were harvested at commercial maturity and subjected to various quality attributes. Fruit size and total soluble solids were measured with the help of vernier calliper and hand refractometer, respectively. Titratable acidity and sugars were estimated by titration method (Horwitz, 1980). To assess the consumer preference, organoleptic evaluation was conducted by a panel of 10 judges as per the method of Hedonic scale (Gould, 1978). Scoring was done out of 10 and their rating was done as per the following scale:

10 - Excellent; 9 - Very good; 8 - Good; 7 - Moderately good; 6 - Fair; 5 - Moderately fair; 4 - Poor; 3 - Very poor; 2 - Not acceptable.

Data relating to various yield and quality contributing characters (Table 1) revealed that all the tested cultivars started to bloom in the beginning of 3rd week of January except Selva wherein blooming was delayed by 5-6 days. The total number of flowers/plant registered significantly higher in Belrubi (16.40) followed by Gorella (13.53) and Confiura (12.87), while their lowest number was recorded in Brighton (7.67) without showing any statistical difference with Selva (9.41). Per cent fruit

Table 1. Mean values for some yield and quality traits in eight strawberry cultivars

Cultivar	Date of first flower emergence	Flower number/ plant	Fruit set (%)	Malformed fruits (%)	Duration of picking (days)	Yield/ plant (g)	Fruit size (LxW) in cm)	Total soluble solids (°B)	Titratable acidity (%)	Total	Sugars (%)		Organoleptic rating
											Reducing	Non-reducing	
Addie	19.01.2001	12.45	74.10	40.00	50.33	54.54	1.95 x 1.34	8.70	0.72	6.97	5.22	1.66	7.27
Belrubi	18.01.2001	16.40	84.51	25.56	50.33	69.53	2.44 x 1.45	7.67	0.86	5.09	4.11	0.93	7.93
Brighton	18.01.2001	7.67	86.21	38.89	49.33	42.47	2.12 x 1.34	7.53	0.73	5.67	4.09	1.50	7.47
Chandler	19.01.2001	12.20	80.71	37.30	49.67	67.64	2.40 x 1.78	7.67	0.71	5.36	4.67	1.26	8.00
Confitura	18.01.2001	12.87	77.40	34.30	49.00	52.52	1.74 x 1.31	6.97	0.63	5.26	4.15	1.19	7.80
Fern	18.01.2001	11.73	80.17	26.81	50.67	36.60	1.40 x 1.07	9.07	0.51	6.62	4.43	2.72	7.73
Gorella	18.01.2001	13.53	81.17	26.88	52.33	81.90	2.40 x 1.67	9.10	0.63	7.08	5.34	1.65	9.63
Selva	24.01.2001	9.41	78.10	42.12	33.00	46.02	2.33 x 1.63	6.57	0.68	4.86	3.92	0.89	6.43
CD (0.05)	—	2.80	6.77	9.05	4.20	17.29	0.49 x 0.38	0.30	0.10	0.56	0.30	0.50	0.98

set was relatively higher in Brighton (86.21%) and no significant difference was recorded among Belrubi Chandler, Fern and Gorella. Malformed fruits were recorded higher than the other cultivars. Fern in Selva (42.12%) and Addie (40.00%)

No significant difference is picking duration was observed in Gorella (52.3 days) followed by Confitura (50.6 days), Addie and Belrubi (each 50.3 days), Chandler (49.67 days), Brighton (49.33 days) and Confitura (49.00 days), difference, while it was shortest in Selva (33.00 days). Of the various cultivars tested, Gorella gave the highest yield (81.90g/plant). Of the 4 cultivars tested by Ivanov (1976), a satisfactory yield was obtained from Belrubi (12194 kg/ha) and Gorella (11656 kg/ha) strawberries. Bringhurst and Voth (1989) suggested Chandler to be the best cultivar for lower elevations.

The physio-chemical fruit characteristics as influenced by different cultivars is given in Table 1. The fruit size was larger in Belrubi (2.44 × 1.45 cm), Chandler (2.40 × 1.78 cm) and Gorella (2.40 × 1.67 cm) than other cultivars tested. Similarly these three varieties were reported notable for large fruit size by Hancock *et al.* (1996). Rosati *et al.* (1982) also observed Gorella to be a large fruited variety.

The content of total soluble solids was quite higher statistically in Fern (9.07°B) and Gorella (9.10°B) cultivars and its lowest value was registered in Selva (6.75°B) (Table 1). The highest and lowest values of fruit acid content were recorded in Belrubi (0.86%) and Fern (0.51%), respectively. The total sugar content was higher and statiscally similar in Gorella (7.08%); Addie (6.97%) and Fern (6.62%) and was registered lowest in Selva (4.86%). Almost similar trend was noticed in case of reducing sugars. The content of non reducing sugar was highest in the fruits of Fern (2.72%). Similar variability in sugars and TSS contents in strawberries was also reported by several researchers (Grewal *et al.*, 1988; Wrolstad *et al.*, 1990; Shamaila *et al.*, 1992).

The fruits of Gorella strawberry were found most acceptable as they scored the highest numerical rating (9.63) followed by Chandler (8.00) and Belrubi (7.93) evaluated through organoleptic test (Table 1). The organoleptic quality of fruits is greatly influenced by sugar content (Alavoine and Crochen, 1989) as also observed in the present studies in case of Gorella.

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References

Alavoine F and M Chrochen (1989) Taste quality of strawberry *Acta. Hort.* **265:** 449-452.

Bringhurst, RS and V Voth (1989). California strawberry cultivars. *Fruit Var. J.* **43:** 12-19.

Gould, WA (1978) *Food Quality Assurance*, AVI Pub. Corp Inc. Westport, Connecticut.

Grewal GPS, GS Dhaliwal and SS Grewal (1998) Evaluation of strawberry varieties for vegetative and fruiting characters under sub-mountain zone. *Punjab Hort. J.* **28:** 87-90.

Hancock JP, DH Scott and FJ Lawrence (1996) Strawberries In: J Janic and JM Moore (eds) *Fruit Breeding Vol II, Vine and Small fruits*, John Willey and Sons, New York, pp 419-470.

Horwitz, W (1980) Official methods of analysis. *Association of Official Analytical Chemists.* 13, Washington, DC USA.

Hughes HM, JB Duggan and MG Banwell (1969) *Strawberry Bul* 95 HMSO 10, 6d Min Agric Fisheries and Food, UK.

Ivanov V (1976) Strawberry varieties suitable for growing in heated greenhouse. Ovoshcharstvo **55:** 35-39.

Rosati P, W Faedi and ND Ercole (1982) Pomological and agronomic data and disease resistance of four new strawberry varieties for the PO valley Addie, Brio, Cesena and Dana. *Frutticoltura* **44:** 47-50.

Sharma RM and R Yamdagni (2000) *Modern Strawberry Cultivation.* Kalyani Publishers. Ludhiana, India, 172 p.

Shamaila M, TE Baumann, GW Eaton, WD Powrie and BJ Skura (1992) Quality attributes of strawberry cultivars grown in British Columbia. *J. Food Sci.* **57:** 696-699.

Westwood MN (1978) Temperate Zone Pomology. WH Freeman and Company, San Francisco, 428p.

Wrolstad RE, JD Culbertson, DA Nagaki and CG Madero (1990) Quality evaluation of strawberry for fresh fruit. Part II. Effect of cultivars on general constituent, organic acid composition, volatile compounds, pectins and physical properties in the edible portion of strawberry. *Bul. Hiroshima Agric. College* **8:** 669-877.

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